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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:03:09 ; Search time 64.1 Seconds

(without alignments)
1.848 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 WSXWS 5

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	507	R06511	EPO receptor sequ
2	30	96.8	508	R06512	EPO receptor. Eryt
3	30	96.8	552	R24017	Fusion protein GM-
4	30	96.8	632	R10795	Human prolactin re
5	30	96.8	400	R10919	Human GM-CSF recep
6	30	96.8	211	R22228	Truncated human pr
7	30	96.8	211	R24273	Truncated human pr
8	30	96.8	284	R23971	MPLV env-vmp1 fusi
9	30	96.8	382	R23970	MPLV env protein w
10	30	96.8	382	R27659	MPLV-env related p
11	30	96.8	184	R27660	Partial MPLV-env r
12	30	96.8	507	R47517	MPL EPO receptor.
13	30	96.8	508	R47518	Human EPO receptor
14	30	96.8	265	R50326	Mouse soluble EPO
15	30	96.8	507	R50327	Mouse soluble EPO
16	30	96.8	507	R69502	Human erythropoiet
17	30	96.8	508	R69503	Human erythropoiet
18	30	96.8	508	R69782	Thrombopoietin-der
19	30	96.8	636	R70032	Human erythropoiet
20	30	96.8	636	R75939	Human erythropoiet
21	30	96.8	635	R75940	Human erythropoiet
22	30	96.8	482	R75941	Human myelopoietic
23	30	96.8	633	R75941	Human myelopoietic
24	30	96.8	633	R79908	Soluble murine MPL
25	30	96.8	633	R79908	Mouse type I MPL recepto
26	30	96.8	633	R79908	Type I MPL recepto
27	30	96.8	633	R79908	Human erythropoiet
28	30	96.8	633	R79908	Human erythropoiet
29	30	96.8	633	R79908	Human erythropoiet
30	30	96.8	633	R79908	Human erythropoiet
31	30	96.8	633	R79908	Human erythropoiet
32	30	96.8	633	R79908	Human erythropoiet
33	30	96.8	633	R79908	Human erythropoiet
34	30	96.8	633	R79908	Human erythropoiet
35	30	96.8	633	R79908	Human erythropoiet
36	30	96.8	633	R79908	Human erythropoiet
37	30	96.8	633	R79908	Human erythropoiet
38	30	96.8	633	R79908	Human erythropoiet
39	30	96.8	633	R79908	Human erythropoiet
40	30	96.8	633	R79908	Human erythropoiet
41	30	96.8	633	R79908	Human erythropoiet
42	30	96.8	633	R79908	Human erythropoiet
43	30	96.8	633	R79908	Human erythropoiet

ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description
44	29	93.5	810	R04574	Derived amino acid
45	29	93.5	218	W40287	Human TSP1 protein

RESULT 1	1
ID	R06511
AC	R06511 standard; protein; 507 AA.
DT	04-JAN-1991 (first entry)
DE	EPO receptor sequence deduced from DNA of clone 190.
KW	Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.
OS	Mus musculus.
FT	Key
FT	peptide
FT	1..24
FT	/label-signal peptide
FT	25..248
FT	/label-extracellular domain
FT	/note-EPO binding region
FT	248..271
FT	/label-transmembrane domain
FT	272..507
FT	/label-intracellular domain
FT	75..77
FT	/label-N-linked-glycos
FT	182..184
FT	/label-N-linked-glycos
FT	184..184
FT	/label-N-linked-glycos
PN	W09008822-A.
PD	09-AUG-1990.
PR	01-FEB-1990; U00635.
PR	03-FEB-1989; US-306503.
PA	(GENE-) GENETICS INST INC.
PI	(WHIT-) WHITEHEAD INST.
PI	D'Andrea A; Wong G;
DR	WPI: 90-260931/34.
DR	N-PSDB; 005747.
PT	Erythropoietin receptor and gene - used for developing reagents
PT	and systems to control and study erythropoiesis.
PS	Disclosure; Fig 1: 53pp; English.
CC	The sequence was deduced from DNA from a clone isolated from a
CC	cDNA library prep. from uninduced murine erythroleukemia cells.
CC	It is a type I transmembrane protein with binding affinity for EPO.
CC	The gene and recombinant EPO receptor produced on expression of
CC	the DNA are used to develop reagents and systems to control and
CC	study erythropoiesis. It is believed that the EPO receptor is
CC	dysfunctional in individuals with Diamond Blackfan anaemia, and
CC	may be hyperactive in polycythemia vera.
CC	See also R06512 (human EPO receptor).
SC	Sequence 507 AA;

Query Match	96.88;	Score 30;	DB 1;	Length 507;
Best Local Similarity	80.08;	Pred. No. 4.4e+02;		
Matches 4;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1 WSXWS 5
DB	232 WSXWS 236

RESULT 2	2
ID	R06512
AC	R06512 standard; protein; 508 AA.
DT	04-JAN-1991 (first entry)
DE	EPO receptor.
KW	Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.
OS	Homo sapiens.
PN	W09008822-A.
PD	09-AUG-1990.
PR	01-FEB-1990; U00635.

PR 03-FEB-1989; US-306503.
 PA (GENE-) GENETICS INST INC.
 PI (WHIT-) WHITEHEAD INST.
 PI D'andrea A, Mong G;
 DR WPI: 90-260931/34.
 DR N-PSDB: 005748.
 PT Erythropoietin receptor and gene - used for developing reagents
 PT and systems to control and study erythropoiesis.
 PS Disclosure; Fig 2; 53pp; English.
 CC The sequence was deduced from DNA obid. from a clone isolated from
 CC a commercially available human genomic cDNA library in phage
 CC Lambda Fix (Stratagene). The sequence encodes a type I trans-
 CC membrane protein with binding affinity for EPO. The gene and
 CC recombinant EPO receptor produced on expression of the DNA are
 CC used to develop reagents and systems to control and study
 CC erythropoiesis. It is believed that the EPO receptor is dys-
 CC functional in individuals with Diamond Blackfan anaemia, and may
 CC be hyperactive in polycythemia vera.
 CC See also R06511 (murine EPO receptor).
 SQ Sequence 508 AA;

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 4,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 233 WSAMS 237

RESULT 3
 R24017 R24017 standard; Protein; 552 AA.
 AC R24017;
 DT 26-NOV-1992 (first entry)
 DE Fusion protein GM-CSFRFC.
 KW Granulocyte macrophage-colony stimulating factor; GM-CSF; IgG1;
 KM Immunoglobulin G1.
 OS Synthetic.
 FH Key
 FT region Location/Qualifiers
 FT 1..318 "human GM-CSF receptor"
 FT 319..336
 FT /note- "linker and hinge"
 FT 337..445
 FT /note- "IgG1 CH2"
 FT 446..552
 FT /note- "IgG1 CH3"
 FT region
 PN EP-488170-A.
 PD 03-JUN-1992.
 PE 26-NOV-1991; 120187.
 PR 28-NOV-1990; DE-037637.
 PA (BEHW) BEHRINGWERKE AG.
 PI Lauffer L, Oquendo P, Zettlmeissl G;
 DR WPI: 92-185084/23.
 PT Cell free receptor binding test contg. recombinant fusion protein -
 PT comprising carrier bound to fusion partner coupled to fixed support,
 PT and second, labelled binding partner, for receptor or antibody
 PT screening etc.
 PS Example; Fig 12; 24pp; German.
 CC The sequence is that of fusion protein GM-CSFRFC comprising the
 CC extracellular domain of granulocyte macrophage-colony stimulating
 CC factor (GM-CSF) fused via a hinge region to the Fc part of the heavy
 CC chain of human IgG1. It may be used as part of a cell free receptor
 CC binding test which can be used for the identification of agonists,
 CC antagonists, antibodies, biological activity of soluble cellular
 CC receptors, functional analysis of modified ligands and diagnostic or
 CC therapeutic substances. See also R24016.
 SQ Sequence 552 AA;

Query Match

96.8%; Score 30; DB 1; Length 552;

Best Local Similarity 80.0%; Pred. No. 4,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 306 WSAMS 310

RESULT 4
 R10795 R10795 standard; Protein; 622 AA.
 AC R10795;
 DT 25-APR-1991 (first entry)
 DE Human prolactin receptor.
 KW Human prolactin receptor; PRL; assay; antibody; growth hormone.
 OS Homo sapiens.
 FH Key
 FT peptide Location/Qualifiers
 FT 1..24
 FT /label- sig_peptide
 FT 25..622
 FT /label- mat_protein
 FT protein
 PN US4992378-A.
 PD 12-FEB-1991.
 PE 16-DEC-1988; 286445.
 PR 16-DEC-1988; US-286445.
 PI (ROYA-) ROYAL INST ADVAN LE.
 PI Kelly PA, Dlane J;
 DR WPI: 91-065341/09.
 DR N-PSDB: Q10550.
 PT Isolated cDNA sequence encoding human prolactin receptor - useful
 PT for expressing the receptor, e.g. for screening assays and antibody
 PT prodn.
 PS Disclosure; Fig. 1 (A-E); 11pp; English.
 CC The human PRL receptor cDNA is isolated by screening a lambda gt 10
 CC library prepared from normal human hepatoma Hep G2 and T47-D breast
 CC cancer cells. Initially, 1x10⁶ recombinants are screened with the
 CC following probe: a complementary RNA of the F3 cDNA of the rat
 CC prolactin receptor. One positive recombinant was isolated from the
 CC Hep G2 library, which was later used as a probe to rescreen the
 CC library. Five additional cDNAs were identified, and by combining
 CC two of the six cDNAs, a PRL receptor cDNA of 2.5 kb was constructed,
 CC contg. a single ORF of 1866 bp. Similar partial length cDNA were
 CC isolated from the T47-D library.
 CC Several regions of sequence identity between the human growth
 CC hormone and PRL receptors can be found, both in the extracellular
 CC and cytoplasmic domains.
 CC The sequence is an important genetic engineering tool which may be
 CC used for the screening of growth hormone variants, for the development
 CC of test kits to measure PRL receptor levels in human breast and prostate
 CC cancer biopsies, for the measurement of bioactive forms of prolactin,
 CC and for the development of drugs to induce stimulation or inhibition of
 CC the immune system.
 SQ Sequence 622 AA;

Query Match 96.8%; Score 30; DB 1; Length 622;
 Best Local Similarity 80.0%; Pred. No. 5,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 215 WSAMS 219

RESULT 5
 R10919 R10919 standard; Protein; 400 AA.
 AC R10919;
 DT 08-MAY-1991 (first entry)
 DE Human GM-CSF receptor.
 KW Granulocyte-macrophage colony-stimulating factor; myeloid leukaemia;
 KW autoimmune disease.
 FH Key
 FT Location/Qualifiers

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FT peptide 1..22
FT /label= signal sequence
FT protein 23
FT /label= GM-CSF receptor
FT domain 321..346
FT /label= transmembrane region
FT modified_site 46
FT /label= N-glycosylation site
FT modified_site 53
FT /label= N-glycosylation site
FT modified_site 99
FT /label= N-glycosylation site
FT modified_site 123
FT /label= N-glycosylation site
FT modified_site 182
FT /label= N-glycosylation site
FT modified_site 195
FT /label= N-glycosylation site
FT modified_site 223
FT /label= N-glycosylation site
FT modified_site 229
FT /label= N-glycosylation site
FT modified_site 272
FT /label= N-glycosylation site
FT modified_site 305
FT /label= N-glycosylation site
FT WO9102063-A.
FT 21-FEB-1991.
FT 10-AUG-1990: AU0342.
FT 11-AUG-1989: AU-005743.
FT 08-MAY-1990: AU-000014.
FT (AMRA-) AMRAD CORP LTD.
FT NICOLA NA, Gough NM, Gearing DP, Metcalf D, King JA.
FT WPI: 91-073539/10.
FT N-PDB: Q10817.
FT Recombinant or synthetic receptor for granulocyte-macrophage
FT colony - used for treatment and diagnosis or related diseases,
FT e.g. myeloid leukaemia or auto-immune reactions
FT Claim 1; Fig 6B; 85pp; English.
FT The sequence was deduced from the combined cDNAs of pGMR138 and
FT pGMR29 which were isolated from a cDNA library prep. from human
FT placental RNA. The DNA can be inserted into expression vectors for
FT the prodn. of recombinant GM-CSF receptor useful for medicinal
FT purposes or to study the mechanism of the receptor binding, etc.
FT Sequence 400 AA:

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Query Match 96.8%; Score 30; DB 1; Length 400;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 WSXWS 5
b 306 WSSWS 310

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ESULT 6
22228
R22228 standard; protein; 211 AA.
R22228:
T 20-JUL-1992 (first entry)
E Truncated human prolactin binding protein.
W hPRLbp; placental lactogen; zinc finger; chelate;
S receptor-ligand complex.
S Homo sapiens.
N WO9203478-A.
D 05-MAR-1992.
F 16-AUG-1991: U05856.
R 17-AUG-1990: US-568936.
A (GENH) GENENTECH INC.
I Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;
I Wells JA;
R WPI: 92-096838/12.

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PT New method of modifying polypeptide hormone-receptor complex - to
PT produce human growth hormone variant, useful for stimulating
PT lactogenic and somatogenic response
PT Disclosure; Page 41; 74pp; English.
CC This truncated human prolactin binding protein is encoded by the
CC insert contained in plasmid pNRLbp(1-211). The hPRLbp gene fragment
CC is transcribed under the control of the alkaline phosphatase
CC promoter and secreted into the host (E.coli) periplasm under the
CC direction of the still signal sequence. A stop codon and Mui
CC restriction site were introduced after the threonine 211 codon which
CC immediately precedes the transmembrane domain of the receptor. The
CC plasmid was used as a template for site-directed mutagenesis to
CC modify the metal-chelating centre of the protein. See e.g. R24273
CC for an example of a preferred variant.
SQ Sequence 211 AA;

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Query Match 96.8%; Score 30; DB 1; Length 211;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSXWS 5
Db 191 WSAMS 195

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RESULT 7
R24273
ID R24273 standard; protein; 211 AA.
AC R24273;
DT 20-JUL-1992 (first entry)
DE Truncated human prolactin binding protein variant.
KW hPRLbp; placental lactogen; zinc finger; chelate;
KW receptor-ligand complex.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_difference 188 /note= "wild-type His replaced by Ala"
FT WO9203478-A.
PD 05-MAR-1992.
PF 16-AUG-1991: U05856.
PR 17-AUG-1990: US-568936.
PA (GENH) GENENTECH INC.
PI Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;
PI Wells JA;
PI WPI: 92-096838/12.
DR New method of modifying polypeptide hormone-receptor complex - to
PT produce human growth hormone variant, useful for stimulating
PT lactogenic and somatogenic response
PS Claim 41; Page 56; 74pp; English.
CC Plasmid pNRLbp(1-211) (see R22228) coding for truncated, soluble
CC prolactin binding protein was mutagenised such that the His codon
CC at position 188 was substituted by an Ala codon. The hPRLbp variant
CC has altered binding affinity for hGH.
SQ Sequence 211 AA;

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Query Match 96.8%; Score 30; DB 1; Length 211;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSXWS 5
Db 191 WSAMS 195

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RESULT 8
R23971
ID R23971 standard; protein; 284 AA.
AC R23971;
DT 05-NOV-1992 (first entry)
DE MPLY env-tmp1 fusion protein.
DE Myeloproliferative leukaemia virus; envelope protein; F-MuLV;
KW

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KM haematopoietic cell; growth factor receptor; gene rearrangement;
 KM Friend replication competent ecotropic murine leukaemia virus.
 OS Myeloproliferative leukaemia virus.
 OS Friend murine leukaemia virus.
 PH Key
 FT peptide
 FT 1.34
 FT /label= signal
 FT /note= "from F-MuLV"
 FT region
 FT 1.64
 FT /note= "N-terminal region of F-MuLV gp70"
 FT 65.100
 FT /note= "central region of F-MuLV env"
 FT 101.284
 FT /note= "MPLV-specific mpl"
 FT 144.165
 FT domain
 FT /note= "putative transmembrane domain"
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24677.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 PS treatment of myeloproliferative diseases
 PS Claim 8; Fig 2b; 75pp; French.
 CC The rearranged env MPLV gene has an open reading frame of 284 amino
 CC acids and deduced mol.wt. of 31kD. The env-mpl fusion protein
 CC comprises the N-terminal 64 amino acids from F-MuLV gp70, including
 CC the signal peptide, 36 amino acids from the central region of the
 CC F-MuLV env gene and 184 amino acids specific to MPLV.
 CC See R23970, Q24674-7.
 SQ Sequence 284 AA;

QY 1 WSXWS 5
 DB 126 WSXWS 130

RESULT 9
 R23970
 ID R23970 standard; protein; 635 AA.
 AC R23970;
 DT 05-NOV-1992 (first entry)
 DE MPLV env protein with growth factor receptor properties.
 KM Myeloproliferative leukaemia virus; haematopoietic cell.
 OS Myeloproliferative leukaemia virus.
 PH Key
 FT Location/Qualifiers
 FT 449.635
 FT /note= "gp70 of MPLV"
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24674.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 PS treatment of myeloproliferative diseases
 PS Claim 1; Page 28; 75pp; French.
 CC This polypeptide is encoded by clone MPV107, isolated from a
 CC genomic bank prepared from clones of Mus dunni cells containing
 CC a unique copy of the MPLV provirus. The bank was screened with two
 CC 300bp long clones specific for MPLV env region. Restriction enzyme

CC analysis showed that clone MPLV107 contained the entire MPLV genome
 CC except for the 3'UTR.
 CC See R23971 and Q24674-7.
 SQ Sequence 635 AA;

QY 1 WSXWS 5
 DB 474 WSXWS 478

Query Match
 Best Local Similarity 96.8%; Score 30; DB 1; Length 635;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 R27659
 ID R27659 standard; protein; 382 AA.
 AC R27659;
 DT 05-NOV-1992 (first entry)
 DE MPLV-env related polypeptide.
 KM Myeloproliferative leukaemia virus; envelope protein; gp70;
 KM haematopoietic cell; growth factor receptor.
 OS Myeloproliferative leukaemia virus.
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24675.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 PS treatment of myeloproliferative diseases
 PS Claim 3; Page 30; 75pp; French.
 CC This polypeptide is an example of a fragment related to the MPLV
 CC env protein having the amino acid sequence assigned GENESQ
 CC accession number R23970. The protein is involved in the
 CC ligand-fixing or signal-transmitting function of haematopoietic
 CC growth factor receptors; is recognised by antibodies to the
 CC protein R23970; when produced from the MPLV genome it can induce/
 CC promote proliferation of haematopoietic cells and/or is involved
 CC in differentiation of haematopoietic cells.
 CC See also Q24674-7.
 SQ Sequence 382 AA;

QY 1 WSXWS 5
 DB 222 WSXWS 226

Query Match
 Best Local Similarity 96.8%; Score 30; DB 1; Length 382;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
 R27660
 ID R27660 standard; protein; 184 AA.
 AC R27660;
 DT 05-NOV-1992 (first entry)
 DE Partial MPLV-env related polypeptide.
 KM Myeloproliferative leukaemia virus; envelope protein; gp70;
 OS Myeloproliferative leukaemia virus.
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;

DR MPI: 92-167154/20.
 DR N-PSDB: Q24676.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 PT treatment of myeloproliferative diseases
 CC Claim 4; Page 31; 75pp; French.
 CC This polypeptide is an example of a fragment related to the MPLV
 CC accesion number R23970. The protein is involved in the
 CC ligand-fixing or signal-transmitting function of haematopoietic
 CC growth factor receptors; is recognised by antibodies to the
 CC protein R23970; when produced from the MPLV genome it can induce/
 CC promote proliferation of haematopoietic cells and/or is involved
 CC in differentiation of haematopoietic cells.
 CC See also Q24674-7.
 SO Sequence 184 AA;

Query Match 96.8%; Score 30; DB 1; Length 184;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 DB 26 WSAWS 30

RESULT 12

R47517
 ID R47517 standard; Protein; 507 AA.

AC R47517;
 DT 24-JUN-1994 (first entry)

DE MEL EPO receptor.
 KW Erythropoietin receptor; recombinant; murine; anaemia.

CS Mus musculus.

FT Key Location/Qualifiers
 FT peptide 1..24
 FT protein 25..507
 FT modified_site 75
 FT modified_site 383
 FT modified_site 250..271
 FT region /note- "putative transmembrane region"

US5278065-A.
 11-JAN-1994.
 03-FEB-1989; 306503.
 03-FEB-1989; US-306503.
 25-MAR-1991; US-678877.
 (CHIL-) CHILDRENS MEDICAL CENT.
 (GENM-) GENETICS INST INC.
 (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 D'Andrea A, Jones SS, Wong GG;
 WPI: 94-025409/03.
 N-PSDB: Q53994.
 T Recombinant DNA encoding erythropoietin receptor - used to
 T develop prods. for study, treatment or diagnosis of disorders in
 T which receptor is dysfunctional.
 T Disclosure; Fig 2; 24pp; English.
 T Mouse erythroleukemia (MEL) cells were used to construct a cDNA
 T library. The cDNA was used to transfect COS-1 cells and these were
 T screened for radiolabeled erythropoietin (EPO) binding to isolate
 T cDNA encoding the EPO receptor. The cDNA may be used to isolate the
 T EPO receptor from other sources and to study, treat or diagnose
 T disorders in which the EPO receptor is dysfunctional. The EPO
 T receptor may also be used to raise antibodies or for treating
 T hypersensitivity to EPO or who have elevated levels of EPO. The prod.
 T is pref. used for treating anaemias, primary proliferative polycythemia
 T and secondary polycythemia.
 T See also R47518.
 C Sequence 507 AA;

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 DB 232 WSAWS 236

RESULT 13

R47518
 ID R47518 standard; Protein; 508 AA.

AC R47518;
 DT 24-JUN-1994 (first entry)

DE Human EPO receptor.
 KW Erythropoietin receptor; recombinant; murine; anaemia.

CS Homo sapiens.

FT Key Location/Qualifiers
 FT peptide 1..24
 FT protein 25..508
 FT modified_site 251..272
 FT region /note- "putative transmembrane domain"

US5278065-A.
 11-JAN-1994.
 03-FEB-1989; 306503.
 03-FEB-1989; US-306503.
 25-MAR-1991; US-678877.
 (CHIL-) CHILDRENS MEDICAL CENT.
 (GENM-) GENETICS INST INC.
 (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 D'Andrea A, Jones SS, Wong GG;
 WPI: 94-025409/03.
 N-PSDB: Q53995.
 T Recombinant DNA encoding erythropoietin receptor - used to
 T develop prods. for study, treatment or diagnosis of disorders in
 T which receptor is dysfunctional.
 T Disclosure; Fig 9; 24pp; English.
 T Mouse erythroleukemia (MEL) cells were used to construct a cDNA
 T library. The cDNA was used to transfect COS-1 cells and these were
 T screened for radiolabeled erythropoietin (EPO) binding to isolate
 T cDNA encoding the EPO receptor. This cDNA was used as a probe to
 T screen a human genomic cDNA library to obtain DNA encoding the human
 T EPO receptor. The cDNA may be used to study, treat or diagnose
 T disorders in which the EPO receptor is dysfunctional. The EPO
 T receptor may also be used to raise antibodies or for treating
 T hypersensitivity to EPO or who have elevated levels of EPO. The prod.
 T is pref. used for treating anaemias, primary proliferative polycythemia
 T and secondary polycythemia.
 T See also R47517.
 C Sequence 508 AA;

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 DB 233 WSAWS 237

RESULT 14

R50326
 ID R50326 standard; Protein; 265 AA.

AC R50326;
 DT 19-OCT-1994 (first entry)

DE Mouse soluble EPO receptor protein fragment.
 KW Murine; soluble; erythropoietin; EPO; receptor protein; sEPO-R; drug;
 KW antigen; diagnostic agent; biochemical reagent.
 OS Mus musculus.

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 DB 233 WSAWS 237

RESULT 14

R50326
 ID R50326 standard; Protein; 265 AA.

AC R50326;
 DT 19-OCT-1994 (first entry)

DE Mouse soluble EPO receptor protein fragment.
 KW Murine; soluble; erythropoietin; EPO; receptor protein; sEPO-R; drug;
 KW antigen; diagnostic agent; biochemical reagent.
 OS Mus musculus.

Job time: 301 sec

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FH Key Location/Qualifiers
FT Peptide 1..25
FT /note- "Signal peptide"
FT protein 26..265
FT /note- "Mature EPO-R fragment"
PN J06038787-A.
PD 15-FEB-1994.
PF 04-MAR-1992; 082865.
PR 04-MAR-1992; JP-082865.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
DR WPI; 94-094847/12.
DR N-PSDB; 044853.
PT Soluble erythropoietin receptor protein - and DNA coding for
PT SEPO-R, useful as diagnostic reagent
PS Disclosure; page 5-6; 9pp; Japanese.
CC This sequence represents a fragment of the murine soluble erythro-
CC poietin (EPO) receptor protein (SEPO-R). This protein is able to
CC bind to EPO and has antigenicity as an EPO receptor. The molecular
CC weight of the full length protein is pref 33 or 29 kD. The protein
CC is useful as a drug, as a diagnostic agent and a biochemical reagent.
SQ Sequence 265 AA;

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Query Match 96.8%; Score 30; DB 1; Length 265;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MSXMS 5
DB 232 WSAMS 236

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RESULT 15
R50327
ID R50327 standard; Protein; 507 AA.
AC R50327.
DT 19-OCT-1994 (first entry)
DE Mouse soluble EPO receptor protein.
KW Murine; soluble; erythropoietin; EPO; receptor protein; SEPO-R; drug;
KW antigen; diagnostic agent; biochemical reagent.
OS Mus musculus.
FH Key Location/Qualifiers
FT modified_site 75..77
FT /note- "N-linked glycosylation site"
PN J06038787-A.
PD 15-FEB-1994.
PF 04-MAR-1992; 082865.
PR 04-MAR-1992; JP-082865.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
DR WPI; 94-094847/12.
DR N-PSDB; 044854.
PT Soluble erythropoietin receptor protein - and DNA coding for
PT SEPO-R, useful as diagnostic reagent
PS Disclosure; fig 1; 9pp; Japanese.
CC This sequence represents the murine soluble erythropoietin (EPO)
CC receptor protein (SEPO-R). This protein is able to bind to EPO and
CC has antigenicity as an EPO receptor. The molecular weight of the
CC full length protein is pref 33 or 29 kD. The protein is useful as a
CC drug, as a diagnostic agent and a biochemical reagent.
SQ Sequence 507 AA;

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Query Match 96.8%; Score 30; DB 1; Length 507;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MSXMS 5
DB 232 WSAMS 236

```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 16, 1999, 19:10:31 ; Search time 53.94 Seconds
(Without alignments)
0.915 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 MSXWS 5

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/1aa/PCTUS9_COMB.pep.*
4: /cgn2_6/prodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	185	1	US-07-676-647-10 Sequence 10, Appl
2	30	96.8	185	1	US-07-676-647-13 Sequence 13, Appl
3	30	96.8	185	1	US-08-184-327A-2 Sequence 2, Appl
4	30	96.8	185	1	US-08-184-327A-4 Sequence 4, Appl
5	30	96.8	482	1	US-08-184-327A-8 Sequence 8, Appl
6	30	96.8	633	1	US-08-250-859-17 Sequence 17, Appl
7	30	96.8	400	1	US-08-351-149-6 Sequence 6, Appl
8	30	96.8	552	1	US-08-243-010-6 Sequence 6, Appl
9	30	96.8	185	1	US-08-449-329-10 Sequence 10, Appl
10	30	96.8	185	1	US-08-449-329-13 Sequence 13, Appl
11	30	96.8	633	1	US-08-490-803-17 Sequence 17, Appl
12	30	96.8	400	1	US-08-384-828-6 Sequence 6, Appl
13	30	96.8	584	2	US-08-313-288B-17 Sequence 17, Appl
14	30	96.8	508	2	US-08-850-293-5 Sequence 5, Appl
15	30	96.8	185	2	US-08-445-073-10 Sequence 10, Appl
16	30	96.8	185	2	US-08-445-073-13 Sequence 13, Appl
17	30	96.8	32	2	US-08-280-864A-13 Sequence 13, Appl
18	30	96.8	185	3	PCT-US91-03896-10 Sequence 10, Appl
19	30	96.8	633	3	PCT-US91-03896-13 Sequence 13, Appl
20	30	96.8	185	3	PCT-US94-08806-17 Sequence 17, Appl
21	30	96.8	626	3	PCT-US95-00670-2 Sequence 2, Appl
22	30	96.8	633	3	PCT-US95-00670-4 Sequence 4, Appl
23	30	96.8	482	3	PCT-US95-00670-8 Sequence 8, Appl
24	30	96.8	633	3	PCT-US95-01775-17 Sequence 17, Appl
25	30	96.8	27	3	PCT-US95-04570-47 Sequence 47, Appl
26	30	96.8	27	3	PCT-US95-04589-47 Sequence 47, Appl
27	30	96.8	633	3	PCT-US95-16626-7 Sequence 7, Appl
28	29	93.5	23	1	US-07-646-531D-6 Sequence 6, Appl
29	29	93.5	70	1	US-07-646-531D-12 Sequence 12, Appl
30	29	93.5	1001	1	US-07-797-556-2 Sequence 2, Appl
31	29	93.5	807	1	US-07-862-021B-10 Sequence 10, Appl
32	29	93.5	807	1	US-07-862-021B-12 Sequence 12, Appl
33	29	93.5	568	1	US-07-862-021B-14 Sequence 14, Appl
34	29	93.5	568	1	US-07-862-021B-19 Sequence 19, Appl
35	29	93.5	56	1	US-07-862-021B-19 Sequence 19, Appl
36	29	93.5	1001	1	US-07-943-843-2 Sequence 2, Appl
37	29	93.5	719	1	US-07-943-843-4 Sequence 4, Appl
38	29	93.5	1097	1	US-07-943-843-6 Sequence 6, Appl
39	29	93.5	372	1	US-07-865-878A-4 Sequence 4, Appl

40	29	93.5	17	1	US-07-801-812A-19	Sequence 19, Appl
41	29	93.5	11	1	US-07-801-812A-22	Sequence 22, Appl
42	29	93.5	372	1	US-07-676-647-2	Sequence 2, Appl
43	29	93.5	188	1	US-07-676-647-8	Sequence 8, Appl
44	29	93.5	185	1	US-07-676-647-9	Sequence 9, Appl
45	29	93.5	184	1	US-07-676-647-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-07-676-647-10
Sequence 10, Application US/07676647

Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furch, Mark E.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: Penite & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676,647

FILING DATE: 19910328

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mastro, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

TELEX: 66141 PENITE

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-676-647-10

Query Match

Best Local Similarity 96.8%; Score 30; DB 1; Length 185;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5

DB 181 MSXWS 185

RESULT 2

US-07-676-647-13

Sequence 13, Application US/07676647

Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furch, Mark E.

```

; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,647
; FILING DATE: 19910328
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-676-647-13

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Query Match 96.8%; Score 30; DB 1; Length 185;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
DB 181 WSSWS 185

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; RESULT 3
; US-08-184-327A-2
; Sequence 2, Application US/08184327A
; Patent No. 5498599
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela
; APPLICANT: Nichol, Janet L.
; TITLE OF INVENTION: Compositions And Methods For Stimulating
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,327A
; FILING DATE: 20-JAN-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-184-327A-4

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; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 626 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-184-327A-2

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Query Match 96.8%; Score 30; DB 1; Length 626;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
DB 466 WSWWS 470

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; RESULT 4
; US-08-184-327A-4
; Sequence 4, Application US/08184327A
; Patent No. 5498599
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela
; APPLICANT: Nichol, Janet L.
; TITLE OF INVENTION: Compositions And Methods For Stimulating
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,327A
; FILING DATE: 20-JAN-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-184-327A-4

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Query Match 96.8%; Score 30; DB 1; Length 635;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
DB 474 WSSWS 478

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; RESULT 5
; US-08-184-327A-8
; Sequence 8, Application US/08184327A
; Patent No. 5498599
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela

```

APPLICANT: Nichol, Janet L.
 TITLE OF INVENTION: Compositions And Methods For Stimulating
 TITLE OF INVENTION: Platelet Production
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
 STREET: 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: CA
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/184,327A
 FILING DATE: 20-JAN-1994
 CLASSIFICATION: 514
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 482 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-184-327A-8

Query Match 96.8%; Score 30; DB 1; Length 482;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 466 WSXWS 470

RESULT 6
 US-08-250-859-17
 Sequence 17, Application US/08250859
 Patent No. 5541085
 GENERAL INFORMATION:
 APPLICANT: Holly, Richard D.
 APPLICANT: Burkhead, Steven K.
 TITLE OF INVENTION: METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zymogenetics, Inc.
 STREET: 4225 Roosevelt Way, N.E.
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/250,859
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, Gary E.
 REGISTRATION NUMBER: 31-648
 REFERENCE/DOCKET NUMBER: 94-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-547-8080 ext 322
 TELEFAX: 206-632-4009
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 633 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-250-859-17

Query Match 96.8%; Score 30; DB 1; Length 633;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 473 WSXWS 477

RESULT 7
 US-08-351-149-6
 Sequence 6, Application US/08351149
 Patent No. 5629283
 GENERAL INFORMATION:
 APPLICANT: Nicola, Nicos A.
 APPLICANT: Gough, Nicholas M.
 APPLICANT: Gearing, David P.
 APPLICANT: Metcalf, Donald
 APPLICANT: King, Julie Ann
 TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
 TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 New York Ave., NW
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/351,149
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fox, Samuel L.
 REGISTRATION NUMBER: 30,353
 REFERENCE/DOCKET NUMBER: 1256.0030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-351-149-6

Query Match 96.8%; Score 30; DB 1; Length 400;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 306 WSXWS 310

RESULT 8
 US-08-243-010-6
 Sequence 6, Application US/08243010
 Patent No. 5639597

GENERAL INFORMATION:
APPLICANT: Lauffer, Leander
APPLICANT: Zeitlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
TITLE OF INVENTION: Production and Use Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einsauid, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-243-010-6

Query Match 96.8%; Score 30; DB 1; Length 552;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
1111
DB 306 MSSWS 310

RESULT 9
US-08-449-329-10
Sequence 10, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-329-10

Query Match 96.8%; Score 30; DB 1; Length 185;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
1111
DB 181 MSWS 185

RESULT 10
US-08-449-329-13
Sequence 13, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-329-10

TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-329-13

Query Match 96.8%; Score 30; DB 1; Length 185;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 181 WSSWS 185

RESULT 11
US-08-490-803-17
Sequence 17, Application US/08490803
Patent No. 5705349
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Burkhead, Steven K.
TITLE OF INVENTION: METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/490,803
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-632-4009
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-490-803-17

Query Match 96.8%; Score 30; DB 1; Length 633;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 473 WSXWS 477

RESULT 12

US-08-384-828-6
Sequence 6, Application US/08384828
Patent No. 5726036
GENERAL INFORMATION:
APPLICANT: Nicola, Micos A.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gearing, David P.
APPLICANT: Metcalf, Donald
APPLICANT: King, Julie Ann
TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,828
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/351,149
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1256.0030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-384-828-6

Query Match 96.8%; Score 30; DB 1; Length 400;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 306 WSSWS 310

RESULT 13
US-08-313-288B-17
Sequence 17, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-288B-17

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 584;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 545 WSXWS 549

RESULT 14
US-08-850-293-5
Sequence 5, Application US/08850293
Patent No. 5843726
GENERAL INFORMATION:
APPLICANT: Lee, Jong Y.
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,293
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/499,643
FILING DATE: 07-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,815
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07004/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
TELEFAX: 612/288-9696

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-850-293-5

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 508;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 233 WSXWS 237

RESULT 15
US-08-445-073-10
Sequence 10, Application US/08445073
Patent No. 5849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Futh, Mark E.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-445-073-10

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 185;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 181 WSXWS 185

- Fri Sep 17 14:52:34 1999

Search completed: September 16, 1999, 20:41:05
Job time: 5434 sec

us-09-037-657-1.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 19:12:07 : Search time 49.27 Seconds
(without alignments)
4.066 Million cell updates/sec

Title: US-09-037-657-1

Sequence: 31
1 MSXMS 5

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR-60:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	508	1 ZOHUR	erythropoietin rec
2	30	96.8	507	1 A32385	erythropoietin rec
3	30	96.8	583	1 C8HUA	complement C8 alph
4	30	96.8	947	1 B44294	unc-5 protein, lon
5	30	96.8	494	2 S60028	ferredoxin-NADP-
6	30	96.8	140	2 S20914	lysozyme (EC 3.2.1
7	30	96.8	140	2 S41573	lysozyme (EC 3.2.1
8	30	96.8	140	2 S41574	lysozyme (EC 3.2.1
9	30	96.8	140	2 S41574	lysozyme (EC 3.2.1
10	30	96.8	81	2 S41580	lysozyme (EC 3.2.1
11	30	96.8	437	2 S69881	phosphopyruvate hy
12	30	96.8	437	2 S67305	phosphopyruvate hy
13	30	96.8	222	2 A26489	placental lactogen
14	30	96.8	507	2 A46713	erythropoietin rec
15	30	96.8	265	2 S14081	erythropoietin rec
16	30	96.8	197	2 JH0602	beta-crystallin A2
17	30	96.8	934	2 A43372	complement C6 prec
18	30	96.8	843	2 A27340	complement C7 prec
19	30	96.8	584	2 I37213	complement C8 alpha
20	30	96.8	191	2 S41317	hypothetical prote
21	30	96.8	284	2 S27931	Enr/v-mpl fusion p
22	30	96.8	222	2 B64635	toxin-like outer m
23	30	96.8	2399	2 H1879	toxin-like outer m
24	30	96.8	218	2 S02828	allicidin resistan
25	30	96.8	394	2 A70504	probable PPE prote
26	30	96.8	2894	2 C64474	hypothetical prote
27	30	96.8	455	2 S66765	hypothetical prote
28	30	96.8	691	2 JEB150	hypothetical prote
29	30	96.8	1584	2 T00026	acetylcholinestera
30	30	96.8	1522	2 T00028	brain-specific an
31	30	96.8	333	2 S13684	granulocyte-macrop
32	30	96.8	400	2 S06945	granulocyte-macrop
33	30	96.8	137	2 S47568	granulocyte-macrop
34	30	96.8	378	2 S50040	granulocyte-macrop
35	30	96.8	984	2 T00326	hypothetical prote
36	30	96.8	422	2 I37891	interleukin-11 rec
37	30	96.8	579	2 B45266	MPL-K protein prec
38	30	96.8	635	2 A45266	MPL-K protein prec
39	30	96.8	206	2 A57018	prolactin receptor

40	30	96.8	622	2 A40144	prolactin receptor
41	30	96.8	625	2 S35317	hematopoietic grow
42	30	96.8	432	2 I48343	interleukin-II rec
43	30	96.8	437	2 S05478	properdin - mouse
44	30	96.8	626	2 S37622	proto-oncogene - m
45	30	96.8	367	2 G71178	hypothetical prote

ALIGNMENTS

RESULT 1
ZOHUR
erythropoietin receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence-revision 05-Apr-1995 #text-change 26-Feb-1999
C:Accession: A43799; A60160; A49824; A53958; A55280; I52563
R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
Blood 76, 31-35, 1990
A>Title: Human erythropoietin receptor: cloning, expression, and biologic characteriz
A:Reference number: A43799; MUID:90304340
A:Accession: A43799
A:Molecule type: mRNA
A:Residues: 1-508 <JON>
A:Cross-references: GB:M60459; NID:g182244; PID:g182245
R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
Blood 76, 24-30, 1990
A>Title: The gene for the human erythropoietin receptor: analysis of the coding seque
A:Reference number: A60160; MUID:90304334
A:Accession: A60160
A>Status: not compared with conceptual translation
A:Molecule type: mRNA, DNA
A:Residues: 1-508 <NOG>
R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wade, Y.; Schechter, A.N.; Hankins, W.D.
Blood 78, 2548-2556, 1991
A>Title: Cloning of the human erythropoietin receptor gene.
A:Reference number: A49824; MUID:92399733
A:Accession: A49824
A:Molecule type: DNA
A:Residues: 1-508 <NOG>
A:Cross-references: GB:S45333; NID:g255496; PID:g255497
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBI:113293, NCBI:113294)
R:Eheman, K.; St. John, T.
Exp. Hematol. 19, 973-977, 1991
A>Title: The erythropoietin receptor gene: cloning and identification of multiple tra
A:Reference number: A53958
A:Accession: A53958
A:Molecule type: mRNA
A:Residues: 1-508 <ENR>
R:Penny, L.A.; Forget, B.G.
Genomics 11, 974-980, 1991
A>Title: Genomic organization of the human erythropoietin receptor gene.
A:Reference number: A55280; MUID:92147143
A:Accession: A55280
A:Molecule type: DNA
A:Residues: 1-17:381-387, 17:395-504-508 <PEN>
A>Note: sequence modified after extraction from NCBI backbone
A>Note: the authors translated the codon GAT for residue 31 as B
R:Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartlon, J.P.; Chretien, S.
Blood 78, 2557-2563, 1991
A>Title: Cloning of the gene encoding the human erythropoietin receptor.
A:Reference number: I52563; MUID:92399734
A:Accession: I52563
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-96 <RES>
A:Cross-references: GB:M76595; NID:g182147; PID:g553281
C:Genetics:
A:Gene: GDB:EPOR
A:Cross-references: GDB:I25242; OMIM:133171
A:Map position: 19p13.3-19p13.2

A: Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
 C: Superfamily: erythropoietin receptor; cytokine receptor homology
 C: Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-508/Product: erythropoietin receptor #status predicted <MAT>
 F: 52-250/Domain: extracellular #status predicted <EXT>
 F: 52-239/Domain: cytokine receptor homology <CRS>
 F: 233-237/Region: WSXWS motif
 F: 251-272/Domain: transmembrane #status predicted <TM>
 F: 273-508/Domain: intracellular #status predicted <INT>
 F: 52-62, 91-107/Disulfide bonds: #status predicted
 F: 76/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 Db 233 WSXWS 237

RESULT 2
 A: 32385
 C: Erythropoietin receptor precursor, membrane-bound form - mouse
 C: Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 05-Sep-1997
 C: Accession: A41866; A32385; S13249
 R: Hino, M.; Tojo, A.; Misawa, Y.; Moril, H.; Takaku, F.; Shibuya, M.
 Mol. Cell. Biol. 11, 5527-5533, 1991
 A: Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
 A: Reference number: A41866; MID:92017832
 A: Accession: A41866
 A: Molecule type: mRNA
 A: Residues: 1-507 <HIN>
 A: Cross-references: GB:559388; NID:9237036; PID:9237037
 A: Experimental source: murine erythroleukemia (MEU) cell line F5-5
 R: D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
 Cell 57, 277-285, 1989
 A: Title: Expression cloning of the murine erythropoietin receptor.
 A: Reference number: A32385; MID:89195238
 A: Accession: A32385
 A: Molecule type: mRNA
 A: Residues: 1-507 <DA>
 A: Cross-references: GB:J04843; NID:9193090; PID:9309219
 A: Experimental source: murine erythroleukemia (MEU) cells, subclone 745
 R: Kuramochi, S.; Ikawa, Y.; Todokoro, K.
 J. Mol. Biol. 216, 567-575, 1990
 A: Title: Characterization of murine erythropoietin receptor genes.
 A: Reference number: S13249; MID:91080149
 A: Accession: S13249
 A: Molecule type: DNA; mRNA
 A: Residues: 1-507 <RUR>
 A: Cross-references: EMBL:X53081; NID:950861; PID:950862
 A: Experimental source: murine erythroleukemia K-1 cells
 C: Genes: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
 C: Superfamily: erythropoietin receptor; cytokine receptor homology
 C: Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-507/Product: erythropoietin receptor #status predicted <MAT>
 F: 52-249/Domain: extracellular #status predicted <EXT>
 F: 52-238/Domain: cytokine receptor homology <CRS>
 F: 550-271/Domain: transmembrane #status predicted <TM>
 F: 272-507/Domain: intracellular #status predicted <INT>
 F: 52-62, 91-106/Disulfide bonds: #status predicted
 F: 75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 Db 232 WSXWS 236

RESULT 3
 C8HUA
 Complement C8 alpha chain precursor - human
 C: Species: Homo sapiens (man)
 C: Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 07-Aug-1998
 C: Accession: A26704
 R: Rao, A.G.; Howard, O.M. 2.; Ng, S.C.; Whitehead, A.S.; Colten, H.R.; Sodetz, J.M.
 Biochemistry 26, 3556-3564, 1987
 A: Title: Complementary DNA and derived amino acid sequence of the alpha subunit of
 A: Reference number: A26704; MID:88000560
 A: Accession: A26704
 A: Molecule type: mRNA
 A: Residues: 1-583 <RAO>
 A: Note: part of the sequence was confirmed by protein sequencing
 C: Comment: C8, a constituent of the cytolytic (membrane attack) complex C5b-C9, con
 C: Comment: The alpha chain binds to the beta chain, gamma chain, and component C9 a
 C: Genes: 1
 A: Gene: GDB:C8A
 A: Cross-references: GDB:119735; OMIM:120950
 A: Map position: 1p32-1p32
 C: Superfamily: Complement C9; EGF homology; LDL receptor ligand-binding repeat hom
 C: Keywords: complement pathway; cytolytic; glycoprotein; membrane attack complex; p
 F: 1-20/Domain: signal sequence #status predicted <SIG>
 F: 21-20/Domain: propeptide #status predicted <PRO>
 F: 31-583/Product: complement C8 alpha chain #status predicted <MPR>
 F: 37-91/Domain: thrombospondin type 1 repeat homology <THR1>
 F: 96-130/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F: 496-527/Domain: EGF homology <EGF>
 F: 537-583/Domain: thrombospondin type 1 repeat homology <THR2>
 F: 43/437/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 1; Length 583;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 Db 544 WSXWS 548

RESULT 4
 B44294
 unc-5 protein, long form - Caenorhabditis elegans
 N: Contains: unc-5 protein, short form
 C: Species: Caenorhabditis elegans
 C: Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 20-Mar-1998
 C: Accession: B44294; A44294
 R: Rieung-Hagstad, J.N.; C. Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.; Hedgecock, E
 Cell 71, 289-299, 1992
 A: Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type
 A: Reference number: A44294; MID:93046629
 A: Accession: B44294
 A: Contents: variety Bergerac
 A: Molecule type: DNA
 A: Residues: 1-947 <LEU>
 A: Cross-references: GB:S47168; NID:9258527; PID:9258529
 A: Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116
 A: Note: authors translated the codon CNA for residue 642 as Val; sequence shown fol
 A: Note: mRNA lacking the first exon is equally prevalent
 C: Genes: 1
 A: Gene: unc-5
 A: Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
 C: Function:
 A: Description: required for guidance of pioneering axons and cells migrating dorsally
 C: Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin
 C: Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane

F:30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F:46-116/Domain: immunoglobulin homology <IG>
 F:153-211/Domain: immunoglobulin homology <IG>
 F:229-300/Domain: thrombospondin type 1 repeat homology <THR1>
 F:301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F:365-390/Domain: transmembrane #status predicted <TM>
 F:512-559/Domain: SH3 homology <SH3>
 F:53-114,65-112,160-209/Disulfide bonds: #status predicted
 F:206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 1; Length 947;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXMS 5
 Db 305 WSAWS 309

RESULT 5
 S60028
 ferredoxin--NADP+ reductase (PC 1.18.1.2) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Feb-1996 #sequence_revision 08-Nov-1996 #text_change 16-Feb-1997
 C:Accession: S60028; 149671
 R:Itch, S.; Iemura, O.; Yamada, E.; Yoshimura, T.; Tsujikawa, K.; Kohama, Y.; Malmure, T.
 Biochim. Biophys. Acta 1264, 159-162, 1995
 A>Title: cDNA cloning of mouse ferredoxin reductase from kidney.
 A:Reference number: 149671; MID:96085117
 A:Accession: S60028
 A:Molecule type: mRNA
 A:Residues: 1-494 <IT0>
 A:Cross-references: EMBL:D4920; NID:g108468; PID:g108469
 C:Genetics:
 A:Genome: nuclear
 C:Superfamily: human ferredoxin--NADP+ reductase
 C:Keywords: FAD; mitochondrion; NADP; oxidoreductase
 F:1-34/Domain: transit peptide (mitochondrion) #status predicted <MP>
 F:35-494/Product: ferredoxin--NADP+ reductase #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 494;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXMS 5
 Db 11 WSAWS 15

RESULT 6
 S20914
 lysozyme (EC 3.2.1.17) D precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Sep-1997
 C:Accession: S20914; S41576
 R:Kylsten, P.; Kimbrell, D.A.; Daffre, S.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 232, 335-343, 1992
 A>Title: The lysozyme locus in Drosophila melanogaster: different genes are expressed in
 A:Reference number: S20914; MID:92269751
 A:Accession: S20914
 A:Molecule type: DNA
 A:Residues: 1-140 <KYL>
 A:Cross-references: EMBL:X58382; NID:g9197; PID:g9198
 R:Daffre, S.; Kylsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapted
 A:Reference number: S41573
 A:Accession: S41576
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAR>
 C:Genetics:

A:Gene: lyso
 A:Cross-references: FlyBase:FBgn0004427
 A:Map position: 3
 C:Superfamily: lysozyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-140/Product: lysozyme D #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXMS 5
 Db 120 WSAWS 124

RESULT 7
 S41573
 lysozyme (EC 3.2.1.17) precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 08-Sep-1997
 C:Accession: S41573; S41575; S32651; S32726
 R:Daffre, S.; Kylsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapt
 A:Reference number: S41573
 A:Accession: S41573
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAR>
 A:Cross-references: EMBL:Z22223; NID:g288920; PID:g288921
 A:Genetics: LYSA
 A:Accession: S41575
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAR>
 A:Cross-references: EMBL:Z22226; NID:g296038; PID:g296039
 A:Genetics: LYSC
 A:Gene: LYSA
 A:Map position: 3
 C:Genetics: <LYSC>
 A:Gene: LYSC
 A:Map position: 3
 C:Superfamily: lysozyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-140/Product: lysozyme A #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXMS 5
 Db 120 WSAWS 124

RESULT 8
 S41574
 lysozyme (EC 3.2.1.17) B precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 26-Feb-1998
 C:Accession: S41574; S32643; S32620
 R:Daffre, S.; Kylsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapt
 A:Reference number: S41574
 A:Accession: S41574
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAR>
 A:Cross-references: EMBL:Z22225; NID:g289001; PID:g289002

A:Genetics: LYSB
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.
 Submitted to the EMBL Data Library, April 1993
 A:Description: The lyszyme locus in Drosophila melanogaster; an expanded gene family ad
 A:Reference number: S32620
 A:Accession: S32643
 A:Molecule type: DNA
 A:Residues: 1-140 <DAF>
 A:Cross-references: EMBL:Z22226
 A:Genetics: LYSB
 C:Genetics: <LYSB>
 A:Gene: LYSB
 A:Cross-references: FlyBase:FBgn0004425
 A:Map position: 3
 C:Genetics: <LYSC>
 A:Gene: FlyBase:LYSC
 A:Cross-references: FlyBase:FBgn0004426
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-140/Product: lyszyme B #status predicted <MAT>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 120 WSAMS 124

RESULT 9
 S41577
 Lyszyme (EC 3.2.1.17) E precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
 C:Accession: S41577; S32634
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.
 M:1. Gen. Genet. 242, 152-162, 1994
 A:Title: The lyszyme locus in Drosophila melanogaster: an expanded gene family adapted
 A:Reference number: S41577
 A:Accession: S41577
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAF>
 A:Cross-references: EMBL:Z22227; NID:g289003; PID:g289004
 C:Genetics:
 A:Gene: LysE
 A:Cross-references: FlyBase:FBgn0004428
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-140/Product: lyszyme E #status predicted <MAT>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 120 WSAMS 124

RESULT 10
 S41580
 Lyszyme (EC 3.2.1.17) X - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C:Date: 25-Dec-1994 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1998
 C:Accession: S41580; S32650
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.

M:1. Gen. Genet. 242, 152-162, 1994
 A:Title: The lyszyme locus in Drosophila melanogaster: an expanded gene family ad
 A:Reference number: S41573
 A:Accession: S41580
 A:Molecule type: mRNA
 A:Residues: 1-81 <DAF>
 A:Cross-references: EMBL:Z22224; NID:g288922; PID:g288923
 C:Genetics:
 A:Gene: LysP
 A:Cross-references: FlyBase:FBgn0004431
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation

Query Match 96.8%; Score 30; DB 2; Length 81;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 60 WSAMS 64

RESULT 11
 S69881
 phosphopyruvate hydratase (EC 4.2.1.11) YMR323w - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-May-1998
 C:Accession: S69881
 R:Churcher, C.M.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: S69876
 A:Accession: S69881
 A:Molecule type: DNA
 A:Residues: 1-437 <CHD>
 A:Cross-references: EMBL:Z54141; NID:g1072408; PID:g1072413; MIPS:YMR323w
 C:Genetics:
 A:Map position: 13R
 A:Note: YMR323w
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:40/Binding site: magnesium 2 (Ser) #status predicted
 F:212,346/Active site: Glu, Lys #status predicted
 F:247,296,321/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2,3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 304 WSAMS 308

RESULT 12
 S67305
 phosphopyruvate hydratase (EC 4.2.1.11) ERRI - yeast (Saccharomyces cerevisiae)
 M:Alternative names: ERRI protein; protein O6788; protein P0304; protein YOR393w; pro
 C:Species: Saccharomyces cerevisiae
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 22-May-1998
 C:Accession: S67305; S67306; S59000; S65314; S65335
 R:Delius, H.; Hedling, U.; Hofmann, B.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67261
 A:Accession: S67305
 A:Molecule type: DNA
 A:Residues: 1-330 <DEF>
 A:Cross-references: EMBL:Z75301; MIPS:YOR393w
 A:Experimental source: strain S288C
 A:Genetics: C15
 R:Wambutt, R.; Medler, H.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67306
 A:Accession: S67306
 A:Molecule type: DNA
 A:Residues: 177-437 <NAME>
 A:Cross-references: EMBL:275301; MIPS:YOR393w
 A:Experimental source: strain S286C
 A:Genetics: C15
 R:Pyde, F.E.; Huckle, T.C.; Louis, E.J.
 Yeast 11, 371-382, 1995
 A:Title: Sequence analysis of the right end of chromosome XV in *Saccharomyces cerevisiae*
 A:Reference number: S59000; MUID:95304651
 A:Accession: S59000
 A:Molecule type: DNA
 A:Residues: 120-230, 'K', 232-437 <PRX>
 A:Cross-references: EMBL:023472; NID:g775202; PID:g775203
 A:Genetics: C15
 R:Duetschhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.; Moestl, D.
 Submitted to the Protein Sequence Database, May 1996
 A:Reference number: S65292
 A:Accession: S65314
 A:Molecule type: DNA
 A:Residues: 1-437 <DUE>
 A:Cross-references: EMBL:273637; MIPS:YPL281c; NID:g1370577; PID:e246987; PID:g1370578
 A:Experimental source: strain S286C (AB972)
 A:Genetics: C16
 C:Genetics: <C15>
 A:Gene: SGD:ERR1
 A:Cross-references: MIPS:YOR393w; SGD:S0005920
 A:Map position: 15R
 A:Note: YOR393w
 C:Genetics: <C16>
 A:Gene: SGD:ERR2
 A:Cross-references: MIPS:YPL281c; SGD:S0006202
 A:Map position: 16L
 A:Note: YPL281c
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:40/Binding site: magnesium 2 (Ser) #status predicted
 F:212/346/Active site: Glu, Lys #status predicted
 F:247,296,321/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 304 MSSWS 308

RESULT 13
 A26489
 Placental lactogen II precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1988 #sequence, revision 05-Oct-1988 #text, change 17-Mar-1999
 C:Accession: A44090; A26489; B23159
 R:Shida, M.M.; Jackson-Grusby, L.L.; Ross, S.R.; Linzer, D.I.H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3864-3868, 1992
 A:Title: Placental-specific expression from the mouse placental lactogen II gene promoter
 A:Reference number: A44090; MUID:92237269
 A:Accession: A44090
 A:Molecule type: DNA

A:Residues: 1-222 <SHI>
 A:Cross-references: GB:M85062
 R:Jackson, L.L.; Colosi, P.; Talamantes, F.; Linzer, D.I.H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8496-8500, 1986
 A:Title: Molecular cloning of mouse placental lactogen cDNA.
 A:Reference number: A26489; MUID:87041482
 A:Accession: A26489
 A:Molecule type: mRNA
 A:Residues: 1-222 <JAC>
 A:Cross-references: GB:M14647; NID:9200404; PID:9200405
 R:Linzer, D.I.H.; Lee, S.J.; Ogren, L.; Talamantes, F.; Nathans, D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4356-4359, 1985
 A:Title: Identification of proliferin mRNA and protein in mouse placenta.
 A:Reference number: A94049; MUID:85242683
 A:Accession: B23159
 A:Molecule type: protein
 A:Residues: 32-50 <LIN>
 C:Comment: Placental lactogen II can bind to mammary gland prolactin receptors.
 C:Superfamily: prolactin
 C:Keywords: hormone; placenta
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-222/Product: Placental lactogen II #status experimental <MAT>

Query Match 96.8%; Score 30; DB 2; Length 222;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 173 WSAMS 177

RESULT 14
 A46713
 erythropoietin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Sep-1993 #sequence, revision 18-Nov-1994 #text, change 20-Mar-1998
 C:Accession: A46713
 R:Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sase
 J. Biol. Chem. 268, 11208-11216, 1993
 A:Title: Functional erythropoietin receptor of the cells with neural characteristics.
 A:Reference number: A46713; MUID:9326574
 A:Accession: A46713
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-507 <MAS>
 A:Cross-references: GB:D13566; NID:9286209; PID:d1003266; PID:9286210
 A:Experimental source: PC12 and erythroid cells
 A:Note: sequence extracted from NCBI backbone (NCBI:132811, NCBI:132813)
 C:Superfamily: erythropoietin receptor; cytokine receptor homology
 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-507/Product: erythropoietin receptor #status predicted <MAT>
 F:25-246/Domain: extracellular #status predicted <EXT>
 F:252-238/Domain: cytokine receptor homology <CRS>
 F:250-271/Domain: transmembrane #status predicted <TM>
 F:272-507/Domain: intracellular #status predicted <INT>
 F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 507;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 232 WSAMS 236

RESULT 15
 S14081
 erythropoietin receptor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-May-1997
C:Accession: S14081; I49653
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A:title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; M01D:91080149
A:Accession: S14081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <RUR>
R:Jacobs, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
J. Biol. Chem. 266, 6952-6956, 1991
A:title: Spleen focus-forming virus long terminal repeat insertional activation of the m
A:Reference number: I49653; M01D:91201346
A:Accession: I49653
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <RBS>
A:Cross-references: GB:M62360; NID:g193199; PID:g193200
C:Superfamily: erythropoietin receptor; cytokine receptor homology
C:Keywords: cytokine receptor; transmembrane protein
F:52-238/Domain: cytokine receptor homology <CRS>

Query Match 96.8%; Score 30; DB 2; Length 265;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
DB 232 MSXMS 236

Search completed: September 16, 1999, 20:42:05
Job time: 5398 sec

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:05:20; Search time 35.09 Seconds

(without alignments)
4.028 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 MSXMS 5

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	494	1	ADRO_MOUSE
2	30	96.8	218	1	ALBR_KLEOX
3	30	96.8	934	1	CO6_HUMAN
4	30	96.8	843	1	CO7_HUMAN
5	30	96.8	584	1	CO8A_HUMAN
6	30	96.8	586	1	CO9_FIGRU
7	30	96.8	196	1	CRBB_BOVIN
8	30	96.8	972	1	CTRL_BACCI
9	30	96.8	508	1	EPOR_HUMAN
10	30	96.8	507	1	EPOR_MOUSE
11	30	96.8	507	1	ERR1_YEAST
12	30	96.8	437	1	GMCR_HUMAN
13	30	96.8	400	1	LYSA_DROME
14	30	96.8	140	1	LYSB_DROME
15	30	96.8	140	1	LYSD_DROME
16	30	96.8	140	1	LYSE_DROME
17	30	96.8	81	1	LYSX_DROME
18	30	96.8	184	1	MPL_MPLV
19	30	96.8	222	1	PLC2_MOUSE
20	30	96.8	622	1	PROR_HUMAN
21	30	96.8	437	1	PROP_MOUSE
22	30	96.8	635	1	SSPO_BOVIN
23	30	96.8	867	1	TPOR_HUMAN
24	30	96.8	635	1	TPOR_MOUSE
25	30	96.8	625	1	TPOR_MOUSE
26	30	96.8	625	1	TPOR_MOUSE
27	29	93.5	507	1	AL15_TOBAC
28	29	93.5	510	1	CEAB_ECOLI
29	29	93.5	697	1	CEAD_ECOLI
30	29	93.5	362	1	CNTR_CHICK
31	29	93.5	372	1	CNTR_HUMAN
32	29	93.5	372	1	CNTR_RAT
33	29	93.5	591	1	CO8B_HUMAN
34	29	93.5	590	1	CO8B_RABIT
35	29	93.5	140	1	CO8B_RAT
36	29	93.5	547	1	CO9_HORSE
37	29	93.5	559	1	CO9_HUMAN
38	29	93.5	528	1	CO9_MOUSE
39	29	93.5	574	1	CO9_MOUSE
40	29	93.5	557	1	CO9_ONCMY
41	29	93.5	554	1	CO9_RABIT
42	29	93.5	494	1	CPSL_HUMAN
43	29	93.5	391	1	CPSD_STRAC

ALIGNMENTS

44 29 93.5 897 1 CYRB_HUMAN P32827 homo sapien
45 29 93.5 517 1 YXWL_CAEL Q20806 caenorhabdi

RESULT 1
ID ADRO_MOUSE STANDARD; PRT; 494 AA.
AC 061578;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NADPH:ADRENODOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (FERREDOXIN-NADP(+) REDUCTASE).
GN FDXR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDA; MORINAE; MUS.
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-KIDNEY;
RX MEDLINE; 96085117.
RA ITOH S., IEMURA O., YAMADA E., YOSHIMURA T., TSUJIKAWA K., KOHANA Y., MIKURA T.;
RT "CDNA cloning of mouse ferredoxin reductase from kidney";
RL BIOCHIM. BIOPHYS. ACTA 1264:159-162(1995).
CC -1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) - OXIDIZED ADRENODOXIN + NADPH.
CC -1- CORRECTOR: FAD FLAVOPROTEIN.
CC -1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TESTIS AND OVARY AND TO A LESSER EXTENT IN THE LIVER AND KIDNEY.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
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CC
CC EMBL; D49920; E212200;
DR MGD; MGI:104724; FDXR.
KW OXIDOREDUCTASE; FLAVOPROTEIN; NADP; FAD; MITOCHONDRION;
KW TRANSIT PEPTIDE.
KW
FT TRANSIT 1 34 MITOCHONDRION (POTENTIAL).
FT CHAIN 35 494 ADRENODOXIN REDUCTASE.
SQ SEQUENCE 494 AA; 54202 MW; 81A18E21 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 494;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
DB 11 MSXMS 15

RESULT 2
ID ALBR_KLEOX STANDARD; PRT; 218 AA.
AC P10488;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-JUL-1989 (REL. 11, LAST ANNOTATION UPDATE)
DE ALBICIDIN RESISTANCE PROTEIN
OS KLEBSIELLA OXYTOCA.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC KLEBSIELLA.

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-JMP4505;
 RC MEDLINE; 89013885.
 RA WALKER M.J., BIRCH R.G., PEMBERTON J.M.;
 RT "Cloning and characterization of an albididin resistance gene from
 RL Klebsiella oxytoca.";
 RM MOL. MICROBIOL. 2:443-454(1988).
 CC -1- FUNCTION: ALBIDIDIN RESISTANCE PROTEIN BINDS TO FORM A COMPLEX
 CC WITHOUT ANTIBIOTIC ACTIVITY BUT WITHOUT CATALYZING ANY FURTHER
 CC CHEMICAL MODIFICATIONS TO ALBIDIDIN.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y00558; G43786;
 DR PIR; S02828; S02828.
 KW ANTIBIOTIC RESISTANCE; PERIPLASMIC.
 SQ SEQUENCE 218 AA; 25838 MW; 87C032C5 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 218;
 Best Local Similarity 80.0%; Pred. No 80;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 57 WSSWS 61

RESULT 3
 CO6_HUMAN STANDARD; PRT; 934 AA.
 AC P13671;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C6 PRECURSOR.
 GN C6.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-31 AND 633-640.
 RX MEDLINE; 90036879.
 RA HAEFLIGER J.-A., TSCHOPE J., VIAL N., JENNE D.E.;
 RT "Complete primary structure and functional characterization of the
 RT C6b-binding domain in complement C6.";
 RT C6b-binding domain in complement C6.";
 RL J. BIOL. CHEM. 264:18041-18051(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89380223.
 RA DISCIPPIO R.G., HUGLI T.E.;
 RT "The molecular architecture of human complement component C6.";
 RL J. BIOL. CHEM. 264:16197-16206(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-BLOOD;
 RX MEDLINE; 93291175.
 RA HOBART M.J., FERNIE B., DISCIPPIO R.G.;
 RT "Structure of the human C6 gene.";
 RL BIOCHEMISTRY 32:6198-6205(1993).
 RN [4]
 RP SEQUENCE OF 1-491 FROM N.A.
 RX MEDLINE; 89202413.
 RA CHAKRAVARTI D.N., CHAKRAVARTI B., PARRA C.A., MOELLER-EBERHARD H.J.;

RT "Structural homology of complement protein C6 with other
 RT channel-forming proteins of complement.";
 RT PROC. NATL. ACADE. SCI. U.S.A. 86:2799-2803(1989).
 RN [5]
 RP VARIANT ALLOTYPES C6 A AND B.
 RX MEDLINE; 93326158.
 RA DEMALD G., NOTHEN M.M., CICHON S.;
 RT "Polymorphism of human complement component C6: an amino acid
 RT substitution (Glu/Ala) within the second thrombospondin repeat
 RT differentiates between the two common allotypes C6 A and C6 B.";
 RL BIOCHEM. BIOPHYS. RES. COMMON. 194:458-464(1993).
 CC -1- FUNCTION: INVOLVED IN THE FORMATION OF THE LYtic C5b-9m COMPLEX.
 CC -1- DOMAIN: C6 CONTAINS NINE DISTINCT STRUCTURAL UNITS (CYSTEINE-RICH)
 CC WHICH HAVE CHARACTERISTIC FEATURES OF MODULES.
 CC -1- PTM: ALL CYSTEINE RESIDUES ARE ASSUMED TO BE CROSS-LINKED TO ONE
 CC ANOTHER. INDIVIDUAL MODULES CONTAINING AN EVEN NUMBER OF CONSERVED
 CC CYSTEINE RESIDUES ARE SUPPOSED TO HAVE DISULFIDE LINKAGES ONLY
 CC WITHIN THE SAME MODULE.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF ALLOTYPIC C6 A.
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C7, C8, C9, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHT (SCR) REPEATS.
 CC -1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC
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 CC
 CC EMBL; J05054; G179704;
 DR EMBL; J05024; G307228;
 DR EMBL; X72177; G825633;
 DR EMBL; J04506; G618466;
 DR PIR; A32109; A32109.
 DR PIR; A34235; A34235.
 DR PIR; A34372; A34372.
 DR MIM; 217050;
 DR PROSITE; PS00279; MAC PERFORIN; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01209; LDLRA_1; 1.
 DR PROSITE; PS00068; LDLRA_2; 1.
 DR PFAM; PF00057; ldl_recept_a; 1.
 DR PFAM; PF00084; sushi; 2.
 DR PFAM; PF00090; tsp_1; 3.
 DR HSP; P01130; 1A01.
 KW COMPLEMENT PATHWAY; GLYCOPROTEIN; PLASMA; MEMBRANE ATTACK COMPLEX;
 KW CYTOLYSIS; SUSHT; REPEAT; SIGNAL; POLYMORPHISM; EGF-LIKE DOMAIN;
 KW TRANSMEMBRANE.
 FT SIGNAL 1 21
 FT CHAIN 934
 FT REPEAT 22
 FT REPEAT 81
 FT REPEAT 137
 FT DOMAIN 175
 FT TRANSMEM 331
 FT TRANSMEM 349
 FT DOMAIN 517
 FT REPEAT 562
 FT DOMAIN 642
 FT DOMAIN 643
 FT REPEAT 643
 FT REPEAT 703
 FT DOMAIN 766
 FT DOMAIN 840
 FT DOMAIN 858
 FT DISULFID 140
 FT DISULFID 146
 FT DISULFID 158
 FT DISULFID 399

COMPLEMENT COMPONENT C6.
 TYPE-1 TSP 1.
 TYPE-1 TSP 2.
 LDL-RECEPTOR CLASS A.
 POTENTIAL.
 EGF-LIKE.
 TYPE-1 TSP 3.
 C5b-BINDING DOMAIN.
 2 X SUSHT (SCR) REPEATS.
 SUSHT 1.
 SUSHT 2.
 COMPLEMENT CONTROL FACTOR I MODULE.
 COMPLEMENT CONTROL FACTOR I MODULE.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.

FT DISULFID 523 539 BY SIMILARITY.
 FT DISULFID 526 541 BY SIMILARITY.
 FT DISULFID 543 552 BY SIMILARITY.
 FT DISULFID 644 666 BY SIMILARITY.
 FT DISULFID 672 699 BY SIMILARITY.
 FT DISULFID 704 746 BY SIMILARITY.
 FT DISULFID 732 761 BY SIMILARITY.
 FT CARBOHYD 324 324 POTENTIAL.
 FT CARBOHYD 855 855 POTENTIAL.
 FT VARIANT 119 119 E -> A (IN ALLOTYPE C6 B).
 SQ SEQUENCE 934 AA; 104843 MW; D03BD9D CRC32;
 Query Match Best Local Similarity 96.8%; Score 30; DB 1; Length 934;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXWS 5
 DB 571 MSWS 575
 RESULT 4
 CO7_HUMAN STANDARD; PRT; 843 AA.
 AC P10643;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C7 PRECURSOR.
 GN C7.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE; 88087145.
 RA DISCIPLIO R.G., CHAKRAVARTI D.N., MUELLER-BERHARD H.J., FEY G.H.;
 RT "The structure of human complement component C7 and the C5b-7 complex."
 CC J. BIOL. CHEM. 263:549-560(1988).
 CC -1- FUNCTION: C7 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.
 CC C7 BINDS TO C5B FORMING THE C5B-7 COMPLEX, WHERE IT SERVES
 CC AS A MEMBRANE ANCHOR.
 CC -1- SUBUNIT: MONOMER OR DIMER; AS A C5B-7 COMPLEX IT CAN ALSO
 CC FORM MULTIMERIC ROSETTES.
 CC -1- PTM: C7 HAS 28 DISULFIDE BRIDGES.
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C6, C8, C9, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: CONTAINS 2 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 CC EMBL; J03507; G179716;
 DR EMBL; A27340; A27340.
 DR MIM; 217070;
 DR PROSITE; PS00279; MAC_PORFORIN.1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01209; LDLR_1; 1.
 DR PROSITE; PS00068; LDLR_2; 1.
 DR PFM; PF00057; Idl_recept_a; 1.
 DR PFM; PF00084; sushi; 2.
 DR PFM; PF00090; tsp_1; 2.
 DR HSP; P10998; IVC.

KM COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
 KM PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; SIGNAL; EGF-LIKE DOMAIN;
 KM REPEAT; SUSHI; TRANSMEMBRANE.
 FT SIGNAL 1 22
 FT CHAIN 23 843
 FT REPEAT 24 83
 FT DOMAIN 83 121
 FT TRANSMEM 271 287
 FT TRANSMEM 292 311
 FT DOMAIN 451 487
 FT REPEAT 497 545
 FT REPEAT 570 689
 FT REPEAT 570 627
 FT REPEAT 630 689
 FT DOMAIN 695 770
 FT DOMAIN 771 843
 FT DISULFID 85 96
 FT DISULFID 91 109
 FT DISULFID 103 119
 FT DISULFID 103 353
 FT DISULFID 337 613
 FT DISULFID 571 613
 FT DISULFID 599 626
 FT DISULFID 631 673
 FT DISULFID 659 688
 FT CARBOHYD 202 202
 FT CARBOHYD 754 754
 SQ SEQUENCE 843 AA; 93514 MW; 0A16E9B4 CRC32;
 Query Match Best Local Similarity 96.8%; Score 30; DB 1; Length 843;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXWS 5
 DB 506 MSWS 510
 RESULT 5
 CO8A_HUMAN STANDARD; PRT; 584 AA.
 AC P07357; Q13668;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR.
 GN C8A.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX TISSUE-LIVER.
 RX MEDLINE; 88000560.
 RA RAO A.G., HOWARD O.M.Z., NG S.C., WHITEHEAD A.S., COLTEN H.R.,
 RA SODETZ J.M.;
 RT "Complementary DNA and derived amino acid sequence of the alpha
 RT subunit of human complement protein C8: evidence for the existence of
 RT a separate alpha subunit messenger RNA."
 RL BIOCHEMISTRY 26:3556-3564(1987).
 RN [2]
 RP REVISIONS TO 467-479.
 RA SODETZ J.M.;
 RL SUBMITTED (FEB-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE; 95278905.
 RA MICHELOTTI G.A., SNIDER J.V., SODETZ J.M.;
 RT "Genomic organization of human complement protein C8 alpha and
 RT further examination of its linkage to C8 beta."
 RL HUM. GENET. 95:513-518(1995).
 CC -1- FUNCTION: C8 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.

CC C8 BINDS TO THE C5B-7 COMPLEX, FORMING THE C5B-8 COMPLEX. C5-B8
 CC BINDS C9 AND ACTS AS A CATALYST IN THE POLYMERIZATION OF C9.
 CC SUBUNIT: C8 IS COMPOSED OF THREE CHAINS: ALPHA, BETA AND GAMMA.
 CC THE ALPHA AND GAMMA CHAINS ARE DISULFIDE BONDED.
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C9, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC -----
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 CC -----
 CC EMBL: M16974; G179718; -
 CC EMBL: U08006; G901864; -
 CC EMBL: U07996; G901864; JOINED.
 CC EMBL: U07997; G901864; JOINED.
 CC EMBL: U07998; G901864; JOINED.
 CC EMBL: U07999; G901864; JOINED.
 CC EMBL: U08000; G901864; JOINED.
 CC EMBL: U08001; G901864; JOINED.
 CC EMBL: U08002; G901864; JOINED.
 CC EMBL: U08003; G901864; JOINED.
 CC EMBL: U08004; G901864; JOINED.
 CC EMBL: U08005; G901864; JOINED.
 CC PIR: A26704; C8HUA.
 CC MIM: 120950; -
 CC DR PROSITE; PS00279; MAC_PERFORIN; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 CC DR PROSITE; PS01209; LDLRA_1; 1.
 CC DR PROSITE; PS00068; LDLRA_2; 1.
 CC DR PFAM; PF00057; ldl_recept_a; 1.
 CC DR PFAM; PF00090; csp_1; 2.
 CC DR HSSP; P01130; ILDR.
 CC DR COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
 CC KW PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; SIGNAL; TRANSMEMBRANE;
 CC EGF-LIKE DOMAIN; REPEAT.
 CC FT SIGNAL 1 20 POTENTIAL.
 CC FT PROPER 21 30 POTENTIAL.
 CC FT CHAIN 31 584 COMPLEMENT COMPONENT C8 ALPHA CHAIN.
 CC FT REPEAT 38 93 TYPE-1 TSP 1.
 CC FT DOMAIN 94 132 LDL-RECEPTOR CLASS A.
 CC FT TRANSMEM 309 325 POTENTIAL.
 CC FT DOMAIN 330 349 POTENTIAL.
 CC FT REPEAT 493 529 EGF-LIKE.
 CC FT DISULFID 536 584 TYPE-1 TSP 2.
 CC FT DISULFID 96 108 BY SIMILARITY.
 CC FT DISULFID 102 121 BY SIMILARITY.
 CC FT DISULFID 115 130 BY SIMILARITY.
 CC FT DISULFID 194 194 INTERCHAIN (WITH C8-GAMMA).
 CC FT DISULFID 375 399 BY SIMILARITY.
 CC FT CARBOHYD 437 437 POTENTIAL.
 CC FT CARBOHYD 437 437 POTENTIAL.
 CC FT CONFLICT 93 93 O -> K (IN REF. 3).
 CC FT CONFLICT 575 575 P -> S (IN REF. 3).
 CC SEQUENCE 584 AA; 65163 MW; 33C94C53 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 584;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 1111
 Db 545 WSXWS 549

RESULT 6

CC09_FUGRU STANDARD; PRT; 586 AA.
 ID C09_FUGRU
 AC P79755;
 DT 01-NOV-1997 (REL. 35, CREATED).
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE).
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE).
 DE COMPLEMENT COMPONENT C9 PRECURSOR.
 GN C9.
 OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
 CC ENKAVORT; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 CC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
 CC TETRAODONTIFORMES; TETRAODONTIDEI; TETRAODONTIDAE; FUGU.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98038993.
 RA YEO G.S.H., ELGAR G., SANDFORD R., BRENNER S.;
 FT Cloning and sequencing of complement component C9 and its linkage to
 FT DOC-2 in the pufferfish *Fugu rubripes*.
 RL GENE 200:203-211(1997).
 CC -1- FUNCTION: C9 IS THE FINAL COMPONENT OF THE COMPLEMENT SYSTEM TO BE
 CC ADDED IN THE ASSEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT IS ABLE
 CC TO ENTER LIPID BILAYERS, FORMING TRANSMEMBRANE CHANNELS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C8, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC -----
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 CC -----
 CC EMBL: U87241; G1845349; -
 CC DR PROSITE; PS00279; MAC_PERFORIN; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 CC DR PROSITE; PS01209; LDLRA_1; 1.
 CC DR PROSITE; PS00068; LDLRA_2; 1.
 CC DR PFAM; PF00057; ldl_recept_a; 1.
 CC DR HSSP; P01130; ILDR.
 CC DR COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
 CC KW PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; SIGNAL; EGF-LIKE DOMAIN;
 CC REPEAT.
 CC FT SIGNAL 1 26 POTENTIAL.
 CC FT CHAIN 27 586 COMPLEMENT COMPONENT C9.
 CC FT REPEAT 36 93 TYPE-1 TSP 1.
 CC FT DOMAIN 94 131 LDL-RECEPTOR CLASS A.
 CC FT TRANSMEM 490 524 POTENTIAL.
 CC FT DOMAIN 540 586 EGF-LIKE.
 CC FT REPEAT 96 108 TYPE-1 TSP 2.
 CC FT DISULFID 103 121 BY SIMILARITY.
 CC FT DISULFID 115 129 BY SIMILARITY.
 CC FT DISULFID 363 389 BY SIMILARITY.
 CC FT DISULFID 494 510 BY SIMILARITY.
 CC FT DISULFID 497 512 BY SIMILARITY.
 CC FT DISULFID 514 523 BY SIMILARITY.
 CC FT CARBOHYD 246 246 POTENTIAL.
 CC FT CARBOHYD 274 274 POTENTIAL.
 CC FT CARBOHYD 354 354 POTENTIAL.
 CC SEQUENCE 586 AA; 65197 MW; 40CEB614 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 586;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
 1111

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Db          549 MSSWS 553

RESULT      7
CRBB_BOVIN ID CRBB_BOVIN STANDARD; PRT: 196 AA.
P26444; AC
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE BETA_CRYSTALLIN A2.
GN CRYBA2.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ACTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
[1]
SEQUENCE FROM N.A.
RC TISSUE-LENS:
RX MEDLINE: 91340151.
VAN REN'S G.L., DRIJSEN H.P.C., NALINI V., SLINGSBY C., DE JONG W.M.,
RA BLOEMENDAL H.;
RT Isolation and characterization of cDNAs encoding beta A2- and beta
RT A4-crystallins: heterologous interactions in the predicted beta
RT A4-beta B2 heterodimer." ;
RL GENE 102:1179-188(1991).
RN [2]
RP SEQUENCE OF 133-196.
RR TISSUE-LENS CORTEX:
RX MEDLINE: 84132067.
BERBERS G.A.M., HOEKMAN W.A., BLOEMENDAL H., DE JONG W.M.,
RA KLEINSCHMIDT T., BRAUNITZER G.;
RT Homology between the primary structures of the major bovine beta-
RT crystallin chains." ;
RL EUR. J. BIOCHEM. 139:467-479(1984).
CC -I FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
OF THE VERTEBRATE EYE LENS.
CC -I SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -I DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
VERY SIMILAR GREEK KEY MOTIFS.
CC -I SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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-----
CC EMBL: MG0329; GI62727; -.
CC PIR: D27898; D27898.
CC PIR: JH0602; JH0602.
CC PROSITE: PS00225; CRYSTALLIN_BETAGAMMA. 3.
CC DR PFM: PF00030; crystal; 2.
CC HSP: P02522; IBLB.
CC EYE LENS PROTEIN; DUPLICATION.
CC INIT_MET 0 0
CC FT DOMAIN 1 10 N-TERMINAL ARM.
CC FT DOMAIN 11 51 MOTIF 1.
CC FT DOMAIN 52 99 MOTIF 2.
CC FT DOMAIN 100 104 CONNECTING PEPTIDE.
CC FT DOMAIN 105 146 MOTIF 3.
CC FT DOMAIN 147 196 MOTIF 4.
CC FT CONFLICT 182 184 OAH -> HAQ (IN REF. 2).
CC ISD SEQUENCE 196 AA; 22099 MM; 9867FFC3 CAC32;

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0Y      1 MSXWS 5
      || ||
      77 MSXWS 81

Db

RESULT 8
CTAL_BACCI
ID      CTAL_BACCI      STANDARD:      PRT:      972 AA.
AC      P94286;
DT      15-JUL-1998 (REL. 36, CREATED)
DT      15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE      15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE      CYCLOISOMALTOLIOSACCHARIDE GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.-)
      (CITASE).
OS      BACILLUS CIRCULANS.
OC      BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC      BACILLUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-T-3040;
RA      OGDWA T.; KUROKAWA T.; TOBE K.; KOBAYASHI M.;
RA      SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC      -1- FUNCTION: PRODUCES CYCLOISOMALTOLIOSACCHARIDE FROM DEXTRAN.
CC      -1- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
CC      -----
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CC      or send an email to license@lsb-sib.ch).
CC      -----
DR      EMBL; D61882; G1780754;
KW      TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL.
FT      SIGNAL      1      38      POTENTIAL.
FT      CHAIN      39      972      CYCLOISOMALTOLIOSACCHARIDE
FT      GLUCANOTRANSFERASE.
SQ      SEQUENCE 972 AA; 107431 MW; E0E01311 CRC32;

Query Match      96.88; Score 30; DB 1; Length 972;
Best Local Similarity 80.08; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

0Y      1 MSXWS 5
      || ||
      832 WSTWS 836

Db

RESULT 9
EPOR_HUMAN
ID      EPOR_HUMAN      STANDARD:      PRT:      508 AA.
AC      P19235;
DT      01-NOV-1990 (REL. 16, CREATED)
DT      01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE      15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE      ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
GN      EPOR.
OS      HOMO SAPIENS (HUMAN).
OC      EDUARDOTA; METAEOA; CHORDATA; VENTERATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 91372359.
RA      ERENNAN K.; ST JOHN T.;
RT      "The erythropoietin receptor gene: cloning and identification of
RT      multiple transcripts in an erythroid cell line OCIM1.";
RL      EXP. HEMATOL. 19:973-977(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 90304340.
RA      JONES S.S.; D'ANDREA A.; HAINES L.L.; WONG G.G.;

```

RT "Human erythropoietin receptor: cloning, expression, and biologic
 RT characterization.";
 RL BLOOD 76:31-35(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 9239773.
 RA NOGUCHI C.T., BAE K.S., CHIN K., WADA Y., SCHECHTER A.N.,
 RA HARKINS W.D.;
 RT "Cloning of the human erythropoietin receptor gene.";
 RL BLOOD 78:2548-2556(1991).
 RN [4]
 RP SEQUENCE OF 1-96 FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 9239773.
 RA MOUCHE L., TOURNAMILLE C., HATTAB C., BOFFA G., CARTRON J.P.,
 RA CHRETIEN S.;
 RT "Cloning of the gene encoding the human erythropoietin receptor.";
 RL BLOOD 78:2557-2563(1991).
 RN [5]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE; 92147143.
 RA PENNY L.A., FORGET B.G.;
 RT "Genomic organization of the human erythropoietin receptor gene.";
 RL GENOMICS 11:974-980(1991).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
 RX MEDLINE; 96291992.
 RA LYNNH O., STURA E.A., JOHNSON D.L., MIDDLETON S.A., MOLCHAY L.S.,
 RA WRIGHTON N.C., DOWE W.J., JOLLIFFE L.K., WILSON I.A.;
 RT "Functional mimicry of a protein hormone by a peptide agonist: the
 RT EPO receptor complex at 2.8 A.";
 RL SCIENCE 273:464-471(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
 RX MEDLINE; 99023198.
 RA LYNNH O., JOHNSON D.L., STURA E.A., FARRELL F.X., BARBONE F.P.,
 RA YU Y., LIU K.D., GOLDSMITH M.A., HE W., KRAUSE C.D., PESTRA S.,
 RA JOLLIFFE L.K., WILSON I.A.;
 RT "An antagonist peptide-EPO receptor complex suggests that receptor
 RT dimerization is not sufficient for activation.";
 RL NAT. STRUCT. BIOL. 5:993-1004(1998).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC
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 CC
 CC EMBL: M34986; G182201;
 CC EMBL: M60453; G182245;
 CC EMBL: S43332; G253497;
 CC EMBL: M76595; G553281;
 CC EMBL: M77244; G182134;
 CC PIR: A43799; A43799.
 CC PIR: A49824; A49824.
 CC PIR: A53958; A53958.
 CC PDB: 1EBP; 29-JUL-97.
 CC PDB: 1EBA; 18-NOV-98.
 CC DR MIM; 133171;
 CC DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAM; PF00041; fn3: 1.
 CC RA RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
 CC SIGNAL 1 24

FT CHAIN 25 508 ERYTHROPOIETIN RECEPTOR.
 FT DOMAIN 25 250 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 251 273 POTENTIAL.
 FT DOMAIN 274 508 CYTOSOLIC (POTENTIAL).
 FT DOMAIN 148 213 FIBRONECTIN TYPE-III.
 FT DISULFID 52 62
 FT DISULFID 91 107
 FT CARBOHYD 76 76
 SO SEQUENCE 508 AA; 55065 MW; A567A994 CRC32; POTENTIAL.

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 DB 233 WSXWS 237

RESULT 10
 EPO_MOUSE
 ID EPO_MOUSE STANDARD; PRT; 507 AA.
 AC P14753; Q63852;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
 OS EPOR.
 GN MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89195238.
 RA D'ANDREA A.D., LODISH H.F., WONG G.G.;
 RT "Expression cloning of the murine erythropoietin receptor.";
 RL CELL 57:277-285(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LIVER;
 RX MEDLINE; 91080149.
 RA KURAMOUCHI S., IKAWA Y., TOOKORO K.;
 RT "Characterization of murine erythropoietin receptor genes.";
 RL J. MOL. BIOL. 216:567-575(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92017832.
 RA HINO M., TOJO A., MISAWA Y., MORII H., TAKAYU F., SHIBUYA M.;
 RT "Unregulated expression of the erythropoietin receptor gene caused by
 RT insertion of spleen focus-forming virus long terminal repeat in a
 RT murine erythroleukemia cell line.";
 RL MOL. CELL. BIOL. 11:5527-5533(1991).
 RN [4]
 RP SEQUENCE OF 1-27 FROM N.A.
 RX MEDLINE; 90287158.
 RA YOUSSEFIAN H., ZON L.I., ORKIN S.H., D'ANDREA A.D., LODISH H.F.;
 RT "Structure and transcription of the mouse erythropoietin receptor
 RT gene.";
 RL MOL. CELL. BIOL. 10:3675-3682(1990).
 RN [5]
 RP SEQUENCE OF 1-24 FROM N.A.
 RX MEDLINE; 91201346.
 RA LACOMBE C., CHRETIEN S., LEMARCHAND V., MAYEUX P., ROMEO P.H.,
 RA GISELBRECHT S., CARTRON J.P.;
 RT "Spleen focus-forming virus long terminal repeat insertion
 RT activation of the murine erythropoietin receptor gene in the T3C1-2
 RT friend leukemia cell line.";
 RL J. BIOL. CHEM. 266:6952-6956(1991).
 RN [6]
 RP MUTAGENESIS.
 RX MEDLINE; 93180826.
 RA MURA O., CLEVELAND J.L., IHLE J.N.;

RT Inactivation of erythropoietin receptor function by point mutations
 RT in a region having homology with other cytokine receptors."
 RL MOL. CELL. BIOL. 13:1788-1795(1993).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J04843; G309219; -
 CC EMBL: X53081; G50862; -
 CC EMBL: M38133; G193093; -
 CC EMBL: M62360; G193200; -
 CC EMBL: S59388; E90908; -
 CC PIR: A32385; A32385.
 CC PIR: A41686; A41686.
 CC PIR: S13249; S13249.
 CC PIR: S14081; S14081.
 CC MGI: MGI:55408; EPOR.
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM: PFM: PF00041; fn3; 1.
 CC HSSP: P19235; 1EBP.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 CC SIGNAL 1 24
 CC CHAIN 1 25
 CC DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
 CC TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 147 212 FIBRONECTIN TYPE-III.
 CC DISULFID 52 62 BY SIMILARITY.
 CC DISULFID 90 106 BY SIMILARITY.
 CC CARBOHYD 75 75 POTENTIAL.
 CC CONFLICT 291 291 E -> D (IN E90908).
 CC SEQUENCE 507 AA; 55194 MW; C90C07B8 CRC32;
 SO

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 1111
 DB 232 WSAMS 236

RESULT 11
 EPOR_RAT STANDARD; PRT; 507 AA.
 AC Q07303;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
 GN EPOR.
 OS RATTUS NORVEGICUS (RAT).
 CC EUDAROTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 9326574.
 RA MASUDA S., NAGAO M., TAKAHATA K., KONISHI Y., GALLYAS F.,
 RA TABIRA T., SASAKI R.,
 RT "Functional erythropoietin receptor of the cells with neural

RT characteristics. Comparison with receptor properties of erythroid
 RT cells."
 RL J. BIOL. CHEM. 268:11208-11216(1993).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13566; G286210; -
 CC PIR: A46713; A46713.
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM: PFM: PF00041; fn3; 1.
 CC HSSP: P19235; 1EBP.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 CC SIGNAL 1 24
 CC CHAIN 1 25
 CC DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
 CC TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 147 212 FIBRONECTIN TYPE-III.
 CC DISULFID 52 62 BY SIMILARITY.
 CC DISULFID 90 106 BY SIMILARITY.
 CC CARBOHYD 75 75 POTENTIAL.
 CC SEQUENCE 507 AA; 55499 MW; 3C20ECC3 CRC32;
 SO

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 1111
 DB 232 WSAMS 236

RESULT 12
 ERRL_YEAST STANDARD; PRT; 437 AA.
 AC P42222;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
 GN ERRL OR YMR33W OR YMR924.15.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUDAROTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
 CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA CHORCHER C.M., LOUIS E.J., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.,
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 120-437 FROM N.A.
 RC STRAIN-S288C / TP1;
 RX MEDLINE; 95304851.
 RA PRYDE F.E., HUCKLE T.C., LOUIS E.J.,
 RT "Sequence analysis of the right end of chromosome XV in Saccharomyces
 RT cerevisiae: an insight into the structural and functional
 RT significance of sub-telomeric repeat sequences."
 RL YEAST 11:371-382(1995).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE

CC + H(2)O.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: 254141; G1072413;
 CC EMBL: 023472; G775203;
 CC SGD: L0002735; ERR1.
 CC PROSITE: PS00164; ENOLASE; 1.
 CC PFM: PF00113; enolase; 1.
 CC HSP: P00924; INEL.
 CC LYSASE, GLYCOLYSIS; MAGNESIUM.
 CC ACT SITE 160 160 BY SIMILARITY.
 CC METAL 247 247 MAGNESIUM (BY SIMILARITY).
 CC METAL 296 296 MAGNESIUM (BY SIMILARITY).
 CC METAL 321 321 MAGNESIUM (BY SIMILARITY).
 CC SEQUENCE 437 AA; 47312 MW; FEE64B47 CRC32;
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 CC Query Match 96.8%; Score 30; DB 1; Length 437;
 CC Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 CC Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 CC 1 MSXWS 5
 CC 1111
 CC 304 MSXWS 308
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 CC RESULT 13
 CC GPCR_HUMAN STANDARD; PRT; 400 AA.
 CC ID P15509; Q14429; Q14430;
 CC AC 01-APR-1990 (REL. 14, CREATED)
 CC DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 CC DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 CC DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA
 CC GN CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CD116) (CD116 ANTIGEN).
 CC OS HOMO SAPIENS (HUMAN).
 CC OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC RN [1]
 CC RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-1).
 CC RC TISSUE-PLACENTA;
 CC RX MEDLINE; 90059966.
 CC RA GEARING D.P., KING J.A., GOUGH N.M., NICOLA N.A.;
 CC RT "Expression cloning of a receptor for human granulocyte-macrophage
 CC colony-stimulating factor.";
 CC RL EMBL J. 8:3667-3676(1989).
 CC RN [2]
 CC RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-2 AND GM-CSF-R-ALPHA-3).
 CC RC TISSUE-BLOOD;
 CC RX MEDLINE; 94368898.
 CC RA HU X., EMMANUEL P.D., ZUCKERMAN K.S.;
 CC RT "Cloning and sequencing of the cDNAs encoding two alternative
 CC splicing-derived variants of the alpha subunit of the
 CC granulocyte-macrophage colony-stimulating factor receptor.";
 CC RL BIOCHIM. BIOPHYS. ACTA 1223:306-308(1994).
 CC RN [3]
 CC RP SEQUENCE OF 1-385 FROM N.A.
 CC RX MEDLINE; 94193800.
 CC RA NAKAGAWA Y., KOSUGI H., MIYAJIMA A., ARAI K.I., YOKOTA T.;
 CC RT "Structure of the gene encoding the alpha subunit of the human
 CC granulocyte-macrophage colony stimulating factor receptor.
 CC Implications for the evolution of the cytokine receptor
 CC superfamily.";
 CC RL J. BIOL. CHEM. 269:10905-10912(1994).
 CC

CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 CC FACTOR.
 CC CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. GM-CSF-R-ALPHA-2
 CC IS PROBABLY SOLUBLE.
 CC CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, GM-CSF-R-ALPHA-1 (SHOWN
 CC HERE) TO GM-CSF-R-ALPHA-3, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: X17648; G32089;
 CC EMBL: D26628; G522102;
 CC EMBL: D26618; G522102; JOINED.
 CC EMBL: D26619; G522102; JOINED.
 CC EMBL: D26620; G522102; JOINED.
 CC EMBL: D26621; G522102; JOINED.
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 CC EMBL: D26670; G522102; JOINED.
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 CC EMBL: D26700; G522102; JOINED.
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 CC EMBL: D26724; G522102; JOINED.
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DB 306 WSSWS 310

RESULT 14
ID LYSB_DROME STANDARD: PRT: 140 AA.
AC P37157;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE LYSOZYME A PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE),
GN LYSB.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYRIDOIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE: 94211204.
RA DAFRE S., KYLSTEN P., SAMAKOVIS C., HULTMARK D.;
RT "The lysozyme locus in Drosophila melanogaster: an expanded gene
family adapted for expression in the digestive tract.";
RL MOL. GEN. GENET. 242:152-162(1994).
CC -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
FOOD.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
N-ACETYL-D-GLUCOSAMINE AND N-ACETYLURAMIC ACID IN PEPTIDOLYCAN
HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC -1- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
SECOND LARVAL INSTARS.
CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL: Z22223; G288921; -
DR PIR: S32651; S32651.
DR PIR: S32726; S32726.
DR FLYBASE: FBgn0011201; LYSB.
DR PROSITE: PS00128; LACTALBUMIN_LYSOZYME; 1.
DR PFAM: PF00062; Lys; 1.
DR HSP: P11941; LMC.
KW HYDROLASE; GLYCOSIDASE; BACTERIOLYTIC ENZYME; SIGNAL;
KW MULTIGENE FAMILY.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 140 LYSOZYME A.
FT DISULFID 24 139 BY SIMILARITY.
FT DISULFID 45 129 BY SIMILARITY.
FT DISULFID 80 96 BY SIMILARITY.
FT DISULFID 92 110 BY SIMILARITY.
FT ACT_SITE 50 50 BY SIMILARITY.
FT ACT_SITE 50 50 BY SIMILARITY.
FT ACT_SITE 68 68 BY SIMILARITY.
FT CONFLICT 17 17 L.
FT CONFLICT 41 42 L -> F (IN G296039).
FT CONFLICT 41 42 AR -> NK (IN G296039).
SQ SEQUENCE 140 AA: 15650 MW: E049BD3D CRC32;

Query Match 96.8%; Score 30; DB 1; Length 140;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 120 WSAWS 124

RESULT 15
ID LYSB_DROME STANDARD: PRT: 140 AA.
AC 008694; P37158;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LYSOZYME B/C PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE),
GN LYSB AND LYSB.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYRIDOIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE: 94211204.
RA DAFRE S., KYLSTEN P., SAMAKOVIS C., HULTMARK D.;
RT "The lysozyme locus in Drosophila melanogaster: an expanded gene
family adapted for expression in the digestive tract.";
RL MOL. GEN. GENET. 242:152-162(1994).
CC -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
FOOD.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
N-ACETYL-D-GLUCOSAMINE AND N-ACETYLURAMIC ACID IN PEPTIDOLYCAN
HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC -1- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
SECOND LARVAL INSTARS.
CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL: Z22225; G289002; -
DR EMBL: Z22226; G296039; -
DR PIR: S32630; S32620.
DR PIR: S32643; S32643.
DR FLYBASE: FBgn0004425; LYSB.
DR FLYBASE: FBgn0004426; LYSB.
DR PROSITE: PS00128; LACTALBUMIN_LYSOZYME; 1.
DR PFAM: PF00062; Lys; 1.
DR HSP: P11941; LMC.
KW HYDROLASE; GLYCOSIDASE; BACTERIOLYTIC ENZYME; SIGNAL;
KW MULTIGENE FAMILY.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 140 LYSOZYME B.
FT DISULFID 24 139 BY SIMILARITY.
FT DISULFID 45 129 BY SIMILARITY.
FT DISULFID 80 96 BY SIMILARITY.
FT DISULFID 92 110 BY SIMILARITY.
FT ACT_SITE 50 50 BY SIMILARITY.
FT ACT_SITE 50 50 BY SIMILARITY.
FT ACT_SITE 68 68 BY SIMILARITY.
FT ACT_SITE 12 13 SG -> CA (IN G296039).
FT CONFLICT 17 17 L -> F (IN G296039).
FT CONFLICT 41 42 AR -> NK (IN G296039).
SQ SEQUENCE 140 AA: 15571 MW: 7FE5302F CRC32;

Query Match 96.8%; Score 30; DB 1; Length 140;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Fri Sep 17 14:52:37 1999

us-09-037-657-1.rsp

Page 10

QY 1 MSXNS 5
11 11
Db 120 MSANS 124

Search completed: September 17, 1999, 03:10:11
Job time: 291 sec

09/11/97 doc to back

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:10 ; Search time 64.1 Seconds

(without alignments)
152.611 Million cell updates/sec

Title: US-09-037-657-13

Sequence: 1 MPAGRGPVAVQASARRPPRL.....WRAMQSKHTRNOVLPARK 413

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2251	100.0%	413	1	M55011	Novel haemopoietin
2	2226.5	98.9%	425	1	M55012	Novel haemopoietin
3	2222.5	98.7%	425	1	M55012	Nucleotide sequence
4	2197.5	97.6	425	1	M70862	Rat zcytoirs protei
5	2098	93.2	425	1	M70861	Allelic variant of
6	2032	92.9	422	1	M70860	Human zcytoirs prot
7	2036	90.4	408	1	M55805	Amino acid sequenc
8	2006.5	89.1	385	1	M70841	Human zcytoirs vari
9	1982	88.0	392	1	M70840	Human zcytoirs vari
10	1970.5	87.5	388	1	M70839	Human zcytoirs vari
11	1967	87.4	389	1	M70840	Human zcytoirs vari
12	1966	87.3	389	1	M70840	Human zcytoirs vari
13	1965	87.3	389	1	M70851	Human zcytoirs vari
14	1964	87.3	389	1	M70852	Human zcytoirs vari
15	1963	87.2	389	1	M70846	Human zcytoirs vari
16	1963	87.2	389	1	M70847	Human zcytoirs vari
17	1963	87.2	389	1	M70849	Human zcytoirs vari
18	1962	87.2	389	1	M70848	Human zcytoirs vari
19	1961	87.1	389	1	M70853	Human zcytoirs vari
20	1954.5	86.8	385	1	M70842	Human zcytoirs vari
21	1772	78.7	350	1	M55015	Amino acid sequenc
22	1602	77.2	303	1	M70843	Human zcytoirs vari
23	1598	71.0	303	1	M70843	Human zcytoirs vari
24	1505	66.9	278	1	M55014	Human zcytoirs vari
25	696	30.9	186	1	M55016	Protein sequence o
26	577	25.6	155	1	M55015	Amino acid sequenc
27	331	14.7	622	1	R10793	Novel haemopoietin
28	331	14.7	622	1	R10793	Human prolactin re
29	330.5	14.7	211	1	R24273	Human gp130-delta-
30	329	14.6	918	1	R10545	Truncated human pr
31	329	14.6	918	1	R46233	Recombinant human
32	329	14.6	658	1	R45576	Human soluble glyce
33	329	14.6	918	1	R75368	Human gp130 splice
34	329	14.6	918	1	R85911	Human gp130 protei
35	329	14.6	951	1	M70798	gp130 N-terminal f
36	329	14.6	859	1	M70796	Human gp130-C-gamm
37	327.5	14.5	329	1	M17859	Rheumatoid arthrit
38	324.5	14.4	211	1	R22228	Truncated human pr
39	320.5	14.2	917	1	R26334	gp130. New mouse G
40	316	14.0	708	1	R37804	Human gp130 N-term
41	261.5	11.6	630	1	R3120	Tilapia prolactin
42	261.5	11.6	606	1	R3121	Tilapia prolactin
43	254.5	11.3	783	1	R11741	Granulocyte colony

ALIGNMENTS

44 254.5 11.3 801 1 R11742 Clone 25-1 encoded
45 254.5 11.3 836 1 R14255 Human GCSF recepto

RESULT 1
ID W55011 standard; Protein; 413 AA.
AC M55011;
DE 29-SEP-1998 (first entry)
DR Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN M09811225-A2.
PD 19-MAR-1998.
PE 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (DZIR/) DZIRGLMSKA H E.
PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J;
DR WPI; 98-260970/23.
DR N-PSDB; V27140.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and it's
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 100.0%; Score 2251; DB 1; Length 413;
Best Local Similarity 100.0%; Pred. No. 5.4e-186;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRGPVAVQASARRPPRLSSIMSPLLCYLGVPRGSGAHTAVSPDDPTLLIGSSIQ 60
DB 1 MPAGRGPVAVQASARRPPRLSSIMSPLLCYLGVPRGSGAHTAVSPDDPTLLIGSSIQ 60
QY 61 AHCSTHGTDPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGDVYCH 120
DB 61 AHCSTHGTDPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGDVYCH 120
QY 121 AADGSLTAGSCLYVGLPPKRPNISCMSNMKDLTCRMVPGAHGFFLTNTSLKYKLM 180
DB 121 AADGSLTAGSCLYVGLPPKRPNISCMSNMKDLTCRMVPGAHGFFLTNTSLKYKLM 180
QY 181 YGQDMTCCEHYTVGPHSCHIRPDALFTPEYIWEATNTLSARSADVTLTDVVTNDP 240
DB 181 YGQDMTCCEHYTVGPHSCHIRPDALFTPEYIWEATNTLSARSADVTLTDVVTNDP 240
QY 241 PPDVAVSRVGLLEDOLSTVWVSPALKDFLFOAKYQIRVEDSDVMKYVDVDSNQTSQR 300
DB 241 PPDVAVSRVGLLEDOLSTVWVSPALKDFLFOAKYQIRVEDSDVMKYVDVDSNQTSQR 300
QY 301 IAGLPGVTVFYOVACNPGYIGSKAGINSMHPTAASIPRSRPPGGVCEPRGGE 360
DB 301 IAGLPGVTVFYOVACNPGYIGSKAGINSMHPTAASIPRSRPPGGVCEPRGGE 360
QY 361 PSSGFVRRELKQFLGMLKHAVCNLSFRLYDQWRANQKSHKTRNOVLPARKL 413

Db 361 PSSGPVRELKQFLGLKKAHCNSLSPFLYDQWRAMQSKRTNRQVLPATL 413

RESULT 2
ID W55012 standard; Protein; 425 AA.
AC W55012.
DE 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN W09611225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGEMSKA H E.
PI Alexander W, Fabry U, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J.
DR WPI: 98-260970/23.
DR N-PSDB: V27141.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 84-87; 182pp; English.
CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 425 AA.

Query Match 98.9%; Score 2226.5; DB 1; Length 425;
Best Local Similarity 98.8%; Pred. No. 7.2e-184;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRPVAVQASARRPPRLSSLSWSPLLCVLGVPRGSGGATAVISPDPTLLIGSSIQ 60
DB 1 MPAGRPVAVQASARRPPRLSSLSWSPLLCVLGVPRGSGGATAVISPDPTLLIGSSIQ 60
QY 61 ATCSIHGDTPGATAGLTYLTNGRLRPSLSRLNTSTLALANLNGSROSGDNLYCH 120
DB 61 ATCSIHGDTPGATAGLTYLTNGRLRPSLSRLNTSTLALANLNGSROSGDNLYCH 120
QY 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLYVTTP 240
DB 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLYVTTP 240
QY 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
QY 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
QY 301 LAGLKPATYVYVQVRCNPFNGIYSGKAGIMSEMSHPTASTRSESRPGGVCPEPRGE 360
DB 301 LAGLKPATYVYVQVRCNPFNGIYSGKAGIMSEMSHPTASTRSESRPGGVCPEPRGE 360
QY 361 PSSGPVRELKQFLGLKKAHCNSLSPFLYDQWRAMQSKRTNRQVLPATL 413
DB 361 PSSGPVRELKQFLGLKKAHCNSLSPFLYDQWRAMQSKRTNRQVLPATL 413

RESULT 3
ID W59804 standard; Protein; 425 AA.
AC W59804.
DE 26-OCT-1998 (first entry)
DE Nucleotide sequence of the murine U4 protein.
KW Murine; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy.
OS Mus sp.
PN W09631811-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M,
PI WPI: 98-414109/35.
DR N-PSDB: V41688.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and autoimmune disease
PS Claim 9; Pages 26-27; 38pp; English.
CC This is the amino acid sequence of the murine U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 425 AA;

Query Match 98.7%; Score 2222.5; DB 1; Length 425;
Best Local Similarity 98.6%; Pred. No. 1.6e-183;
Matches 408; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 MPAGRPVAVQASARRPPRLSSLSWSPLLCVLGVPRGSGGATAVISPDPTLLIGSSIQ 60
DB 1 MPAGRPVAVQASARRPPRLSSLSWSPLLCVLGVPRGSGGATAVISPDPTLLIGSSIQ 60
QY 61 ATCSIHGDTPGATAGLTYLTNGRLRPSLSRLNTSTLALANLNGSROSGDNLYCH 120
DB 61 ATCSIHGDTPGATAGLTYLTNGRLRPSLSRLNTSTLALANLNGSROSGDNLYCH 120
QY 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEPKPENISCSWNRMDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLYVTTP 240
DB 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLYVTTP 240
QY 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
QY 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVAGLEDLSTRWVSPALAKDFLQAKQIRRVSDVDMKYVDVSNQTSR 300
QY 301 LAGLKPATYVYVQVRCNPFNGIYSGKAGIMSEMSHPTASTRSESRPGGVCPEPRGE 360
DB 301 LAGLKPATYVYVQVRCNPFNGIYSGKAGIMSEMSHPTASTRSESRPGGVCPEPRGE 360
QY 361 PSSGPVRELKQFLGLKKAHCNSLSPFLYDQWRAMQSKRTNRQVLPATL 413
DB 361 PSSGPVRELKQFLGLKKAHCNSLSPFLYDQWRAMQSKRTNRQVLPATL 413

RESULT 4
ID W70862 standard; Protein; 425 AA.

RESULT 6
W70860 6
ID W70860 standard; Protein; 422 AA.
AC W70860;
DT 17-MAR-1999 (first entry)
DE Human zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PE 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (Zymo) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehnner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR N-PSDB; V70894.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
PT in blood.
PS Claim 1: Page 66-67; 55pp; English.
CC The present sequence represents a protein designated zcyto5, which is
CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and the
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 422 AA;

Query Match 92.9%; Score 2092; DB 1; Length 422;
Best Local Similarity 93.5%; Pred. No. 2.7e-172;
Matches 387; Conservative 8; Mismatches 13; Indels 6; Gaps 3;
QY 1 MPAGRPVPAQASRRPRLSSLSMPLLCVGVPRGSGAHTAVISPDPTLLIGSSSLQ 60
DB 1 MPAGRGPAQASRRP-PLPLLL--LLLCVGAAPRAGSGAHTAVISPDPTLLIGSSSL 57
QY 61 ATCSIHGDTPGAATAGELVTLNGRRLLPSLSRLNTSTALALANLNGSGDNLVCH 120
DB 58 ATCSVHGDPGATAGELVTLNGRRLLPSLSRLNTSTALALANLNGSGDNLVCH 117
QY 121 ARDSGLIAGSCLVGLPPEKPNISCSNMKDLCTPAGHGETFLHTNSLKYKLRW 180
DB 118 ARDSGLIAGSCLVGLPPEKPNISCSNMKDLCTPAGHGETFLHTNSLKYKLRW 177
QY 181 YGQDNTCEHYHTVGHSHCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDP 240
DB 178 YGQDNTCEHYHTVGHSHCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDP 237
QY 241 PPDVAVSRVGGLEDOLSTRWSPPLAKDFLFQAKIQIRYVEDSDVMKVVDDVNSQTSR 300
DB 238 PPDVAVSRVGGLEDOLSTRWSPPLAKDFLFQAKIQIRYVEDSDVMKVVDDVNSQTSR 297
QY 301 LAGLPGTIVYFQVNCNFGIYGSKKAGIWSHPTAASIPRSRPPGGGVCPEPRGGE 360
DB 298 LAGLPGTIVYFQVNCNFGIYGSKKAGIWSHPTAASIPRSRPPGGGVCPEPRGGE 357
QY 361 PSSGVRRELKQFLGMLKKHAYCSNLSPRLYDQWRAMQKSHKTRNO---VLPA 411
DB 358 PSSGVRRELKQFLGMLKKHAYCSNLSPRLYDQWRAMQKSHKTRNO---VLPA 411

RESULT 7
W59805 7
ID W59805 standard; Protein; 408 AA.
AC W59805;
DT 26-OCT-1998 (first entry)
DE Amino acid sequence of the human U4 protein.
KW Human: U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW auto-immune disease; cancer; allergy.
OS Homo sapiens.
PN M09831811-A1.
PD 23-JUL-1998.
PE 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENE) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whiters M;
DR WPI; 98-414109/35.
DR N-PSDB; V41689.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and auto-immune disease
PS Claim 9; Pages 29-30; 38pp; English.
CC This is the amino acid sequence of the human U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 408 AA;

Query Match 90.4%; Score 2036; DB 1; Length 408;
Best Local Similarity 94.0%; Pred. No. 1.7e-167;
Matches 376; Conservative 7; Mismatches 11; Indels 6; Gaps 3;
QY 15 RPPRLSSLSMPLLCVGVPRGSGAHTAVISPDPTLLIGSSSLQATCSINGDPGATA 74
DB 1 RPP-PLPLLL--LLLCVGAAPRAGSGAHTAVISPDPTLLIGSSSLQATCSINGDPGATA 57
QY 75 EGLYTLNGRRLLPSLSRLNTSTALALANLNGSGDNLVCHARDGSLIAGSCLV 134
DB 58 EGLYTLNGRRLLPSLSRLNTSTALALANLNGSGDNLVCHARDGSLIAGSCLV 117
QY 135 GLPPEKPNISCSNMKDLCTPAGHGETFLHTNSLKYKLRWYQDNTCEHYHTVG 194
DB 118 GLPPEKPNISCSNMKDLCTPAGHGETFLHTNSLKYKLRWYQDNTCEHYHTVG 177
QY 195 PHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDPDPPDVHVSRYGLED 254
DB 178 PHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDPDPPDVHVSRYGLED 237
QY 255 QLSYRWSPPLAKDFLFQAKIQIRYVEDSDVMKVVDDVNSQTSRGLGTPGYFQV 314
DB 238 QLSYRWSPPLAKDFLFQAKIQIRYVEDSDVMKVVDDVNSQTSRGLGTPGYFQV 297
QY 315 RCNPFGIYGSKKAGIWSHPTAASIPRSRPPGGGVCPEPRGGEPSGVRRELKQFL 374
DB 298 RCNPFGIYGSKKAGIWSHPTAASIPRSRPPGGGVCPEPRGGEPSGVRRELKQFL 357
QY 375 GMLKKHAYCSNLSPRLYDQWRAMQKSHKTRNO---VLPA 411
DB 358 GMLKKHAYCSNLSPRLYDQWRAMQKSHKTRNO---VLPA 411

AC W70841; (first entry)
 DT 17-MAR-1999
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE.
 DR MPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1: Page 83-84; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 385 AA.

Query Match 89.1%; Score 2006.5; DB 1; Length 385;
 Best Local Similarity 98.4%; Pred. No. 5.5e-165;
 Matches 368; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 41 AHFAVISPDPPTLLIGSSSLQATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTSTA 100
 DB 1 AHFAVISPDPPTLLIGSSSLQATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTSTA 60
 QY 101 LALANLNGSRSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRWTP 160
 DB 61 LALANLNGSRSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRWTP 120
 QY 161 GAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 220
 DB 121 GAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 180
 QY 221 GSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVWVSPPALKDLFOAKYQIRX 280
 DB 181 GSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVWVSPPALKDLFOAKYQIRX 240
 QY 281 VADSDVMKYVDVSNQTSCLAGLKPRTYFYQVRCNPFGIYGSKAGIWMSEMSHTAAS 340
 DB 241 VADSDVMKYVDVSNQTSCLAGLKPRTYFYQVRCNPFGIYGSKAGIWMSEMSHTAAS 300
 QY 341 TRSRPFGGVCPEPGEPSGPRRLKQFLGWLKHAHCNSLSPFLYDQWRAMAK 400
 DB 301 TRSRPFGGVCPEPGEPSGPRRLKQFLGWLKHAHCNSLSPFLYDQWRAMAK 360
 QY 401 SHKTRNQ--VLPAA 411
 DB 361 SHKTRNQDEGLIPS 374

DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE.
 DR MPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 392 AA.

Query Match 88.0%; Score 1982; DB 1; Length 392;
 Best Local Similarity 92.9%; Pred. No. 7.3e-163;
 Matches 364; Conservative 5; Mismatches 7; Indels 16; Gaps 1;

QY 38 GSARHFAVISPDPPTLLIGSSSLQATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTS 97
 DB 1 GSARHFAVISPDPPTLLIGSSSLQATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTS 60
 QY 98 TALANLNGSRSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRWTP 157
 DB 61 TALANLNGSRSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRWTP 120
 QY 158 WTPGAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 217
 DB 121 WTPGAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 180
 QY 218 NTLGSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVWVSPPALKDLFOAKYQIR 277
 DB 181 NTLGSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVWVSPPALKDLFOAKYQIR 240
 QY 278 RYRVSDSDVMKYVDVSNQTSCLAGLKPRTYFYQVRCNPFGIYGSKAGIWMSEMSHT 337
 DB 241 RYRVSDSDVMKYVDVSNQTSCLAGLKPRTYFYQVRCNPFGIYGSKAGIWMSEMSHT 300
 QY 338 AASTPSESPFGGVCPEPGEPSGPRRLKQFLGWLKHAHCNSLSPFLYDQWRAMAK 397
 DB 301 AASTPSESPFGGVCPEPGEPSGPRRLKQFLGWLKHAHCNSLSPFLYDQWRAMAK 360
 QY 398 WOKSHKTRNQ-----VLPAA 413
 DB 361 WOKSHKTRNQHRTGSCPRADGARRVLPDXL 392

RESULT 9
 W70840
 W70840 standard; Protein; 392 AA.
 W70840;
 W70840;

RESULT 10
 W70839
 W70839 standard; Protein; 388 AA.
 AC W70839;
 DT 17-MAR-1999 (first entry)

DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KM cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 45
 FN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 80-81; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 388 AA;

Query Match 87.5%; Score 1970.5; DB 1; Length 388;
 Best Local Similarity 95.2%; Pred. No. 7e-162;
 Matches 359; Conservative 8; Mismatches 7; Indels 3; Gaps 1;
 QY 38 GSGAHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLTMTS 97
 DB 1 GSGAHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLTMTS 60
 QY 98 LALANLNGSRQSGDNLYCHARDGSLAGSCLYVGLPEKPEFNISCSWNNKDLTCRTP 157
 DB 61 LALANLNGSRQSGDNLYCHARDGSLAGSCLYVGLPEKPEFNISCSWNNKDLTCR 120
 QY 158 WTPGAGETFLHTNTSLKTKLWYGODNTCEYHTVGPCHIRKDLALFTPEIWEATNRL 217
 DB 121 WTPGAGETFLHTNTSLKTKLWYGODNTCEYHTVGPCHIRKDLALFTPEIWEATNRL 180
 QY 218 NPLGARSVDLTLDVLTVDPPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKQIR 277
 DB 181 NPLGARSVDLTLDVLTVDPPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKQIR 240
 QY 278 RRVEDSVDMKVVYDVDSNQTSCRLAGLKPQIVYFVOVRCNPFGISKKAGIWSMSHPT 337
 DB 241 RRVEDSVDMKVVYDVDSNQTSCRLAGLKPQIVYFVOVRCNPFGISKKAGIWSMSHPT 300
 QY 338 AASTPSEPPGGGVCERPGEGSSGPRRELKQFLGMLKKHAYCSNLSFRLDQWAMNOK 397
 DB 301 AASTPSEPPGGGVCERPGEGSSGPRRELKQFLGMLKKHAYCSNLSFRLDQWAMNOK 360
 QY 398 MOKSHKTRNQ-----VLPAL 411
 DB 361 MOKSHKTRNQDEGLIPS 377

RESULT 11
 W70850
 ID W70850 standard; Protein; 389 AA.

AC W70850:
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KM cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 45
 FN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 95-96; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.4%; Score 1967; DB 1; Length 389;
 Best Local Similarity 93.1%; Pred. No. 1.4e-161;
 Matches 362; Conservative 4; Mismatches 7; Indels 16; Gaps 1;
 QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLTMTS 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLTMTS 60
 QY 101 LALANLNGSRQSGDNLYCHARDGSLAGSCLYVGLPEKPEFNISCSWNNKDLTCRTP 160
 DB 61 LALANLNGSRQSGDNLYCHARDGSLAGSCLYVGLPEKPEFNISCSWNNKDLTCRTP 120
 QY 161 GAGETFLHTNTSLKTKLWYGODNTCEYHTVGPCHIRKDLALFTPEIWEATNRL 220
 DB 121 GAGETFLHTNTSLKTKLWYGODNTCEYHTVGPCHIRKDLALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDVLTVDPPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKQIR 280
 DB 181 GSARSDVLTLDVLTVDPPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKQIR 240
 QY 281 VEDSVDMKVVYDVDSNQTSCRLAGLKPQIVYFVOVRCNPFGISKKAGIWSMSHPTAS 340
 DB 241 VEDSVDMKVVYDVDSNQTSCRLAGLKPQIVYFVOVRCNPFGISKKAGIWSMSHPTAS 300
 QY 341 TPSEPPGGGVCERPGEGSSGPRRELKQFLGMLKKHAYCSNLSFRLDQWAMNOK 400
 DB 301 TPSEPPGGGVCERPGEGSSGPRRELKQFLGMLKKHAYCSNLSFRLDQWAMNOK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGAREVLPDL 389

RESULT 12
 W70844
 ID W70844 standard; Protein; 389 AA.
 AC W70844;

DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SO Sequence 389 AA;

Query Match 87.3%; Score 1966; DB 1; Length 389;
 Best Local Similarity 92.8%; Pred. No. 1.7e-161;
 Matches 361; Conservative 5; Mismatches 7; Indels 16; Gaps 1;
 QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGIYWTNGRRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGIYWTNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSWKNMDLTCRMT 160
 DB 61 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSWKNMDLTCRMT 120
 QY 161 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 220
 DB 121 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 180
 QY 221 GSARSDVLTLDVLTDDPPDVHVSRYVGLLEDOLSVRWSPPALKDFLFOAKQIYR 280
 DB 181 GSARSDVLTLDVLTDDPPDVHVSRYVGLLEDOLSVRWSPPALKDFLFOAKQIYR 240
 QY 281 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFGIYSGKAGIWSWSHPTAAS 340
 DB 241 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFGIYSGKAGIWSWSHPTAAS 300
 QY 341 TPRSRRPFGGACVCPRGEPSSGVRRELKQFLGMLKKHAYCSNLSRFLYDQWAMAK 400
 DB 301 TPRSRRPFGGACVCPRGEPSSGVRRELKQFLGMLKKHAYCSNLSRFLYDQWAMAK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGARREVLDPDL 389

RESULT 13
 W70851
 ID W70851 standard; Protein; 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)

DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SO Sequence 389 AA;

Query Match 87.3%; Score 1965; DB 1; Length 389;
 Best Local Similarity 92.5%; Pred. No. 2.1e-161;
 Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;
 QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGIYWTNGRRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGIYWTNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSWKNMDLTCRMT 160
 DB 61 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSWKNMDLTCRMT 120
 QY 161 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 220
 DB 121 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 180
 QY 221 GSARSDVLTLDVLTDDPPDVHVSRYVGLLEDOLSVRWSPPALKDFLFOAKQIYR 280
 DB 181 GSARSDVLTLDVLTDDPPDVHVSRYVGLLEDOLSVRWSPPALKDFLFOAKQIYR 240
 QY 281 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFGIYSGKAGIWSWSHPTAAS 340
 DB 241 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFGIYSGKAGIWSWSHPTAAS 300
 QY 341 TPRSRRPFGGACVCPRGEPSSGVRRELKQFLGMLKKHAYCSNLSRFLYDQWAMAK 400
 DB 301 TPRSRRPFGGACVCPRGEPSSGVRRELKQFLGMLKKHAYCSNLSRFLYDQWAMAK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGARREVLDPDL 389

RESULT 14
 W70852
 ID W70852 standard; Protein; 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.

KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (Zymo) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.3%; Score 1964; DB 1; Length 389;
 Best Local Similarity 92.5%; Pred. No. 2.6e-161;
 Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;

QY 41 AHAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRRLPSELRLNTSTA 100
 DB 1 AHAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRRLPSELRLNTSTA 60
 QY 101 LALANLNGSRQSGDNLYVCHARDGSLAGSCLYVGLPEKPNISCSWNNMFLTCRMT 160
 DB 61 LALANLNGSRQSGDNLYVCHARDGSLAGSCLYVGLPEKPNISCSWNNMFLTCRMT 120
 QY 161 GAHGETFLHTNLSKTKLRMGQDNCEHYHVGPHSCHIPDLALFTPEIWEATNRL 220
 DB 121 GAHGETFLHTNLSKTKLRMGQDNCEHYHVGPHSCHIPDLALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWMSPPALKDLFOAKQIIR 280
 DB 181 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWMSPPALKDLFOAKQIIR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLKGTYVFOVRCNPFGIYSKAKAGIWSMSHPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLKGTYVFOVRCNPFGIYSKAKAGIWSMSHPTAAS 300
 QY 341 TPRESERPGGGVCPEPSSGPRRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 400
 DB 301 TPRESERPGGGVCPEPSSGPRRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHTRGSCPRADGARREVLDPKL 389

KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (Zymo) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 89-90; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.2%; Score 1963; DB 1; Length 389;
 Best Local Similarity 92.5%; Pred. No. 3.1e-161;
 Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;

QY 41 AHAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRRLPSELRLNTSTA 100
 DB 1 AHAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRRLPSELRLNTSTA 60
 QY 101 LALANLNGSRQSGDNLYVCHARDGSLAGSCLYVGLPEKPNISCSWNNMFLTCRMT 160
 DB 61 LALANLNGSRQSGDNLYVCHARDGSLAGSCLYVGLPEKPNISCSWNNMFLTCRMT 120
 QY 161 GAHGETFLHTNLSKTKLRMGQDNCEHYHVGPHSCHIPDLALFTPEIWEATNRL 220
 DB 121 GAHGETFLHTNLSKTKLRMGQDNCEHYHVGPHSCHIPDLALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWMSPPALKDLFOAKQIIR 280
 DB 181 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWMSPPALKDLFOAKQIIR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLKGTYVFOVRCNPFGIYSKAKAGIWSMSHPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLKGTYVFOVRCNPFGIYSKAKAGIWSMSHPTAAS 300
 QY 341 TPRESERPGGGVCPEPSSGPRRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 400
 DB 301 TPRESERPGGGVCPEPSSGPRRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHTRGSCPRADGARREVLDPKL 389

Search completed: September 17, 1999, 03:08:12
 Job time: 303 sec

RESULT 15
 W70846
 ID W70846 standard; Protein: 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 19:07:29 ; Search time 68.96 Seconds

(without alignments)
4,462 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 MSXMS 5

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :

SPTREMBL.10:*
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_undefined:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	96.8	2894	1	Q58791	Q58791 methanococ
2	30	96.8	367	1	O59408	O59408 pyrococcus
3	30	96.8	2529	2	O25579	O25579 helicobacte
4	30	96.8	394	2	O33205	O33205 mycobacteri
5	30	96.8	528	2	P70733	P70733 acetomonas c
6	30	96.8	2399	2	O92K59	O92K59 helicobacte
7	30	96.8	455	3	O08231	O08231 saccharomyc
8	30	96.8	437	3	O12007	O12007 saccharomyc
9	30	96.8	446	4	O43384	O43384 homo sapien
10	30	96.8	410	4	O14431	O14431 homo sapien
11	30	96.8	333	4	O16564	O16564 homo sapien
12	30	96.8	1522	4	O60242	O60242 homo sapien
13	30	96.8	984	4	O60297	O60297 homo sapien
14	30	96.8	1584	4	O14514	O14514 homo sapien
15	30	96.8	206	4	O16354	O16354 homo sapien
16	30	96.8	422	4	O16542	O16542 homo sapien
17	30	96.8	4123	4	O75851	O75851 homo sapien
18	30	96.8	52	4	O16340	O16340 homo sapien
19	30	96.8	820	4	O92489	O92489 homo sapien
20	30	96.8	328	4	O95061	O95061 homo sapien
21	30	96.8	72	5	O43983	O43983 cryptospori
22	30	96.8	291	5	O20991	O20991 caenorhabdi
23	30	96.8	947	5	O44171	O44171 caenorhabdi
24	30	96.8	769	5	O00816	O00816 toxoplasma
25	30	96.8	254	5	O19092	O19092 caenorhabdi
26	30	96.8	654	5	O19284	O19284 caenorhabdi
27	30	96.8	860	5	O22580	O22580 caenorhabdi
28	30	96.8	660	5	O23832	O23832 cryptospori
29	30	96.8	687	5	O23729	O23729 cryptospori

30	30	96.8	238	5	O76510	O76510 cryptospori
31	30	96.8	1207	5	O21535	O21535 caenorhabdi
32	30	96.8	1444	5	O17591	O17591 caenorhabdi
33	30	96.8	947	5	O26262	O26262 caenorhabdi
34	30	96.8	229	6	O27950	O27950 bos indicus
35	30	96.8	229	6	O28205	O28205 bos taurus
36	30	96.8	425	6	O02661	O02661 bos taurus
37	30	96.8	234	6	O97888	O97888 bos taurus
38	30	96.8	162	9	O38069	O38069 bacterioph
39	30	96.8	375	9	O92X59	O92X59 mycobacteri
40	30	96.8	316	11	O35545	O35545 iatus norv
41	30	96.8	147	11	O61427	O61427 mus musculu
42	30	96.8	898	11	O08721	O08721 iatus norv
43	30	96.8	1077	11	O62217	O62217 mus musculu
44	30	96.8	432	11	O64385	O64385 mus musculu
45	30	96.8	191	12	O65971	O65971 cucurbit ap

ALIGNMENTS

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RESULT 1
ID      O58791      PRELIMINARY;      PRT; 2894 AA.
AC      O58791      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE      HYPOTHETICAL PROTEIN MJ1396.
GN      MJ1396.
OS      Methanococcus jannaschii.
OC      Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC      Methanococcus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 96337999.
RA      BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA      STUTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCYNE J.D.,
RA      KERVILANGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA      OVERBERGER R., KIRNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLOCKER A.,
RA      SCOTT J.L., GEORGEAGIS N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA      UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA      COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BOROVOSKY M.,
RA      KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT      "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT      jannaschii."
RL      Science 273:1058-1073(1996).
CC      -1- SIMILARITY: TO A.FULGIDUS AF2090-N AND IN THE C-TERMINAL, TO
CC      AF2090-C.
DR      EMBL; U67579; AAB99406.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 2894 AA; 322361 MW; 4CF899EC9 CRC32;

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Query Match. 96.8%; Score 30; DB 1; Length 2894;

Best Local Similarity 80.0%; Pred. No. 2.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5

DB 792 WSTWS 796

RESULT 2

ID O59408 PRELIMINARY; PRT; 367 AA.

AC O59408; 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DE 01-JAN-1999 (TREMBLrel. 09, Last annotation update)

GN PH1708. 367AA LONG HYPOTHETICAL PROTEIN.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-073;
 RX MEDLINE; 98344137.
 RA KARABAYAN Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
 RA YAMAMOTO S., SENE M., BABA S., KOSUGI H., HOSOTAMA A., NAGAI Y.,
 RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMITA M., OHKUBO Y.,
 RA FUJAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OUCHI A.,
 RA AOKI K., NAKAMURA Y., ROBE T.F., HORIKOSHI K., MASUCHI Y., SHIZUTA H.,
 RA KIRUCHI H.,
 RT "Complete sequence and gene organization of the genome of a
 RT hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76(1998).
 DR EMBL: AP000007; BAA30822.1;
 SQ SEQUENCE 367 AA; 41785 MW; B135C4EA CRC32;

Query Match 96.8%; Score 30; DB 2; Length 367;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXMS 5
 DB 262 WSXMS 266

RESULT 3
 ID 025579 PRELIMINARY; PRT; 2529 AA.
 AC 025579;
 DT 01-JAN-1998 (TRENBLREL. 05, Created)
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE TOXIN-LIKE OUTER MEMBRANE PROTEIN.
 GN HP0922.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695;
 RX MEDLINE; 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
 RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
 RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
 RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., MATTHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.,
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori."
 RL Nature 388:539-547(1997).
 DR EMBL: AE000602; AAD07969.1;
 DR TIGR: HP0922;
 KW Hypothetical protein.
 SQ SEQUENCE 2529 AA; 274561 MW; 31AE6AC CRC32;

Query Match 96.8%; Score 30; DB 2; Length 2529;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXMS 5
 DB 87 WSXMS 91

RESULT 4
 ID 033205 PRELIMINARY; PRT; 394 AA.

AC 033205;
 DT 01-JAN-1998 (TRENBLREL. 05, Created)
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE HYPOTHETICAL 39.8 KD PROTEIN.
 GN MTC1125.28C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA OLIVER K., HARRIS D.,
 RT Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA PARKHILL J., BARRELL B.G., RAJANDREAN M.A.,
 RT Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMAYER K., PASCOBELLA L.,
 RA BALSUBRAMANIAN V., HEIM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.,
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL: 298268; CAB10963.1;
 DR PFM; PF00823; PFI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 394 AA; 39778 MW; 3F5F0DD5 CRC32;

Query Match 96.8%; Score 30; DB 2; Length 394;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXMS 5
 DB 300 WSXMS 304

RESULT 5
 ID P70733 PRELIMINARY; PRT; 528 AA.
 AC P70733;
 DT 01-FEB-1997 (TRENBLREL. 02, Created)
 DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
 DT 01-JAN-1999 (TRENBLREL. 09, Last annotation update)
 DE ENDO-XYLANASE.
 GN XYN3.
 OS Aeromonas caviae.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
 OC Aeromonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W-61;
 RA OKAI N., NGUYEN D.V., NARAYAN R., MURAMOTO K., KANEKO J., TOMITA T.,
 RA KAMIO Y.,
 RT "Molecular cloning of new xylanase from Aeromonas caviae W-61."
 RT Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: D88553; BAA13641.1;
 KW Xylan degradation; Hydrolyase; Glycosidase.
 SQ SEQUENCE 528 AA; 58533 MW; 8D84F6AD CRC32;

Query Match 96.8%; Score 30; DB 2; Length 528;
 Best Local Similarity 80.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 517 MSTWS 521

RESULT 6

Q9ZKS9 PRELIMINARY; PRT: 2399 AA.
AC Q9ZKS9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PUTATIVE VACUOLATING CYTOTOXIN (VACA) PARALOG.
GN JHP0856.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-J99;
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUID B.C., DEJONGE B.L., CARREL G.,
RA TUMMINO P.J., CARUSO A., URICA-NICKELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRIST T.J.;
RT "Genomic Sequence Comparison of Two Unrelated Isolates of the Human
RT Gastric Pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
DR EMBL; AE001515; AAD06432.1;
SQ SEQUENCE 2399 AA; 260015 MW; 9B40A7A6 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 2; Length 2399;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 86 WSSWS 90

RESULT 7

Q08231 PRELIMINARY; PRT: 455 AA.
AC Q08231;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE CHROMOSOME XV READING FRAME ORF Y01072M.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
CC Saccharomycetaceae; Saccharomyces.
RN (1)
RN SEQUENCE FROM N.A.
RA ALEXANDRAKI D., KATSIOLOU C., TZERMIA M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA MITS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 274814; CA99082.1;
SQ SEQUENCE 455 AA; 52678 MW; 15DC3CC3 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 3; Length 455;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 78 WSAWS 82

RESULT 8

Q12007 PRELIMINARY; PRT: 437 AA.
AC Q12007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
DE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
GN ENRL.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
CC Saccharomycetaceae; Saccharomyces.
RN (1)
RP SEQUENCE OF 1-331 FROM N.A.
RA DELTUS H., HEBLING U., HOFMANN B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 176-437 FROM N.A.
RA WABUTT R., WEDLER H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA DELTUS H., HEBLING U.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RA DUESTERHOEF A., FLOETH M., FRITZ M., HILBERT H., MOESTL D.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE +
CC H(2)O.
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
DR EMBL; 275301; CA99725.1;
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DR EMBL; 275719; CA99999.1;
DR EMBL; 275720; CA99999.1;
DR EMBL; 275721; CA99999.1;
DR EMBL; 275722; CA99999.1;
DR EMBL; 275723; CA99999.1;
DR EMBL; 275724; CA99999.1;
DR EMBL; 275725

Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004160; AAC03417.1;
 DR PF00090: tsp_1; 3.
 FT NON_TER 1
 FT NON_TER 446 446
 SQ SEQUENCE 446 AA; 50444 MW; B793521E CRC32;

Query Match 96.8%; Score 30; DB 4; Length 446;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 396 WSSWS 400

RESULT 10
 ID 014431 PRELIMINARY; PRT; 410 AA.
 AC 014431;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE GM-CSF RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91352066.
 RA CROSTIER K.E., WONG G.G., MATHYX-PRYOR B., NATAN D.G., SIEFF C.A.;
 RT "A functional isoform of the human granulocyte/macrophage
 RT colony-stimulating factor receptor has an unusual cytoplasmic
 RT domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).
 DR EMBL: M64445; AAA35908.1;
 KW Transmembrane.
 SQ SEQUENCE 410 AA; 46901 MW; 30CE1609 CRC32;

Query Match 96.8%; Score 30; DB 4; Length 410;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 306 WSSWS 310

RESULT 11
 ID 016564 PRELIMINARY; PRT; 333 AA.
 AC 016564;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE GM-CSF RECEPTOR PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91376112.
 RA RAINES M.A., LIO U., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.;
 RT Identification and molecular cloning of a soluble human
 RT granulocyte-macrophage colony-stimulating factor receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91088339.
 RA ASHWORTH A., KRAFT A.;

RT "Cloning of a potentially soluble receptor for human GM-CSF."
 RL Nucleic Acids Res. 18:7178-7178(1990).
 DR EMBL: M73832; AAA35909.1;
 DR EMBL: X54935; CAA38697.1;
 KW Signal; Alternative splicing.
 FT SIGNAL 1
 FT CHAIN 23
 FT CHAIN 23
 SQ SEQUENCE 333 AA; 38438 MW; 48178079 CRC32;

Query Match 96.8%; Score 30; DB 4; Length 333;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 306 WSSWS 310

RESULT 12
 ID 060242 PRELIMINARY; PRT; 1522 AA.
 AC 060242;
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
 DT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
 DE BAI 3.
 GN BAI 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 98194217.
 RA SHIRATSUCHI T., NISHIMORI H., ICHISE H., NAKAMURA Y., TOKINO T.;
 RT "Cloning and characterization of BAI2 and BAI3, novel genes
 RT homologous to brain-specific angiogenesis inhibitor 1 (BAI1)."
 RL Cytogenet. Cell Genet. 79:103-108(1997).
 DR EMBL: AB005299; BAA25363.1;
 DR PFAM: PF00090; tsp_1; 4.
 SQ SEQUENCE 1522 AA; 171490 MW; 740FCBCE CRC32;

Query Match 96.8%; Score 30; DB 4; Length 1522;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 406 WSSWS 410

RESULT 13
 ID 060297 PRELIMINARY; PRT; 984 AA.
 AC 060297;
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
 DT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
 DE KIA00580 PROTEIN.
 GN KIA00580.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 98290545.
 RA NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
 RA OHARA O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.
RL DNA Res. 5:31-39(1998).
DR EMBL; AB011122; BAA25476.1; -
PFAM; PF00090; tsp_1; 4
SO SEQUENCE 984 AA; 110897 MW; 39A158F8 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 4; Length 984;
Matches 4; Conservative 0; Pred. No. 8e+02; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 406 WSSWS 410

RESULT 14

ID 014514 PRELIMINARY; PRT; 1584 AA.
AC 014514
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE BAI 1.
GN BAI 1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA NISHIMORI H., SHIRATSUCHI T., URANO T., KIMURA Y., KIYONO K.,
RA TATSUMI K., YOSHIDA S., ONO M., KIWANO M., NAKAMURA Y.;
RL Oncogene 0:0-0(1997).
DR EMBL; AB005297; BAA23647.1; -
DR PFAM; PF00090; tsp_1; 5.
SO SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 4; Length 1584;
Matches 4; Conservative 0; Pred. No. 1.2e+03; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 473 WSSWS 477

RESULT 15

ID 016354 PRELIMINARY; PRT; 206 AA.
AC 016354
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
cancer cell lines."
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL; S78505; AAB34470.1; -
DR PFAM; PF00041; fn3; 2.
FT NON_TER 1
SO SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match

96.8%; Score 30; DB 4; Length 206;

Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 191 WSSWS 195

Search completed: September 16, 1999, 20:40:03
Job time: 5594 sec

Db 265 DASTSQIPEDTASTRSSFTVODLKPTEYFIRIC-----MKEDGKGYSDMSEASG 319
QY 340 STPRSERP 347
Db 320 IT-YEDRP 326

RESULT 2

US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 14.6%; Score 329; DB 2; Length 708;
Best Local Similarity 28.6%; Pred. No. 1.2e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSLOATCSHG---DIPGATAGELVTLNGRRLPSELSTLNTSLALA 102
Db 31 ISPESPVQLHSNTAVCLAKCKMDYFHNANTYWKTHFTTPKQYTIINRTASSVT 90
QY 103 LANNGSROOSGDNLVCHARDGSIILAGSLYGLPPEKPNISCSWRNMKDLCTRWTPGA 162
Db 91 FTDIASINIQLTNIIILFQLEQNVYGIITISGLPEKRNLSICIYNEGKMKCENDGGR 150
QY 163 HGEFTLHTNYSKAKLWYGODNTCEHYTVGPHSCHIRPDALFTPEYIWEATNRIGS 222
Db 151 --ETHLETNTLSEWATKHFADCKAKRDT--PTSCYVDYSTYFVNIWVEAENALGK 206
QY 223 ARSDVTLVLDVYTTDPPDVHVSRYVGLDOLSVRWSPPALKDFLPAKQIQRIVE 282
Db 207 VTSQHINFDVYKPKPNNHLSVINESEELSIKLTWTN-PSIKSYIT-LKTNIOYRTR 264

QY 283 DSYDMKVY---DVSNOTSCLAGLKPGTYFVGRNCNPFICYSKAGIWSMHPRA 339
Db 265 DASTSQIPEDTASTRSSFTVODLKPTEYFIRIC-----MKEDGKGYSDMSEASG 319
QY 340 STPRSERP 347
Db 320 IT-YEDRP 326

RESULT 3

PCT-US95-06530-2
Sequence 2, Application PC/RUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 14.6%; Score 329; DB 3; Length 708;
Best Local Similarity 28.6%; Pred. No. 1.2e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSLOATCSHG---DIPGATAGELVTLNGRRLPSELSTLNTSLALA 102
Db 31 ISPESPVQLHSNTAVCLAKCKMDYFHNANTYWKTHFTTPKQYTIINRTASSVT 90
QY 103 LANNGSROOSGDNLVCHARDGSIILAGSLYGLPPEKPNISCSWRNMKDLCTRWTPGA 162
Db 91 FTDIASINIQLTNIIILFQLEQNVYGIITISGLPEKRNLSICIYNEGKMKCENDGGR 150
QY 163 HGEFTLHTNYSKAKLWYGODNTCEHYTVGPHSCHIRPDALFTPEYIWEATNRIGS 222
Db 151 --ETHLETNTLSEWATKHFADCKAKRDT--PTSCYVDYSTYFVNIWVEAENALGK 206
QY 223 ARSDVTLVLDVYTTDPPDVHVSRYVGLDOLSVRWSPPALKDFLPAKQIQRIVE 282

Db 207 VTSCHINFDVYKVPNPHNLVINESELSIKLWLN-PSIKSVII-LKYNIOYRTK 264
QY 283 DSYDMKVY---DVSNOTSCLAGLKPQTYVOVRCNPFQISKKGKAGISEMHP1AA 339
Db 265 DASWWSIPEDRSTSTSSFFVODLKPFTEYFVIRK-----MEDGKGYSWDSSEANS 319
QY 340 STPSRSP 347
Db 320 IT-YEDRP 326

RESULT 4

US-07-923-976-4
Sequence 4, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA: JP 176629/1990
APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500

TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-923-976-4

Query Match 11.3%; Score 254.5; DB 1; Length 836;
Best Local Similarity 28.9%; Pred. No. 1.5e-15;
Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 16;

QY 21 SLSWSPLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTGATAE-GLYW 79
Db 8 SLTWALIIILL-----PGSIECGHSVSAPYVHLGDPITASCIIKQNSHLDPEQILW 63
QY 80 TLNGRRLPSELSELN--TSTLALALANLNGSRQSGDNVYCHARDS---ILAGSCLYV 134
Db 64 RLGAELQPGRGQRRLSDGTQESITILPHLNHTQA---FLSCCLMNGNSLQIILDQVELRA 119

QY 135 GLPPEKPEINIS-WSRNMKDLTCRWTPGANGFTLHNTYSIK-YKLWYGO---DNICEE 189
Db 120 GYPALPNNLSLMLNLTSSLICQWEPG--ETHLPSTFLKSKSGKNCQTOGDSILDC 177
QY 190 YHTVGPSCHIP-KDLLETPYEIWEATNRLSGARSVDLILDLVDV-----TTDP 240
Db 178 VPKDGOSHCIPRKHLHLLYQNMGIWQAEMLGTSMSPOLCLDNDVYKLEPPMLRTMDP 237
QY 241 PPDVYSRVGGLDQLSVRWVSPALDFFLEQANKYQIRYVE-DSYDMKVYDVSNOT-S 298
Db 238 SPEAAPQAGCLQ-----LCW--EPMQPLHINQKCELRHKQREASAMALVGPPLLEALQ 291
QY 299 CRLAGLKPQTYVOVRCNPFQISKKGKAGISEMWS 334
Db 292 YELGGLPATATYTLQIRCIKRWPL-----PGHWSWDS 322

RESULT 5

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA: JP 176629/1990
APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500

TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-923-976-6

Query Match 11.3%; Score 254.5; DB 1; Length 771;
Best Local Similarity 28.9%; Pred. No. 1.3e-15;
Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 16;

QY 21 SLSWSPLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTGATAE-GLYW 79
Db 8 SLTWALIIILL-----PGSIECGHSVSAPYVHLGDPITASCIIKQNSHLDPEQILW 63
QY 80 TLNGRRLPSELSELN--TSTLALALANLNGSRQSGDNVYCHARDS---ILAGSCLYV 134
Db 64 RLGAELQPGRGQRRLSDGTQESITILPHLNHTQA---FLSCCLMNGNSLQIILDQVELRA 119

Db 8 SLTMAALLILL----PGSLECGHISVSAPIVHLDPTIASCIIKQNSHLDPEQIIM 63
 QY 80 TLNGRLPSELRLN--ISTALALANLNGSRQSGDNLYCHARGS---ILAGSCLYV 134
 Db 64 RLGAELQPGGROQRSLDQESITTLPHLNHTQA---FLSCCLMNGNSLIQIDQVELRA 119
 QY 135 GLPPEKPFNISC-WSRNMKDLTCRWTPGAHGEFTHTNYSK-YKLRWGO---DNICEE 189
 Db 120 GYPAIPHLNLSCLMNLITSSILCQWEPGP--ETHLPSTLTKSFKSRGNCQTOGDSILDC 177
 QY 190 YHTVPHSCHIP-KDLAFETPEIWEATNRLGSARSVDLTLDVLYV-----TTDP 240
 Db 178 VPKDQSHCCIPRKHLILLYQNGIWIWQAENALGTSMSPOLCLDPMDVYKLEPMLRTMDP 237
 QY 241 PDVAVSRVGLGLEDLSRWVSPPAKDLFOAKIQIRYVE-DSVDRKVVDDVSNQT-S 298
 Db 238 SPEAAPQAGCLQ---LCW--EPWQPGIHNOKCELRRKPRGEGASWALVGPLLEALQ 291
 QY 299 CRLAGLKPGTYEVOVRCNPFGIYSKKGIMSEWS 334
 Db 292 YELCGLPRATATYTIQIRCIKRWPL-----PGHWSWMS 322

RESULT 6
 US-07-923-976-8
 ; Sequence 8, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullat & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923, 976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/J991/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 514853
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1500
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 863 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-923-976-8

Query Match 11.3%; Score 254.5; DB 1; Length 863;
 Best Local Similarity 28.9%; Pred No. 1.5e-15;
 Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 15;
 QY 21 SLSMSPLLICVLGVPGGSGAHTAVISPODPTLLIGSSIQANCSIHDPGATAE-GLYV 79
 Db 8 SLTMAALLILL----PGSLECGHISVSAPIVHLDPTIASCIIKQNSHLDPEQIIM 63
 QY 80 TLNGRLPSELRLN--ISTALALANLNGSRQSGDNLYCHARGS---ILAGSCLYV 134
 Db 64 RLGAELQPGGROQRSLDQESITTLPHLNHTQA---FLSCCLMNGNSLIQIDQVELRA 119
 QY 135 GLPPEKPFNISC-WSRNMKDLTCRWTPGAHGEFTHTNYSK-YKLRWGO---DNICEE 189
 Db 120 GYPAIPHLNLSCLMNLITSSILCQWEPGP--ETHLPSTLTKSFKSRGNCQTOGDSILDC 177
 QY 190 YHTVPHSCHIP-KDLAFETPEIWEATNRLGSARSVDLTLDVLYV-----TTDP 240
 Db 178 VPKDQSHCCIPRKHLILLYQNGIWIWQAENALGTSMSPOLCLDPMDVYKLEPMLRTMDP 237
 QY 241 PDVAVSRVGLGLEDLSRWVSPPAKDLFOAKIQIRYVE-DSVDRKVVDDVSNQT-S 298
 Db 238 SPEAAPQAGCLQ---LCW--EPWQPGIHNOKCELRRKPRGEGASWALVGPLLEALQ 291
 QY 299 CRLAGLKPGTYEVOVRCNPFGIYSKKGIMSEWS 334
 Db 292 YELCGLPRATATYTIQIRCIKRWPL-----PGHWSWMS 322

RESULT 7
 US-07-923-976-2
 ; Sequence 2, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullat & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923, 976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/J991/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 514853
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1500
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 837 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-2

Query Match 11.28; Score 252.5; DB 1; Length 837;
Best Local Similarity 27.8%; Pred. No. 2,3e-15;
Matches 107; Conservative 56; Mismatches 163; Indels 59; Gaps 20;

29 LCYGVPRGSGAHTAVISPODPLLLGSSLAQATCSIHGDPGATAG-LYWTNGRRLL-87
14 LITLLRLRSLSCGHIFIS-PYVRLGDPYLAACITISPNCSKLDQOAKILMRLODEPIQ-71
87 PSELSRL--NTSTLALALANLNGSRQSGDNVCHARDGSIILAGSLYGLPREKFN1144
72 PGRQHHLPGQTQESLITLHLANT-QAFLECLVPMEDSVOLQOAEHLHAGYPPASSNL130
145 SCMSR-NMKDLTRMTPGAGETFLHNTSLK-YKLR--WYGDNCEHYTVGPHSCH199
131 SCMLHLTNSLVQMEGCP--ETHLPSTFKSPRADQYQGDITIPDVAKKRNCS188
200 IP-KDLALFPYILWEATNRLSARSVDVLTLDVLYTTDPP-----PDVHVSRYG250
189 IPKKNLLLYQYMAIWOAEKMLSSSPKLCLEPMDVYKLEPMLQALDIGPDVYSHQPG248
251 GLEDQSVRWVS-PPALKDFLFOAKQIERYVE-DSYDMKYVDVY-SNOTSCLRLAGLRPG307
249 CL-----WLSKPKPKPSYMEQECLEKIQPOLKGNMTLVHLPSKQOFLCGLHQA301
308 TYFVQVRCNPFEGISYKSKAGIWSMS-----HPT-AASTPRSERPGGVCPEPRGCEP361
302 PYVTLQMRG-----IRSSLEGFWSPPSGQLAPRTMKAPIRLDT-----WCKKRLDP350
362 SS-----GPRRELKQFLGML377
351 GYVSVOLFWKPTPLQEDSGQIQGYL375

RESULT 8

US-07-865-878A-4

Sequence 4, Application US/07865878A

Patent No. 5332672

GENERAL INFORMATION:

APPLICANT: Yancopoulos, George D. et al.

TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
Factor/Receptor Complex

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/865,878A

FILING DATE: 19911202

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/801/562

FILING DATE: 02-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-082

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-865-878A-4

Query Match 9.8%; Score 220.5; DB 1; Length 372;
Best Local Similarity 26.2%; Pred. No. 6.8e-13;
Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPQDPTLL-----IGSSLAQATCSIHGDPGATAGLYWTNGRRLSLS91
15 AAAYVYAGHSPQENAPHQYERLGSVYTLPGCTANMDAAVT-----WRVNGTDLAPD--68
92 RLNTSTLALALANLNGSRQSGDNVCHARDGSIILAGS-CLYVGLPREKFNISCMRN150
68 -LNGSGLV-----LHGLELGHSGLYACFHRDSMHLRHQVYLHVGLPREPV-LSCRSNT120
151 M-KDLQCRW-----TPGAGHETFLHNTSLKYLKRTGQDNVCEHYTVGPHSCHIRK202
121 YPKGFICSMHLPPTIIPNTFNTVYLGSKIM-----VCEKDAL-KNRCHI-R167
203 DLALFT--PYEIWEATNRLSARSVDVLTLDVLYTTDPPDVHVSRYGLEDQSVRW260
168 YMLFSTIKKVISISVSNLGH-NATAITDEFTYKPPDPPEVAVARPPSNRRLLEVIM226
261 VSPPALKD-FLFOAKQIERYVEDSVDMKYVDVSNQTSORLAGLPGTYFVQVRCNPF319
227 QTSPTWDPDSFPLKEFLRPLILQWQH-V-ELSDGTALHTIDAVAGEXYLIQVAAK--284
320 GIGSKKAGIWSMS-----HPTAASIPRSEPRGPGGVCPEPRG358
284 ----DNEIGTWSMVAHAHTPTEPRHLTTEQAARETTSTSLAPPPTKIDP--338
359 GEPSSG364
338 GELGSG343

RESULT 9

US-07-676-647-2

Sequence 2, Application US/07676647

Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squitro, Stephen P.

APPLICANT: Furtth, Mark E.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676,647

FILING DATE: 19910328

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-676-647-2

Query Match 9.8%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 6.8e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

QY 41 AHTAVI-----SPDPTLL-----IGSSLQATCSIHGDTFGATAEGLYWTNGRLPSELS 91
 DB 15 AAAAVYAOHSPQEAHPHYERLGSVDYLPCTANMDAAVT-----WRVNGTDLAPD-- 68
 QY 92 RLINTSTLALANLNGSRQSGDNLYCHARDGSIAGS-CLYVGLPPEKPPENISQMSRN 150
 DB 68 -LINGSQLV-----LHGLELGHSGLYACFHRDSMHLRHQVLLHVGLPPEPV-LSCRSM 120
 QY 151 M-KDLICRW-----TPGAGETFLHTNLSLKYLRWIGQNTCEHYHTVGPCHIRP 202
 DB 121 YPKGFYCSWHLPTPIYIPNTFNTVLHGSKIM-----VCEKDPAL-KNRCHI-R 167
 QY 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVDTTPDPDVHRSRGLEDOLSVYM 260
 DB 168 YMLFSTIKKVISISVSNLGH-NATAITDEFITKPPDPENAVARPPSPNRRLLEVTV 226
 QY 261 VSPPALKD-FLFOAKQIQRVEDSVDMKYVDVSNQSCRLAGLPGTVYEVQVQCNPF 319
 DB 227 QTPSTWDPDESFLKFLKRLRPILDDQOHV-ELSDGTHTITDAAGKEYIIQVAAK-- 284
 QY 320 GIYSKKGAIWSEMS-----HPTAASPPRSERPDPGGVCEPRG 358
 DB 284 ----DNEIGTWSMSVAHAATPTEPRHLTTEAQAETTTSTSLAPPPTTKICDP-- 338
 QY 359 GEPSSG 364
 DB 338 GELGSG 343

RESULT 10
 US-08-449-329-2
 Sequence 2, Application US/08449329
 Patent No. 5648334
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn, Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,329

FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/700,677
 FILING DATE: 15-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-449-329-2

Query Match 9.8%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 6.8e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

QY 41 AHTAVI-----SPDPTLL-----IGSSLQATCSIHGDTFGATAEGLYWTNGRLPSELS 91
 DB 15 AAAAVYAOHSPQEAHPHYERLGSVDYLPCTANMDAAVT-----WRVNGTDLAPD-- 68
 QY 92 RLINTSTLALANLNGSRQSGDNLYCHARDGSIAGS-CLYVGLPPEKPPENISQMSRN 150
 DB 68 -LINGSQLV-----LHGLELGHSGLYACFHRDSMHLRHQVLLHVGLPPEPV-LSCRSM 120
 QY 151 M-KDLICRW-----TPGAGETFLHTNLSLKYLRWIGQNTCEHYHTVGPCHIRP 202
 DB 121 YPKGFYCSWHLPTPIYIPNTFNTVLHGSKIM-----VCEKDPAL-KNRCHI-R 167
 QY 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVDTTPDPDVHRSRGLEDOLSVYM 260
 DB 168 YMLFSTIKKVISISVSNLGH-NATAITDEFITKPPDPENAVARPPSPNRRLLEVTV 226
 QY 261 VSPPALKD-FLFOAKQIQRVEDSVDMKYVDVSNQSCRLAGLPGTVYEVQVQCNPF 319
 DB 227 QTPSTWDPDESFLKFLKRLRPILDDQOHV-ELSDGTHTITDAAGKEYIIQVAAK-- 284
 QY 320 GIYSKKGAIWSEMS-----HPTAASPPRSERPDPGGVCEPRG 358
 DB 284 ----DNEIGTWSMSVAHAATPTEPRHLTTEAQAETTTSTSLAPPPTTKICDP-- 338
 QY 359 GEPSSG 364
 DB 338 GELGSG 343

RESULT 11
 US-08-445-073-2
 Sequence 2, Application US/08445073
 Patent No. 5849897
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073

FILING DATE:

CLASSIFICATION: 435

Prior APPLICATION DATA:

APPLICATION NUMBER: US 07/676,647

FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-048

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-445-073-2

Query Match 9.88; Score 220.5; DB 2; Length 372;

Best Local Similarity 26.28; Pred. No. 6.8e-13;

Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDDPTLL-----IGSSLAQATCSIHGDTPGATAEGLYWTNGRLRPSSELS 91
15 AAAAVYVQRRHSPOEAPHVQYERLGSVDTLPCGTANMDAAYT-----WRVNGTDLADP-- 68
92 RLNTSTLALANLNGSRQSGDNLVCHARDGSIAGS-CLYVGLPEPEKPFNISCNRSN 150
68 -LNGSGLV-----LHGELGHSGLYACFHRDSWHLRHOVLHVGLEPPEPV-LSCSRNT 120
151 M-KDLTCRW-----TPGAGETFLHTNYSIKYKLRWYGODNTCEEYHTVGPSCHIPK 202
121 YPKGFYSWHLPTFTYIPNTENVYLVGSKIM-----VCEKDPAL-KNRCHI-R 167
203 DLALFT--PEIWEATNRUGSARSVDLTLDVYTTDPPDVHVSRYGLEDOLSVRW 260
168 YMLFSTIKYKVSISVSNAIGH-NATAITDEFITVAKDPDENVAVRPVSNPRRLLEVTV 226
261 VSPPALMD-FLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKFGTYFVQVRCNPF 319
227 QTPSTWDPDSFPLKFLRYRPLILDQMOHV-ELSDGTAHTITDAYAKKEYIIQVAAK-- 284
320 GIYSKKAGIWSMS-----HPTASTPRSRPRPGGVCPCPRG 358
284 ----DNELGWSMSVAHAHATPWTPEERHLLTTEAOAAETTTSTSSILAPPPTTKICDP-- 338
359 GEPSSG 364
338 GELGSG 343

RESULT 12
PCT-US91-03896-2

Sequence 2, Application PC/TUS9103896

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Futh, Mark E.

APPLICANT: Yancopoulos, George D.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penzie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896

FILING DATE: 19910603

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-065-228

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: AMINO ACID

TOPOLOGY: unknown

MOLECULE TYPE: protein

PCT-US91-03896-2

Query Match 9.88; Score 220.5; DB 3; Length 372;

Best Local Similarity 26.28; Pred. No. 6.8e-13;

Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDDPTLL-----IGSSLAQATCSIHGDTPGATAEGLYWTNGRLRPSSELS 91
15 AAAAVYVQRRHSPOEAPHVQYERLGSVDTLPCGTANMDAAYT-----WRVNGTDLADP-- 68
92 RLNTSTLALANLNGSRQSGDNLVCHARDGSIAGS-CLYVGLPEPEKPFNISCNRSN 150
68 -LNGSGLV-----LHGELGHSGLYACFHRDSWHLRHOVLHVGLEPPEPV-LSCSRNT 120
151 M-KDLTCRW-----TPGAGETFLHTNYSIKYKLRWYGODNTCEEYHTVGPSCHIPK 202
121 YPKGFYSWHLPTFTYIPNTENVYLVGSKIM-----VCEKDPAL-KNRCHI-R 167
203 DLALFT--PEIWEATNRUGSARSVDLTLDVYTTDPPDVHVSRYGLEDOLSVRW 260
168 YMLFSTIKYKVSISVSNAIGH-NATAITDEFITVAKDPDENVAVRPVSNPRRLLEVTV 226
261 VSPPALMD-FLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKFGTYFVQVRCNPF 319
227 QTPSTWDPDSFPLKFLRYRPLILDQMOHV-ELSDGTAHTITDAYAKKEYIIQVAAK-- 284
320 GIYSKKAGIWSMS-----HPTASTPRSRPRPGGVCPCPRG 358
284 ----DNELGWSMSVAHAHATPWTPEERHLLTTEAOAAETTTSTSSILAPPPTTKICDP-- 338
359 GEPSSG 364
338 GELGSG 343

RESULT 13
US-08-685-118-2

Sequence 2, Application US/08685118

Patent No. 5840530

GENERAL INFORMATION:

APPLICANT: Gudley, Ulrich A

APPLICANT: Presky, David R

TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 9.7%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.5e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 LLIGSLATGCSIHGDTGATAGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILGSLVITCSL-----KPRGCFHYSRRNKLILYFDRRINHHGSHLSNSQYTGJPL 94
QY 95 NSTLALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISGWSRNMK-D 153
DB 95 GTTLFVCKLACINSEIQ-----ICGAELFVGVAEPQPNLSCIQAGEGT 140
QY 154 LTCRMTGPAHGETPLHNTSLKY---KLRYGQ--DNICEYHTVG-----PHSCHI 200
DB 141 VACTWERRG--DTHLYTEYTLQSGPKNLTWOKCKDIYC-DYLDGGINLPESPESNFT 197
QY 201 PKDALFTPEIWEATNRLGARSADVLTLDVYTTDPPPDVHVSRYGLEDQLSVRW 260
DB 198 AK-----VTAVNSLGSSSSSLPSTFTFLDIVRPLPMDIRIKOKASVSCITLW 246
QY 261 VSPPLAKDFLOAKQOIRYVEDSVDMKVVDDVSNQTSCLAGLPGTVYVQVRCNPG 320
DB 247 -----RDEGLVLLNRLRYRSPNSRLMMNVNTAKAGRHLDLDLPFTYEYEQI-SSKLH 299
QY 321 IYGSKKAIGWSESHPTAATPRSERPG 348
DB 300 LY-----KGSWSDWSESLRAQTPEEPPTG 323

RESULT 14
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5832176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 9.7%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.5e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 LLIGSLATGCSIHGDTGATAGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILGSLVITCSL-----KPRGCFHYSRRNKLILYFDRRINHHGSHLSNSQYTGJPL 94
QY 95 NSTLALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISGWSRNMK-D 153
DB 95 GTTLFVCKLACINSEIQ-----ICGAELFVGVAEPQPNLSCIQAGEGT 140
QY 154 LTCRMTGPAHGETPLHNTSLKY---KLRYGQ--DNICEYHTVG-----PHSCHI 200
DB 141 VACTWERRG--DTHLYTEYTLQSGPKNLTWOKCKDIYC-DYLDGGINLPESPESNFT 197
QY 201 PKDALFTPEIWEATNRLGARSADVLTLDVYTTDPPPDVHVSRYGLEDQLSVRW 260
DB 198 AK-----VTAVNSLGSSSSSLPSTFTFLDIVRPLPMDIRIKOKASVSCITLW 246
QY 261 VSPPLAKDFLOAKQOIRYVEDSVDMKVVDDVSNQTSCLAGLPGTVYVQVRCNPG 320
DB 247 -----RDEGLVLLNRLRYRSPNSRLMMNVNTAKAGRHLDLDLPFTYEYEQI-SSKLH 299
QY 321 IYGSKKAIGWSESHPTAATPRSERPG 348
DB 300 LY-----KGSWSDWSESLRAQTPEEPPTG 323

RESULT 15
US-08-419-652-6
Sequence 6, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chue, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05 ; Search time 49.27 Seconds

(without alignments)
335,844 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251
Sequence: 1 MPAGRPVAVQASRRPRPL.....MPAMQKSHKTRNYLPKAL 413

Scoring table: BLOSUM62

Searched: 122810 seqs, 40055486 residues

Database :

PIR-60:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	14.7	622	A40144	prolactin receptor
2	329	14.6	918	A35337	membrane glycoprot
3	324.5	14.4	206	A57018	prolactin receptor
4	319.5	14.2	917	I49699	glycoprotein 130 -
5	317.5	14.1	918	A44257	interleukin-6 sign
6	314	13.9	830	I50455	interleukin-6 sign
7	312	13.9	610	A34631	lactogen receptor
8	312	13.9	610	A36116	prolactin receptor
9	312	13.9	412	A41070	prolactin receptor
10	312	13.9	310	A29884	prolactin receptor
11	307.5	13.7	616	A30304	prolactin receptor
12	307.5	13.7	303	I77524	prolactin receptor
13	307.5	13.7	292	I77525	prolactin receptor
14	307.5	13.7	608	I53269	prolactin receptor
15	306	13.6	831	J01655	prolactin receptor
16	302.5	13.4	581	I45971	prolactin receptor
17	261.5	11.6	630	I51086	prolactin receptor
18	254.5	11.3	783	JH0329	granulocyte colony
19	254.5	11.3	771	B38252	granulocyte colony
20	254.5	11.3	863	C38252	granulocyte colony
21	252.5	11.2	837	A34898	granulocyte colony
22	234	10.4	372	I58141	ciliary neurotroph
23	220.5	9.8	372	I58141	ciliary neurotroph
24	209.5	9.3	422	I37891	interleukin-11 rec
25	208.5	9.3	432	I48343	interleukin-11 rec
26	203.5	9.0	460	JL0145	growth promoting a
27	203.5	8.9	468	A41242	interleukin-6 rece
28	200.5	8.9	468	A41242	interleukin-6 rece
29	199	8.8	156	A33868	prolactin receptor
30	194.5	8.6	440	JL0144	interleukin-6 rece
31	192.5	8.6	579	B45266	interleukin-6 rece
32	192.5	8.6	635	A45266	interleukin-6 rece
33	191.5	8.5	894	S68437	MPL-K protein prec
34	191.5	8.5	900	S68440	leptin receptor (V
35	191.5	8.5	805	S68441	leptin receptor (V
36	190	8.4	1097	S11308	leptin receptor (V
37	190	8.4	625	S35317	leukemia inhibitor
38	190	8.4	150	B34631	hematopoietic grow
39	188.5	8.4	894	JC4797	lactogen receptor
					leptin receptor pr

40 188.5 8.4 1162 2 PC4184 leptin receptor, O
41 188.5 8.4 805 3 JC4897 leptin receptor, O
42 186 8.3 626 2 S37622 proto-oncogene - m
43 185 8.2 1092 2 JX0312 differentiation-st
44 185 8.2 719 2 JC2181 differentiation-st
45 182 8.1 895 2 S74225 leptin receptor, I

ALIGNMENTS

RESULT 1

A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
C:Accession: A40144
R:Boutin, J.M.; Ederly, M.; Shirota, M.; Jolicoeur, C.; Lesneur, L.; Ali, S.; Gould
Mol. Endocrinol. 3:1455-1461, 1989
N>Title: Identification of a cDNA encoding a long form of prolactin receptor in hu
A:Reference number: A40144; MUID:90114212
A:Accession: A40144
A:Molecule type: mRNA
A:Residues: 1-622 <BOD>
A:Cross-references: GB:M31661; NID:g190361; PID:g190362
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAY>
F:59,104,233/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 14.7%; Score 331; DB 2; Length 622;
Best Local Similarity 37.5%; Pred. No. 3.5e-19;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILASGLVYG-LPPEKPFNISCMSRMKDLCTRMFGAGHFLHTNYLTKLRWYGOD 184
DB 15 LFLNLCNLGQLPQKPELFCRSPKKEFTCTWNRGTGG--LPINLYLTHRGETLM 72
QY 185 NTCEHYHTVGPSPHCHPNK-LALFTPEYELWEATNRLGARSVDLTLDVDTTDPDP 243
DB 73 HECPDITGGPNSCHGKQYTSMMRTYIMVNAITNGSSFDDELVDVDTYIVQDPPE 132
QY 244 VHSRYGGLLEDOLSVRW--SPALKDF--LPQAKYQIRYVEDSVDMKVVDVSNOTS 298
DB 133 LAV-EVKQPEDKRPYLMIMSPPTLIDLCTGMFTLLYEIRLPEKAEWE-IHFAQOTE 190
QY 299 CRLAGIKPQTYFVYRCNPFYIGSKKRGIMSEWHPAAATP 342
DB 191 FFLSLHPQKYLVOVRKP-----DHGYSAMSPTFTIOP 227

RESULT 2

A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
C:Accession: A36337
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
N>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:g186353; PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05 ; Search time 49.27 seconds
(without alignments)
335.844 Million cell updates/sec

Title: US-09-037-657-13
Perfect score: 2251

Sequence: 1 MPARPGPVAAQSARRPPRL.....WRAMQSKHTRNOVLPKAL 413

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR_60:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331	14.7	622	2	A40144	prolactin receptor
2	329	14.6	918	2	A36337	membrane glycoprotein
3	324.5	14.4	206	2	A57018	prolactin receptor
4	319.5	14.2	917	2	I49699	glycoprotein 130
5	317.5	14.1	918	2	A44257	interleukin-6 sign
6	314	13.9	830	2	I50455	prolactin receptor
7	312	13.9	610	2	A4631	prolactin receptor
8	312	13.9	412	2	A36116	prolactin receptor
9	312	13.9	610	2	A41070	prolactin receptor
10	312	13.9	310	2	A39884	prolactin receptor
11	307.5	13.7	616	2	A30304	prolactin receptor
12	307.5	13.7	303	2	I77524	prolactin receptor
13	307.5	13.7	292	2	I77525	prolactin receptor
14	307.5	13.7	608	2	I53269	prolactin receptor
15	306	13.6	831	2	J01655	prolactin receptor
16	302.5	13.4	581	2	I45971	prolactin receptor
17	281.5	11.6	630	2	I51086	prolactin receptor
18	274.5	11.3	783	2	JH0329	granulocyte colony
19	254.5	11.3	771	2	B38252	granulocyte colony
20	254.5	11.3	863	2	C38252	granulocyte colony
21	252.5	11.2	837	2	A34898	granulocyte colony
22	234	10.4	372	2	I58141	ciliary neurotroph
23	230.5	9.8	372	1	UHR0CN	ciliary neurotroph
24	209.5	9.3	422	2	I37891	interleukin-11 rec
25	208.5	9.3	432	2	I48343	interleukin-11 rec
26	208	9.2	362	2	S60614	growth promoting a
27	203.5	9.0	460	2	JU0145	interleukin-6 rece
28	200.5	8.9	468	1	A41242	interleukin-6 rece
29	199	8.8	156	2	A32868	prolactin receptor
30	194.5	8.6	440	2	JU0144	interleukin-6 rece
31	192.5	8.6	579	2	B45266	MPL-K protein prec
32	192.5	8.6	635	2	A45266	MPL-K protein prec
33	191.5	8.5	894	2	S68437	leptin receptor (v
34	191.5	8.5	900	2	S68440	leptin receptor (v
35	191.5	8.5	805	2	S68441	leptin receptor (v
36	190	8.4	1097	2	I57308	leukemia inhibitor
37	190	8.4	625	2	S35317	hematopoietic grow
38	190	8.4	150	2	B34631	lactogen receptor
39	188.5	8.4	894	2	JC4797	leptin receptor pr

40 188.5 8.4 1162 2 PC4184 leptin receptor, O
41 188.5 8.4 805 2 JC4897 leptin receptor, O
42 186 8.3 626 2 S37622 proto-oncogene - m
43 185 8.2 1092 2 JU0312 differentiation-st
44 185 8.2 719 2 JC2181 differentiation-st
45 182 8.1 895 2 S74225 leptin receptor, 1

ALIGNMENTS

RESULT 1
A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C:Accession: A40144

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A:Reference number: A40144; MUID:90114212

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOD>

A:Cross-references: GB:M31661; NID:G190361; PID:G190362

C:Genetics:

A:Gene: GDB:PIR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F.1-24/Domains: signal sequence #status predicted <SIG>

F.25-622/Product: prolactin receptor, long form #status predicted <MAT>

F.59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7% Score 331; DB 2; Length 622;

Best Local Similarity 37.5% Pred. No. 3.5e-15;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

DB 15 LFNLCILNGOLPPKPRFIFKCRSPKRTFTCWPRPGDGG--LPTNLSLYHDEGTLM 72

QY 185 NTCEHYHTVGPCHSIPRD-LALFTPEIWEATNRGASRDVLLDVLDTVTDPDPD 243

DB 73 HECPPYITGPNCSHFQYQYSMTYIMVNAIOMSSPSDELYDVYIVQPPPLE 132

QY 244 VHSVNGGLEQOLSTRV--SPALKDF--LFOAKIQRIRVEDSVDMKYVDVSNQTS 298

DB 133 LAV-EVKQPEDRKPYLMTKWSPPPLIDKTGMFTLLYEIRLKPKAEME-IHFGQOTE 190

QY 299 CRLAGLKPGTYFVQVRCNPGIYSGKAGISEMSHPTASTP 342

DB 191 FKILSLHFGQYTLVQVCKRP-----DHGIWSAMSPATFIQIP 227

RESULT 2

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C:Accession: A36337

R:HLBI, M.; Murakami, M.; Saito, M.; Hirano, T.; Tega, T.; Kishimoto, T.

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MUID:91084844

A:Accession: A36337

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:G186353; PID:G186354

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 14.6%; Score 329; DB 2; Length 918;

Best Local Similarity 28.6%; Pred. No. 8.6e-19; Mismatches 151; Indels 18; Gaps 8;

46 ISPPDPTLLIGSSLAATCSHG---DTPGATAGLWTLNGRLSELRLNTSTLALA 102
 31 ISPSFVQVHNSFTAVCLAKKCDYFVNANVYWKTNHTTPEQDTIIRFASSTV 90
 103 LANLNGSRQSGDNLVCHARDGSIAGSLVGLPPEKPFNISCWRMKDLTCRMTGCA 162
 91 FTDIASLNTQILCNILTFEQGQNYGIIISGLPPEKKNKSLCVINSEKKNRCMDGR 150
 163 HGETFLHTNYSKLYKLRWYQDNTCEHYHTVGPCHSPKDLALTPPEIWEATNRLGS 222
 151 --ETHELETNLTSEWATKRFADCKAKRDT--PTSCYDYSTVYFVNIEVWEALNALGK 206
 223 ARSDVLTDLVLTDPDPDVHVSRYGLEDQLSVRWSPALDKDFLQAKYQIRYRV 282
 207 VTSDHINFDVYKVPKPNHNSVINSELSILKLTWTN-PSISVLI-LKYNQYRFX 264
 283 DSDVDRKV---DVSNOTSCRLAGLKPQTVYFVQVRCNPFYIGSKKAGINSESHPTAA 339
 265 DASTWSQIPEDTASTRSSEFTVQDLKPFTEYFRIRC-----MKDGGKYNDSMSEASG 319
 340 STPRSERP 347
 320 IT-YEDRP 326

RESULT 3

Prolectin receptor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996

C:Accession: A57018

R:Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolectin receptor antagonists that inhibit the growth of breast cancer cell 11

A:Reference number: A57018; MUID:95286597

A:Accession: A57018

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-206 <RES>

A:Cross-references: GB:S78505; NID:9999114; PID:9999115

Query Match

14.4%; Score 324.5; DB 2; Length 206;

Best Local Similarity 38.0%; Pred. No. 2.8e-19; Mismatches 90; Indels 17; Gaps 7;

136 LPPKPFNISCWRMKDLTCRMTGAGETFLHTNYSKLYLRWYQDNTCEEHYVGP 195
 2 LPPGKPEIFKCRSPKKEFTTCMRKGTGDS--LPINYSILYHREGETLMHCEPDYITGCP 59
 136 HSCHPKD-LALFTPEIWEATNRLGSASDVLTLVDVLTDPDPDVHVSRYGLED 254
 60 NSCHGKQYTSKMRFTYIMVNTNONGSSELDYVYIYQDPPELAV-EVKQPED 118
 255 QLSVWV--SPALKDF---LQAKYQIRYRVSDVMDVVDVNSQSCRLAGLKPQTV 309
 119 KRPYLMIKWSPPTLIDLTGKGTFTLYELRLKPKAAWE-IHFAQQQTEFKILSHPOK 177
 310 YFVQVRCNPFYIGSKKAGINSESHPTAASP 342
 178 YLYVQRCRP-----DHGYWASMSPTFIQIP 203

RESULT 4

149699

glycoprotein 130 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997

C:Accession: 149699; I48370

R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.

J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, g

A:Reference number: I48370; MUID:92291532

A:Accession: 149699

A:Status: translated from GB/EMBL/DBJ

A:Residues: 1-917 <RES>

A:Molecule type: mRNA

A:Cross-references: GB:M83336; NID:9193591; PID:9193592

A:Accession: I48370

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PID:9840817

C:Genetics:

A:Gene: gp130

C:Keywords: glycoprotein

Query Match

14.2%; Score 319.5; DB 2; Length 917;

Best Local Similarity 29.6%; Pred. No. 5e-18; Mismatches 146; Indels 23; Gaps 10;

46 ISPPDPTLLIGSSLAATCSHG---DTPGATAGLWTLNGRLSELRLNTSTLALA 102
 31 IYPEFPVQGRSNTFAICVLKQACQHYVNASYVWKTNAAVREQVATINRTTSVT 90
 103 LANLNGSRQSGDNLVCHARDGSIAGSLVGLPPEKPFNISCWRMKDLTCRMTGCA 162
 91 FTDVAVPQVQLTNCILSFGQEQNYGVYTMISGPPDPKPNLTGIVNCKMMLCOMPGR 150
 163 HGETFLHTNYSKLYKLRWYQDNTCEHYHTVGPCHSPKDLALTPPEIWEATNRLG 221
 151 --ETHELETNLTSEWATKRFADCKAKRDT--PTSCYDYSTVYFVNIEVWEALNALGK 203
 222 SARSDVLTDLVLTDPDPDVHVSRYGLEDQLSVRWSPALDKDFLQAKYQIRYRV 281
 204 KYSSSINFDVYKVPKPNHNSVINSELSILKLTWTN-PSISVLI-LKYNQYRFX 261
 282 EDSVDRKV---DVSNOTSCRLAGLKPQTVYFVQVRCNPFYIGSKKAGINSESHPTA 338
 262 KDASTWQVPLEDTPMSPRTSTVQDLKPFTEYFRIRC-----SIRDGK-GYWSMSEAS 316
 339 AST--PRSERP 347
 317 GTTYEDRPSRP 327

RESULT 5

A44257

Interleukin-6 signal transducing molecule gp130 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997

C:Accession: A44257

R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.

Genomics 14, 666-672, 1992

A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transdu

A:Reference number: A44257; MUID:93053397

A:Accession: A44257

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-918 <RAN>

A:Experimental source: liver

A>Note: sequence extracted from NCBI backbone (NCBIP:118488)

C:Keywords: transmembrane protein

Query Match

14.1%; Score 317.5; DB 2; Length 918;

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; I55417
 R:Alt: S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (NB2) expresses a mutant form of prolactin
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALIT>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 R:O'Neil, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, NB2, and long prolactin receptor
 A:Reference number: I55417; MUID:95014432
 A:Accession: I55417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: NB2-11C cell line
 C:Keywords: transmembrane protein

Query Match 13.9% Score 312; DB 2; Length 412;
 Best Local Similarity 35.4% Pred. No. 7.2e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

125 SILGSCLYVGLPEKPNISCSNMKDLTCRWTGAGHGETFLHTNYSKTKLRMGOD 184
 15 SLKSGS-----PQKPEIHKCRSPDKETFCMNPBGDGG--LPTNLSLTYSK--GEK 65
 185 NT--CEEHYTVGPHSCHLPND-LALFPEYELWEATNLSARSDDVLTLDVLTDP 241
 66 TTCEPDYKTSKGNCSFSSKQYTSIMKYLITVATNOMSSSDPLVDTYVEPEPP 125
 242 PDVHVSXVGLGLEDOLSRWV--SPALKDF--LFOAKYQIRYVESVDMKVVDVSNQ 296
 126 RNLLT-EVKQDKRKTYLWVMSPTITDVTGFTMEYERLPEEAEME-THFTGHQ 183
 297 TSCRLAGLKPGTYFVQVRCNPFYIGSKKAGIWEWSHPTASTP 342
 184 TQFVFDLYGQKYLIVQTRCKP-----DHGYSRMSQSSVEMP 222

RESULT 10
 A29884
 prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A29884
 R:Boulin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shlrota, M.; Banville
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc
 A:Reference number: A29884; MUID:88165035
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 13.9% Score 312; DB 2; Length 310;
 Best Local Similarity 35.4% Pred. No. 5e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

125 SILGSCLYVGLPEKPNISCSNMKDLTCRWTGAGHGETFLHTNYSKTKLRMGOD 184
 15 SLKSGS-----PQKPEIHKCRSPDKETFCMNPBGDGG--LPTNLSLTYSK--GEK 65
 185 NT--CEEHYTVGPHSCHLPND-LALFPEYELWEATNLSARSDDVLTLDVLTDP 241

DB 66 TTCEPDYKTSKGNCSFSSKQYTSIMKYLITVATNOMSSSDPLVDTYVEPEPP 125
 242 PDVHVSXVGLGLEDOLSRWV--SPALKDF--LFOAKYQIRYVESVDMKVVDVSNQ 296
 126 RNLLT-EVKQDKRKTYLWVMSPTITDVTGFTMEYERLPEEAEME-THFTGHQ 183
 297 TSCRLAGLKPGTYFVQVRCNPFYIGSKKAGIWEWSHPTASTP 342
 184 TQFVFDLYGQKYLIVQTRCKP-----DHGYSRMSQSSVEMP 222

RESULT 11
 A30304

prolactin receptor 2 precursor - rabbit
 N:Alternate names: prolactin receptor, mammary gland
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
 C:Accession: A30304; A60380
 R:Edey, M.; Jolicoeur, C.; Levi-Meyueis, C.; Dusanter-Fourt, I.; Petridou, B.; Bou
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A:Title: Identification and sequence analysis of a second form of prolactin receptor
 A:Reference number: A30304; MUID:89184578
 A:Accession: A30304
 A:Molecule type: mRNA
 A:Residues: 1-616 <EDE>
 A:Cross-references: GB:J04510; NID:g165669; PID:g165670
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rece
 A:Reference number: A60380; MUID:91146782
 A:Accession: A60380

A:Molecule type: protein
 A:Residues: 41-58, 'Y', 60-66-90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NK', 108, 150-154, 'XX',
 A>Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domain: transmembrane #status predicted <TM>
 F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 13.7% Score 307.5; DB 2; Length 616;
 Best Local Similarity 36.3% Pred. No. 2.8e-17;
 Matches 77; Conservative 28; Mismatches 90; Indels 17; Gaps 7;

137 PPKFPNISCWNRKMDLTCRWTGAGHGETFLHTNYSKTKLRMGODNTCEEHYTVGP 196
 27 PPKFPNISCWNRKMDLTCRWTGAGHGETFLHTNYSKTKLRMGODNTCEEHYTVGP 196
 197 SCHI-PKDALFPEYELWEATNLSARSDDVLTLDVLTDPDPDVHVSXVGLGLEDQ 255
 85 SCFFSKHNSIMYITVATNOMSSSDPLVDTYVEPEPPNLT-EKKHPEDR 143
 256 LSVRWVS--PPALKDF--LFOAKYQIRYVESVDMKVVDVSNQTSCLAGLKPGTY 310
 144 KPLWYKWLPELTIVDRSGMLTQYEIRLKPKEAAEME-THFTGQGTQFNLISLYPGOKY 202
 311 FVQVRCNPFYIGSKKAGIWEWSHPTASTP 342
 203 LVQVRCNP-----DHGYSRMSQSSVEMP 222

RESULT 12
 I77524

prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: I57699; MUID:89261824

A:Accession: 177524
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-303 <RES>
 A:Cross-references: GB:M22958; NID:g200479; PID:g200480

Query Match 13.7%; Score 307.5; DB 2; Length 303;
 Best Local Similarity 32.6%; Pred. No. 1,1e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLVLSISLNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRWTPGANGFELHTNYSLKYLWYGODNT--CEEHYVGPSCHIPKD-LAL 206
 35 DKETTCWMPGSDGG--LPTNYSLTYSKE--GEKNTYECPEYKTSGPNSCFPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVANATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLWVWLP 149
 265 ALKDF---LFOAKQIRRVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVYTGFTMEYERLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOGRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGWSRMGOEKSEIEIP 222

RESULT 13
 177525
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text, change 02-Aug-1996
 A:Accession: 177525
 R:Davis, J.A.; Linzer, D.I.H.
 Moll. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:9261824
 A:Accession: 177525
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:g200481; PID:g200482

Query Match 13.7%; Score 307.5; DB 2; Length 292;
 Best Local Similarity 32.6%; Pred. No. 1,1e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLVLSISLNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRWTPGANGFELHTNYSLKYLWYGODNT--CEEHYVGPSCHIPKD-LAL 206
 35 DKETTCWMPGSDGG--LPTNYSLTYSKE--GEKNTYECPEYKTSGPNSCFPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVANATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLWVWLP 149
 265 ALKDF---LFOAKQIRRVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVYTGFTMEYERLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOGRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGWSRMGOEKSEIEIP 222

RESULT 14
 153269

prolactin receptor, long form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text, change 29-Jan-1999
 A:Accession: 153269; J0671; S34356
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993

A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary
 A:Reference number: 153269; MUID:93307149
 A:Accession: 153269

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:g293769; PID:g293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J0671; MUID:94085788
 A:Accession: J0671

A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:g347398; PID:g347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: S34356
 A:Accession: S34356

A:Molecule type: mRNA
 A:Residues: 1-557, 559-608 <EDE>
 A:Cross-references: EMBL:X13372; NID:g312696; PID:g312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from a
 C:Comment: This long form receptor is capable of transducing a signal to milk protein
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domin: transmembrane #status predicted <TM>

Query Match 13.7%; Score 307.5; DB 2; Length 608;
 Best Local Similarity 32.6%; Pred. No. 2,8e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLVLSISLNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRWTPGANGFELHTNYSLKYLWYGODNT--CEEHYVGPSCHIPKD-LAL 206
 35 DKETTCWMPGSDGG--LPTNYSLTYSKE--GEKNTYECPEYKTSGPNSCFPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVANATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLWVWLP 149
 265 ALKDF---LFOAKQIRRVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVYTGFTMEYERLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOGRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGWSRMGOEKSEIEIP 222

RESULT 15
 J01655

prolactin receptor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text, change 10-Sep-1997
 A:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
 A:Reference number: J01655; MUID:93075121

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:11 : Search time 35.09 Seconds

(without alignments)
332,710 Million cell updates/sec

Title: US-09-037-657-13

Sequence: 1 MPAGRGPVQASARRPPRL.....WRAMQSHKTRNYLPAKL 413

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: Swissprot_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331	14.7	622	1	PLRL_HUMAN
2	329	14.6	918	1	IL6B_HUMAN
3	319.5	14.2	917	1	IL6B_MOUSE
4	317.5	14.1	918	1	IL6B_RAT
5	314	13.9	810	1	PLRL_COLLI
6	312	13.9	610	1	PLRL_RAT
7	307.5	13.7	608	1	PLRL_MOUSE
8	307.5	13.7	616	1	PLRL_RABIT
9	306	13.6	831	1	PLRL_CHICK
10	305	13.5	831	1	PLRL_MEIGA
11	303	13.5	581	1	PLRL_CEREL
12	302.5	13.4	581	1	PLRL_BOVIN
13	261.5	11.6	630	1	PLRL_ORENI
14	254.5	11.3	836	1	GCSS_HUMAN
15	252.5	11.2	837	1	GCSS_MOUSE
16	234	10.4	372	1	CNTR_RAT
17	222.5	9.9	372	1	CNTR_HUMAN
18	208	9.2	362	1	CNTR_CHICK
19	203.5	9.0	460	1	IL6A_MOUSE
20	200.5	8.9	468	1	IL6A_HUMAN
21	196.5	8.7	462	1	IL6A_RAT
22	192.5	8.6	635	1	TPOR_HUMAN
23	191.5	8.5	1162	1	LEPR_MOUSE
24	190	8.4	1097	1	LIFR_HUMAN
25	190	8.4	625	1	TPOR_MOUSE
26	185	8.2	1092	1	LIFR_MOUSE
27	175	7.8	427	1	IL13_HUMAN
28	174.5	7.8	1165	1	LEPR_HUMAN
29	170	7.6	888	1	UFO_MOUSE
30	164.5	7.3	638	1	GHR_RABIT
31	158.5	7.0	508	1	EPOR_HUMAN
32	157	7.0	507	1	EPOR_RAT
33	156.5	7.0	638	1	GHR_PIG
34	155	6.9	507	1	EPOR_MOUSE
35	151	6.7	638	1	GHR_HUMAN
36	147	6.5	1040	1	AXO1_RAT
37	146.5	6.5	424	1	IL13_MOUSE
38	145	6.4	634	1	GHR_SHEEP
39	143.5	6.4	380	1	IL13_HUMAN
40	143	6.4	638	1	GHR_RAT
41	142	6.3	897	1	GHR_MOUSE
42	140.5	6.2	897	1	GHR_MOUSE
43	140.5	6.2	297	1	GHR_MOUSE

ALIGNMENTS

44 139.5 6.2 608 1 GHR_CHICK
45 136.5 6.1 1036 1 AXO1_CHICK
002092 gallus gall
P28685 gallus gall

RESULT 1
ID PRLR_HUMAN STANDARD: PRT: 622 AA.
AC P16471:
DE 01-AUG-1990 (REL. 15, CREATED)
DE 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DE 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS HOMO SAPIENS (HUMAN).
OC EUCARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATAARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90114212.
RA BOTTIN J.-M., EDERY M., SHIROTA M., JOLICOEUR C., LESUEUR L.,
RA ALI S., GOUUD D., DJIANE J., KELLY P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells."
RL MOL. ENDOCRINOL. 3:1455-1461(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE; 95075462.
RA SOMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;
RT "The x-ray structure of a growth hormone-prolactin receptor complex."
RL NATURE 372:478-481(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb.ch).
CC -----
CC EMBL: M31661; GI90362; -
CC PIR: A40144; A40144.
CC PDB: 1BP3; 23-SEP-98.
CC MIM: 176761; -
CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
CC DR PFAM: PF00041; fn3; 2.
CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
CC FT SIGNAL 1 24
CC FT CHAIN 25 622
CC FT DOMAIN 25 234
CC FT TRANSMEM 235 258
CC FT DOMAIN 235 258
CC FT DOMAIN 25 122
CC FT DOMAIN 123 227
CC FT DISULFID 36 46
CC FT DISULFID 75 86
CC FT CARBOHYD 59 59
CC FT CARBOHYD 104 104
CC FT CARBOHYD 233 233
CC SQ SEQUENCE 622 AA; 69505 MW; 69244E155 CRC32;
PROLACTIN RECEPTOR
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.

Query Match 14.7%; Score 331; DB 1; Length 622;
Best Local Similarity 37.5%; Pred. No. 1.2e-19;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAASCTIYV-LPEKFPNISCNRNKKDLTCAWTGASGETLHTNYSUKYLRWYGD 184
 DB 15 LFLNLTCLLNQOLPFGKPEIKFCRSPNKEFTLCWRPGLDGG--LPTNYSILYHREBETLM 72
 QY 185 NTCBEVHTVGPHSCHIPKD-LALFTPEIIVENTNRGASRDVLTLDVDTVTTPPPD 243
 DB 73 HECDDITTGDPNSCHFEKQYTSMTKRYIMVNVNTNMGSSFSBELVDVTVYVQPPPLE 132
 QY 244 VHSRVGLEDQSLSVRWV--SPPALKDF--LFOAKYQIRYVEDSVDMRVVDVSNQTS 298
 DB 133 LAV-EVQOPEDRKRYELIKMSPTLLDLKGTWFTLLYLEILNKEPKALEWE-IHFAQQTG 130
 QY 299 CRLAGLKPGTVYVQVNCNPFGLYGSKKACIMSEWSHPAASRP 342
 DB 191 FKILSLHFGQKLYVQVCKP-----DHGYMSMSPATRIQIP 227
 RESULT 2
 IL6B_HUMAN STANDARD: PRT; 918 AA.
 ID IL6B_HUMAN
 AC P40189;
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSUPPRESSOR
 DE RECEPTOR) (CDW130) (CD130 ANTIGEN).
 GN IL6ST.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATHARTINI; HOMINIDAE; HOMO.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-MYELOMA, AND PLACENTA.
 RX MEDLINE: 91084844.
 RA HIRI M., MORAKAMI M., SAITO M., HIRANO T., TNGA T., KISHIMOTO T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RT gp130.";
 RL CELL 63:1149-1157(1990).
 RN (2)
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE: 98169383.
 RA BRAVO J., STANTON D., HEATH J.K., JONES E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD GUIDE CD130 ENTRY;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
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 CC or send an email to license@sdb.ch).
 CC EMBL: M57230; G186354.
 DR PIR: A36337, A36337.

DR PDB: 1BQJ; 26-AUG-98.
 DR MIM: 600694;
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PRAM: PRO0041; f03; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT; 3D-STRUCTURE.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 619
 FT TRANSMEM 620 641
 FT DOMAIN 642 918
 FT DOMAIN 26 120
 FT DOMAIN 124 222
 FT DOMAIN 223 324
 FT DOMAIN 325 423
 FT DOMAIN 424 517
 FT DOMAIN 518 613
 FT DOMAIN 725 755
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT CARBOHYD 43 43
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 227 227
 FT CARBOHYD 379 379
 FT CARBOHYD 383 383
 FT CARBOHYD 390 390
 FT CARBOHYD 553 553
 FT CARBOHYD 564 564
 SQ SEQUENCE 918 AA; 103522 MW; 7CC06F05 CRC32;
 Query Match 14.6%; Score 329; DB 1; Length 918;
 Best Local Similarity 28.6%; Pred. No. 3e-19;
 Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPOPTLLIGSLATNCISHG---DTGATGGLTWTNGRLPSELRLNTSLAL 102
 DB 31 ISPEVYVGLHNTFAVCLAKKCKNDYFHVANNIYKWNHTTIREQYTTIKRASVY 90
 QY 103 LANLNGSSROQSDNIVCHARDGSIAGSLYVGLPEKFPNISCNRNKKDLTCAWTG 162
 DB 91 FTDIASLNIQLNCNLTILFGLQBNVYGIITISGLPEKKNKNCIYNEKKKRCWDG 150
 QY 163 HETPLHTYYSKYLKRWGONTCEHYTVGPHSCHIPKDALFTPEIIVENTNRG 222
 DB 151 --ETHLENTFTLSEWATKHFADCKAKRDT--PTCTVDYSTVYFVNIEVWEAENAL 206
 QY 223 ARSDVLTLDVLDVTTDPPDVHVSRLGLEDQSLSVRWVSPPALKDFLQAKYQIRY 282
 DB 207 VYSDHNDPVAKYKPNPNHNISVNSELSILKLTWTN-PSISVIT-LKYNIOYRK 264
 QY 283 DSDVKKVY--DVSNGQSCRLAGLKPGTVYVQVNCNPFGLYGSKKACIMSEWSHP 339
 DB 265 DASTSQIPEDPTASTRSSTFYQDLKPFREYFRIRC-----MKEDGKGYNDWSEEN 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326
 RESULT 3
 IL6B_MOUSE STANDARD: PRT; 917 AA.
 ID IL6B_MOUSE
 AC Q000560;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 GN IL6ST.
 OS MUS MUSCULUS (MOUSE).

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Best Local Similarity 29.6%; Pred. No. 1,8e-18;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10

QY 46 ISPODPLLIGSSLOATCSIHG---DRPGATAEGLYTLNGRRRLPSELSRLNTSTLALA 102
   |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 31 IYPEFPVQGSNFTACIVLEKACLQHYYNASYIWKTHNAANPRQOVIYNITTSVT 90
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 103 LANLNGRROOSGNLYNCVHADGSLILAGSCLYGLPPKPFENISCSNRMDLTGRTPGA 162
   :||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 91 FTVVLPLSPVOLTCNNISLFEGIEQNVYGVTMLSGEPFKPNLTICIVEGKKMQLCMPGR 150
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 163 HGEFLHTNTSLKYKLKWYGOD--NTCEHYTGVGHSHCHIKDLALFPEYLWVATRLG 221
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 151 --ETYLETNITTLSE--WATEKEPDCDSKGT---SCWVSYPMTYYINIWVEAEALNG 203
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 222 SANSDYLLTDLDLVYTDPDPDVHVSXVGLEDQLSVRWYSPALNKDFLEQAKQIRRV 281
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 204 KYSESSEINFDPVDKVPPTPYNLSTVNSELSSLILKSWSGSL--GGLLDKSDIOYRT 261
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 282 EDSVDMKVY---DVDNSQJSCRLAGLKPGTVYFYOVQRCPFGYIGSKRKAGISEWSHP7A 338
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 262 KASTYIQVPLEDEMTSPRSFTVQDKLPFEYEFYRFR---SIKDSOK-GYMDWSMEAS 316
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 339 AST--PRSERP 347
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 317 GTTYEDRPSPR 327
   ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 4
IL6B_RAT ID IL6B_RAT STANDARD: PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHENTIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATIOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE; 93052397.
RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130."
RL GENOMICS 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
EMBYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-----
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EMBL; M92340; NOT ANNOTATED CDS

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DR PIR: A44257; A44257.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 3.
 DR HSSP; P40189; 180U.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618
 FT TRANSMEM 619 640
 FT DOMAIN 641 918
 FT DOMAIN 26 120
 FT DOMAIN 124 221
 FT DOMAIN 222 323
 FT DOMAIN 324 422
 FT DOMAIN 423 516
 FT DOMAIN 517 612
 FT DOMAIN 724 754
 FT DISULFID 134 144
 FT DISULFID 172 181
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 137 157
 FT CARBOHYD 205 205
 FT CARBOHYD 226 226
 FT CARBOHYD 382 382
 FT CARBOHYD 389 389
 FT CARBOHYD 477 477
 FT CARBOHYD 552 552
 SQ SEQUENCE 918 AA; 102450 MW; BEDECD0 CRC32;

Query Match 14.1%; Score 317.5; DB 1; Length 918;
 Best Local Similarity 29.1%; Pred. No. 2,6e-18;
 Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISPOPTLLIGSSLOATCSHG---DTPGATAGLWTLNGRLRPSLSRLNTSLIALA 102
 DB 31 IYEPFVVGROGNSFNATCYLKEKCLQVSVNATYIWKKNHVAVREQVTVINRTASSVT 90
 QY 103 LANLSSROQSGDNLYCHARDSSILAGSCLYVGLPEPEKFNISCSRNKKDLTCRTPGA 162
 DB 91 FTDVVFQONQVLCNMLISFGQIBQNYGIRILSGYPPDIPNLSCLYNEGKNLQDLPGR 150
 QY 163 HGETLHTYSLKYLKRWGOD--NCEEHYTGPHSCHLPKDLAFTPEIYVETATNRLG 221
 DB 151 --ETYLEINVTLKSE--WATERKFPDCRTKH--GTSSCMAGYTPPIYFVNLEVVAEMLAG 204
 QY 222 SARSDVLLDVLVDVVTDPDPVHVSRYVGLDQLSVRVSPALKDFFQAKYQIRYRV 281
 DB 205 NVSSSEINEDPYDKYKPSPHLSVTNSELSSILKLANVNSGL--DSLRLKSDIQRT 262
 QY 282 EDSDVMKVV---DVSNOTSCLAGLKPGTVYFVQVRCNPFQIYSSKAGIWSHPTGA 338
 DB 263 KDASTWIOVPLDEDVSPRSTFVQDLKPTVEYVRLR---SIKENGR-GYSDMSSE-EA 316
 QY 339 ASTPRSERP 347
 DB 317 SETTYEDRP 325

RESULT 5
 PRIR COLLI STANDARD; PRT: 830 AA.
 AC 090374;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS COLUMBA LIVIA (DOMESTIC PIGEON).

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CROPSAC;
 RX MEDLINE; 94283267.
 RA CHEN X., HORSEMAN N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor".
 RL ENDOCRINOLOGY 135:269-276(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----

DR EMBL; U07694; G466382;
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFAM; PF00041; fn3; 4.
 DR HSSP; P16471; 1BP3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 25 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 163 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SQ SEQUENCE 830 AA; 94507 MW; 5EFAD51 CRC32;

Query Match 13.9%; Score 314; DB 1; Length 830;
 Best Local Similarity 37.1%; Pred. No. 4,4e-18;
 Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PPEKPFNISCWRNKKDLTCRTPGAAGETFLH--TNSLKYLRNYGQDNCEETHVGP 195
 DB 231 PPEKPTIIRKSPKPEKETTCWKKPSSDGG---HPTNYTLKSKSEGEERYECPDYTAGP 287
 QY 196 HSCHT--PRDLAFTPEIYVETATNRLGSASDVLVDVLTDPDPD--HVSRYVGL 252
 DB 288 NSCFDKKHTSWITNYITVATNLTGNSVSDPLVDTYIVQDPPVNVLELKTIVNR 347
 QY 253 EDQLSVRVNSPALKDF---LFOAKYQIRYVEDSDVMKVVDDVSNQTSCLAGLKPGTV 309
 DB 348 KPYLVLTN--SPPPLADVNSGWLTLDELRNLPRAEAEKETI--FVGQOYHYMFLSNPKK 405
 QY 310 YFVQVRCNPFQIYSSKAGIWSHPTGA 334
 DB 406 YIVQIHCKP-----DHHGSWSHWS 424

RESULT 6

PRIR_RAT STANDARD: PRT: 610 AA.
 ID PRIR_RAT STANDARD: PRT: 610 AA.
 AC P05710; 063451; 063723; 062832; 064274; 065479;
 DT 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1987 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
 GN PRLR.
 OS RATUS NORVIGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MORIDAE; MORINAE; RATIUS.
 CC (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91155946.
 RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
 EDERY M., DUJANE J., KELLY P.A.;
 KT "Expression of two forms of prolactin receptor in rat ovary and
 liver."
 MOL. ENDOCRINOL. 4:1136-1143(1990).
 (2)
 RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
 CP STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 MEDLINE; 90241201.
 RA ZHANG R., BUCZKO E., TSAI-MORRIS C.H., HU Z.Z., DUFAU M.L.;
 KT "Isolation and characterization of two novel rat ovarian lactogen
 receptor cDNA species."
 J. BIOL. BIOPHYS. RES. COMMUN. 168:415-422(1990).
 (3)
 RP SEQUENCE OF 281-610 FROM N.A.
 RA BANVILLE D., STOCO R., MURPHY K.K., BOLE Y., KELLY P.A.;
 KT SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 (4)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
 CP TISSUE-LIVER;
 MEDLINE; 88165059.
 RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
 SHIROTA M., BANVILLE D., DUSANTER-FOURTE I., DUJANE J., KELLY P.A.;
 KT "Cloning and expression of the rat prolactin receptor, a member of
 the growth hormone/prolactin receptor gene family."
 CELL. 53:69-77(1988).
 (5)
 RP SEQUENCE FROM N.A. (FORM NB2).
 CP TISSUE-LYMPHOMA;
 MEDLINE; 92041834.
 RA ALI S., PELLIGRINI I., KELLY P.A.;
 KT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
 of prolactin receptor."
 J. BIOL. CHEM. 266:20110-20117(1991).
 (6)
 RP SEQUENCE FROM N.A. (FORM NB2).
 CP MEDLINE; 95014432.
 RA O'NEAL K.D., YU-LEE L.Y.;
 KT "Differential signal transduction of the short, Nb2, and long
 prolactin receptors. Activation of interferon regulatory factor-1 and
 cell proliferation."
 J. BIOL. CHEM. 269:26076-26082(1994).
 (7)
 RP EDUCATION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 (8)
 RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 (9)
 RP ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING OF THE PRLR GENE.
 (10)
 RP SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 (11)
 RP SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 (12)
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 or send an email to license@sib-sib.ch).

CC EMBL; M57668; G206367; -
 DR EMBL; M34083; G205123; -
 DR EMBL; L48060; G1019651; -
 DR EMBL; U34730; G1238859; -
 DR EMBL; M19304; G206365; -
 DR EMBL; M74152; G206390; -
 DR EMBL; U07567; G641864; -
 DR PIR; A29884; A29884.
 DR PROSITE; P500241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; P500340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 2.
 DR HSP; P16471; 1BP3.
 KW RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL, REPEAT;
 KW ALTERNATIVE SPLICING.
 FT SIGNAL 1 19
 FT CHAIN 20 610
 FT DOMAIN 20 229
 FT TRANSMEM 230 253
 FT DOMAIN 254 610
 FT DOMAIN 20 117
 FT DOMAIN 119 222
 FT DISULFID 31 41
 FT DISULFID 70 81
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT VARSPLIC 131 150
 FT VARSPLIC 151 610
 FT VARSPLIC 281 310
 FT VARSPLIC 311 610
 FT VARSPLIC 342 539
 FT CONFLICT 236 236
 FT CONFLICT 345 345
 FT CONFLICT 465 465
 FT CONFLICT 466 466
 FT CONFLICT 469 469
 FT CONFLICT 541 541
 FT CONFLICT 555 555
 SO SEQUENCE 610 AA; 68599 MW; C579BC43 CRC32;
 Query Match 13.9%; Score 312; DB 1; Length 610;
 Best Local Similarity 35.4%; Pred. No. 4.3e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;
 QY 125 SIAGSCLYVGLPPEKPFNISCWSRNKDLCTCRWTPGAGGEFLHTNYSLSKTKLRWYGD 184
 DB 15 SLKGS-----PQKPELHKCRSPDKETFCWNPNDG--LPTNLSLSKE--GK 65
 QY 185 NT--CEHYTVGPHSCHPKD-LAETPYEIVEATNTRGSASDYLTDVLYVTTDP 241
 DB 66 TYECPDYKTSQNFSCFFSKQYTSIKYIIVNATNMGSSSDPLVDVYIYEP 125
 QY 242 PNYHSRVGGLDQLSVKRV--SPRLADF---LQAKYQIRYEDSVKRVVDVDSNQ 296
 DB 126 RWTLT-EVQQLDKKTYLWVWVSPPTIDVKTGWFTMEIILKPEAEWE-EHFTGHQ 183
 QY 297 TSCRLAGLKPQTVYEVQVNCNPFGLYGSKKAGISEMSHPTAASP 342
 DB 184 TQFKYFDLYPGOKYIVORCKP-----DHGIYRWSSQESSVEMP 222
 RESULT 7
 PRIR_MOUSE STANDARD: PRT: 608 AA.
 ID PRIR_MOUSE STANDARD: PRT: 608 AA.
 AC 008501; 062099; P15213; P15212;
 DT 01-APR-1980 (REL. 14, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J04510; G165670; -
 CC PIR: A30304; A30304.
 CC PDB: 1AN3; 03-DEC-97.
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAM: PF00041; fn3; 2.
 CC DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT: 3D-STRUCTURE.
 CC FT SIGNAL 1 24
 CC FT CHAIN 1 24
 CC FT FT 25 616
 CC FT FT 25 234
 CC FT TRANSMEM 235 258
 CC FT DOMAIN 259 616
 CC FT FT 25 122
 CC FT DOMAIN 124 227
 CC FT FT 36 46
 CC FT DISULFID 75 86
 CC FT FT 59 59
 CC FT CARBOHYD 104 104
 CC FT CARBOHYD 132 132
 CC FT SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;
 CC -----
 CC Query Match 13.7%; Score 307.5; DB 1; Length 616;
 CC Best Local Similarity 36.3%; Pred. No. 1e-17; Indels 17; Gaps 7;
 CC Matches 77; Conservative 28; Mismatches 90;
 CC Y 137 PEKPNISCSNMKDLTCRWTPGAHGETFLHTNYSLKRLMYGQDNCEHYHVGPH 196
 CC Y 27 PGKPEIFCRSEPEKFTFCWMPRGADG--LPTNTLTLYHNGEETTHCPRDKTGSPN 84
 CC Y 197 SCGHI-PKDLALFTPYEINWEATNRLGSASDVLTLDVLDVTTDPPDVHVSRYGLEDQ 255
 CC Y 85 SCYFSKHTSTWITITITVATNATNOMGSSVSDPRYVDVTVIYEPDPVYNLT-L-EVKRDEDR 143
 CC Y 256 LSVRWVS--PALKDF---LFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLAKGTVY 310
 CC Y 144 KPLVWKMPLPLVDVRSGLWLTLEYIRLKPKEAAEME-TTFAGQOTOFKILSLYPGOKY 202
 CC Y 311 FVQVRCNPFGIYSGSKKAGIWMSESHPTAASP 342
 CC Y 203 LVQVRCKP-----DHGFWSVMSPESSIOIP 227
 CC -----
 CC RESULT 9
 CC PRLR-CHICK STANDARD: PRT: 831 AA.
 CC D 004594;
 CC T 01-JUN-1994 (REL. 29, CREATED)
 CC T 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 CC T 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 CC PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CDRLP).
 CC PRLR.
 CC S GALLUS GALLUS (CHICKEN).
 CC S EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC S NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-WHITE LECHORN; TISSUE-KIDNEY;
 CC MEDLINE: 93075121.
 CC TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
 CC "Double antenna structure of chicken prolactin receptor deduced from

FT the cDNA sequence."
 RE BIOCHEM. BIOPHYS. RES. COMMUN. 168:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 CC EMBL: D13154; G222849; -
 CC PIR: J01655; J01655.
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 CC DR PFAM: PF00041; fn3; 4.
 CC DR HSSP: P16471; 1BP3.
 CC DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 CC FT SIGNAL 1 23
 CC FT CHAIN 1 23
 CC FT FT 24 831
 CC FT FT 24 438
 CC FT TRANSMEM 439 459
 CC FT DOMAIN 460 831
 CC FT FT 25 122
 CC FT DOMAIN 123 225
 CC FT FT 228 325
 CC FT DOMAIN 326 428
 CC FT FT 36 46
 CC FT DISULFID 75 86
 CC FT FT 59 59
 CC FT CARBOHYD 91 91
 CC FT CARBOHYD 100 100
 CC FT FT 112 112
 CC FT CARBOHYD 112 112
 CC FT FT 132 132
 CC FT CARBOHYD 262 262
 CC FT FT 303 303
 CC FT CARBOHYD 315 315
 CC FT SEQUENCE 831 AA; 94102 MW; B977BF07 CRC32;
 CC -----
 CC Query Match 13.6%; Score 306; DB 1; Length 831;
 CC Best Local Similarity 35.0%; Pred. No. 2e-17; Indels 18; Gaps 8;
 CC Matches 76; Conservative 27; Mismatches 96;
 CC Y 137 PEKPNISCSNMKDLTCRWTPGAHGETFLH-TNYSLKRLMYGQDNCEHYHVGPH 195
 CC Y 230 PEKPTIICRSPREKFTFCWMPRGIDG--HPTNTLTLSKEEEOVTECPDYRTGP 286
 CC Y 196 HSGHI-PKDLALFTPYEINWEATNRLGSASDVLTLDVLDVTTDPPDVH--HVSAGGL 252
 CC Y 287 NSCYFDKHTSEMTITITVATNEMGSSSDPRYVDVTVIYQPPVANNVLELKKPINR 346
 CC Y 253 EQGLSVRWVSPALKDF---LFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLAKGTV 309
 CC Y 347 KPLVLTW-SPPPLADVRSGLWLTLEYIRLKPKEEEMETI-FVQOQYQYKMFSLNPGK 404
 CC Y 310 FVQVRCNPFGIYSGSKKAGIWMSESHPTAASPGR 346
 CC Y 405 YIIQIHCKP-----DHGWSMSSENYIOPNDR 435
 CC -----
 CC RESULT 10
 CC PRLR-MELGA STANDARD: PRT: 831 AA.
 CC ID PRLR-MELGA
 CC AC 091094; 091091; 091092;
 CC DT 01-NOV-1997 (REL. 35, CREATED)
 CC DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

[illegible]

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SQ      SEQUENCE# 630 AA; 70810 MW; E9A4E553 CRC32;
Query Match          11.6%; Score 261.5; DB 1; Length 630;
Best Local Similarity 33.2%; Pred. No. 6, 1e-14;
Matches 71; Conservative 26; Mismatches 94; Indels 23; Gaps 9
OY      138 PEKPNISGWSNMNDLCRMTPGANGEFELTNTSLAKTKLRNGCDNTEETHTVGPSS 197
DQ      29 PPKPEIKCRSEKELETCWMPKPSGG--LEPTTALYYLKRKGSDVHECPDYHTRGNKS 86
DB      198 CHIPDAL-FEPYEIWEATNRIGSARSDVTLVDIVDTDPEDPVRSRYGLEDQ- 256
DB      87 CFENNNMLIMWSYITVATNALKITYSDPDIDIVYIQGHFPEKLEYT---VKDDQG 143
OY      256 ---LSRVNSPALKDF---LEQARYQIRVED-SVDMKVYDVSNQTSCLAGLKPT 308
Db      144 WPLFLVSN-EPRKADRTSGWTLLTYELRKLEDESENE-NHAAGQCKMNFSLRSRG 201
OY      309 VYFYVRNCNPRIYSKKAGISEMSHPAASTP 342
Db      202 TLLIQVRCKP-----DHGFSEWSSTSYKYVP 228

RESULT 14
GCSR_HUMAN         STANDARD:     PRF:   836 AA.
AC      QG9062;
DT      01-FEB-1995 (REL. 31, CREATED)
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE      GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
DE      (CD114 ANTIGEN).
DE      CSF3R OR GCSFR.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAPOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CAVIARHINI; HOMINIDE; HOMO.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PLACENTA;
RX      MEDLINE; 91011257.
RA      LARSEN A., DAVIS T., CURTIS B.M., GIMBEL S., SIMS J.E., COSMAN D.,
RA      PARK L., SORENSON E., MARCH C.J., SMITH C.A.;
RT      "A cDNA clone expressed in natural killer and T cells that likely
RT      encodes a secreted protein.";
RL      J. EXP. MED. 172:1559-1570(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PLACENTA;
RX      MEDLINE; 91062348.
RA      FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
RT      "Three different mRNAs encoding human granulocyte colony-stimulating
RT      factor receptor.";
RL      PROC. NATL. ACAD. SCI. U.S.A. 87:8702-8706(1990).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 92091782.
RA      SETO Y., FUKUNAGA R., NAGATA S.;
RT      "Chromosomal gene organization of the human granulocyte colony-
RT      stimulating factor receptor";
J      J. IMMUNOL. 148:259-266(1992).
RN      [4]
RP      DOMAINS STRUCTURE.
RX      MEDLINE; 92007729.
RA      FUKUNAGA R., ISHIZAKA-IKEDA E., PAN C.-X., SETO Y., NAGATA S.;
RT      "Functional domains of the granulocyte colony-stimulating factor
RT      receptor.";
RL      EMBO J. 10:2855-2865(1991).
RN      [5]
RP      STRUCTURE BY NMR OF 227-334.
RX      MEDLINE; 97331337.
RA      YANASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
RT      "Solution structure of an extracellular domain containing the WSXWS
```

RT		motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand."
RL	NAT.	STRUCT. BIOL. 4:498-503(1997).
RN	[6]	
RP	3D-STRUCTURE MODELLING OF 125-331.	
RX	MEDLINE; 98037802.	
RA	LATION J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;	
RT	"Identification of a ligand-binding site on the granulocyte colony-	
RL	stimulating factor receptor by molecular modeling and mutagenesis";	
J. BIOC. CHEM. 272:29735-29741(1997).		
-1	FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.	
-1	SUBUNIT: DIMER (PROBABLE).	
-1	SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM, WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM OF THE RECEPTOR.	
-1	TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MELOBLASTOS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.	
-1	ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER), GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-TERMINAL PORTION.	
-1	DISEASE: DEFECTS IN GCSFR ARE A CAUSE OF KOSTMANN SYNDROME; ALSO KNOWN AS SEVERE CONGENITAL NEUTROPHENIA (SCN).	
-1	SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.	
-1	SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.	
-1	SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
-1	DATABASE: NAME-PROV; NOTE=CD guide CD114 entry:	
WWW-HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD114.HTM"		
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	
DR	EMBL; X55721; G31697; -	
DR	EMBL; X55720; G31699; -	
DR	EMBL; S71484; G240884; -	
DR	EMBL; M59818; G183047; -	
DR	EMBL; M59819; G485364; -	
DR	EMBL; M59820; G183049; -	
DR	PIR; JHO329; JHO329.	
DR	PIR; JHO330; JHO330.	
DR	PIR; A38252; A38252.	
PDB; 1A27; 28-JAN-98.		
DR	MIR; 138971; -	
DR	MIM; 202700; -	
DR	PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.	
DR	PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.	
KW	PFAM: PF00041; fn3: 3.	
KM	RECEPTOR_TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT; ALTERNATIVE SPLICING; 3D-STRUCTURE.	
FT	SIGNAL	1 24
FT	CHAIN	25 836
FT	DOMAIN	25 627
FT	TRANSSEM	628 650
FT	DOMAIN	651 836
FT	DOMAIN	25 117
FT	DOMAIN	121 227
FT	DOMAIN	228 332
FT	DOMAIN	333 428
FT	DOMAIN	429 525
FT	DOMAIN	526 621
FT	DOMAIN	131 142
FT	DISULFID	
CC	-----	
CC	GRANULOCYTE COLONY STIMULATING FACTOR	
CC	RECEPTOR	
CC	EXTRACELLULAR (POTENTIAL).	
CC	CYTOPLASMIC (POTENTIAL).	
CC	IG-LIKE C2-TYPE DOMAIN.	
CC	FIBRONECTIN TYPE-II.	
CC	FIBRONECTIN TYPE-III.	
CC	FIBRONECTIN TYPE-III.	
CC	FIBRONECTIN TYPE-III.	
CC	FIBRONECTIN TYPE-III.	
CC	BY SIMILARITY.	

Query Match	11.3%	Score 254.5;	DB 1;	Length 836;
Best Local Similarity	28.9%	Pred. NO. 3.3e-13;		
Matches 97;	Conservative 48;	Mismatches 148;	Indels 43;	Gaps 16

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0Y      21  SLSMSPLLCYLVSPRGSGAHTVVISPODPTLLIGSSLATCGSHGDTPGATAE-GLWY 79
Db      8  SLTMAALITELL-----GSGTECHGISVAPVYHGLDPTFASCIIRKQNSHLDEPQIM 63
QY      80  TLNGRRRLPELSRLLN--TPTLALALNLNLSRQSGDNLVGHARDS--TLAGCLVY 134
Db      64  RLAAELDPPGRROOGLSNGTQESITTLPHLHTQA---FLSCCLMNNSLIQILDQVELRA 119
QY      135  GLDPPEKPFNIS-WSRNMKDUTCRWPTGAGETPLHTNYSIK-YKLWYQG---DNICEE 188
Db      120  GYPPALPHNLSCLMNLTTSSLICOMEGR--ETHLPISFLTKSRKSGNCOQOGDSILDC 177
QY      190  YHNVGPHSCHIP-KDALFTPYELIWEATNRLGSARSDVLTLDIVY-----TTPD 240
Db      178  VPPDGGSHCCIPKRKHLLYONMGIMVQAEALGSMSPQCLDPMQVYKLEPPLKRTMDP 237
QY      241  PRPVHVSRYNGLEDOLSVRVVSPALKDOLFQAKYQIRYVE-DSYDMKYVDVDSNOT-S 298
Db      238  SPRAADPPQACLD-----LCW-EPWOPGLHINOCIELRHKPRQGEASMAVYGLPLEALQ 291
QY      299  CRLAGLKPQVYVFOVORCNPFGLYGSKKIGWSEMS 334
Db      292  YELCGLLPATATYTLQIRCTKMP-----PGRHSDWS 322

:ESULT 15
:CSR_MOUSE
:GCSR_MOUSE      STANDARD;      PRT;      837 AA.
C P40223;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GRAUDOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
CSFBR OR CSFG.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA.
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
MEDLINE: 90235283.

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RA  FUDUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;
RT  "Expression cloning of a receptor for murine granulocyte colony-
RL  stimulating factor";
RN  CELL 61:341-350(1990).
RX  [2]
RP  STRUCTURE BY NMR OF 225-333.
RA  YAMASAKI K., MATO S., ANAGUCHI H., OHKUBO T., OTA Y.;
RT  "Solution structure of an extracellular domain containing the WSWS
RL  motif of the granulocyte colony-stimulating factor receptor and its
RN  interaction with ligand";
RM  NMR. STRUCT. BIOL. 4:498-504(1997).
CC  "- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
CC  ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
CC  THE CELL SURFACE.
CC  "- SUBUNIT: DIMER (PROBABLE).
CC  "- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC  "- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
CC  "- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC  ONE IG-LIKE DOMAIN.
CC  "- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC  "- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M58288; G193455;
DR  PIR; A34898; A34898.
DR  PDB; 1GCF; 22-OCT-97.
DR  PDB; 1CRO; 22-OCT-97.
DR  MGD; MGI:88533; CSFGR.
DR  PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR  PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW  PFAM; PF00041; fn3; 3.
KW  RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW  REPEAT; 3D-STRUCTURE.
FT  SIGNAL 1 25
FT  CHAIN 26 837
FT  FT
FT  FT
FT  DOMAIN 26 626 POTENTIAL.
FT  TRANSMEM 627 650 GRANULOCYTE COLONY STIMULATING FACTOR
FT  DOMAIN 651 837 RECEPTOR.
FT  DOMAIN 26 118 EXTRACELLULAR (POTENTIAL).
FT  DOMAIN 122 228 CYTOPLASMIC (POTENTIAL).
FT  DOMAIN 229 333 IG-LIKE C2-TYPE DOMAIN.
FT  DOMAIN 334 431 FIBRONECTIN TYPE-III.
FT  DOMAIN 432 528 FIBRONECTIN TYPE-III.
FT  DOMAIN 529 624 FIBRONECTIN TYPE-III.
FT  DISULFID 132 143 BY SIMILARITY.
FT  DISULFID 249 296 BY SIMILARITY.
FT  DISULFID 267 310 BY SIMILARITY.
FT  CARBOHYD 51 51 POTENTIAL.
FT  CARBOHYD 94 94 POTENTIAL.
FT  CARBOHYD 129 129 POTENTIAL.
FT  CARBOHYD 186 186 POTENTIAL.
FT  CARBOHYD 279 279 POTENTIAL.
FT  CARBOHYD 392 392 POTENTIAL.
FT  CARBOHYD 408 408 POTENTIAL.
FT  CARBOHYD 474 474 POTENTIAL.
FT  CARBOHYD 487 487 POTENTIAL.
FT  CARBOHYD 582 582 POTENTIAL.
FT  CARBOHYD 613 613 POTENTIAL.
FT  CARBOHYD 613 613 POTENTIAL.
SQ  SEQUENCE 837 AA; 93406 MW; D55F84D4 CRC32;

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OY 29 LCVLGVPRGGSGANTAVISPODPELLIGSSLOACSIHGDPGALLBG-LYMTLNGRRU- 87
Dd 14 LIFLLPRSLSESCHIEISP-PVVRKADPVLASTCISPNCSKIDQOAKITMLKIDPEPIQ 71
OY 87 PSELRLU--WTSTLALALANLNGSRROOSGNLVCCHARDSILLAGSCLYGLRPPKPFNI 144
Dd 72 PGDRQHHLPODSTOESILTLPLHANT-QAFLECLVPWEDSVQILDOALHNGVYPPASPSNI 130
OY 145 SCWRS-NKKDLTCMTGTGANGETLHNTYSIK-YKLR---WYGDNTCEBYHTVGPSPCH 199
Dd 131 SCLMHLTNTNSLYVCQMEGPP-ETHLPRSFILKSPRSRADCQOYGDITPDCVANKRONNCS 188
OY 200 IP-KDLAFPEYEIVENETNLSGARSADVLTLDVADVTTPD-----PVRHVSRYG 250
Dd 189 IPRKNLLIYQYMAIYVQAEHLNGSSBSPKICLDPMDVYKLEPPQLQALMDIGPVSHPQ 248
OY 251 GLEDOLSVRWVS-PPALKDELFOAKYIRRYVE-DSVDMKVVVDY-SNQTSCYLAGLKRG 307
Dd 249 CL-----WLSMKPWRKSEYMEQECLELRQPOQLKANMTLVYHLPSKQOFLGCLGHQA 301
OY 308 TVTYVQVRCNFGILYSGKKAGINSFMS-----HPT-AASTPRSEBPGGGVCEPRGGE 361
Dd 302 PVYTLQNMCC-----IRSLPEFMSPMSPGLOLRMTAKAPITRLDT-----WCOKKOLDP 350
OY 362 SS-----GPVRELKQELGR 377
Dd 351 GTVASVOLFMRKPTPLQEDSGQIOGVL 375

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Search completed: September 17, 1999, 03:10:12
Job time: 292 sec

Result	No.	Score	Query Match	Length	DB	ID	Description
1	2096	93.1	422	4	075462	075462 homo sapien	
2	355.5	15.8	881	13	057519	057519 xenopus lae	
3	324.5	14.4	206	4	016334	016334 homo sapien	
4	306	13.6	581	6	046551	046551 ovis aries	
5	302.5	13.4	296	6	018880	018880 bos taurus	
6	268.5	11.9	346	13	093404	093404 oreochromis	
7	234.5	10.4	217	6	046336	046336 mustela vis	
8	230.5	10.2	198	6	018985	018985 cervus elap	
9	226.5	10.1	335	6	P79203	P79203 ovis aries	
10	226	10.0	372	11	088307	088307 mus musculus	
11	217.5	9.7	862	4	099655	099655 homo sapien	
12	215.5	9.6	874	11	P97378	P97378 mus musculus	
13	209.5	9.3	422	4	016542	016542 homo sapien	
14	208.5	9.3	432	11	064385	064385 mus musculus	
15	201	8.9	432	11	P70025	P70025 mus musculus	
16	194.5	8.6	440	11	000343	000343 mus musculus	
17	193.5	8.6	710	13	057520	057520 xenopus lae	
18	187.5	8.3	1165	6	002671	002671 sus scrofa	
19	182	8.1	895	11	026260	026260 rattus norv	
20	177	7.9	316	11	035545	035545 rattus norv	
21	174.5	7.8	958	4	092930	092930 homo sapien	
22	174.5	7.8	958	4	092921	092921 homo sapien	
23	174.5	7.8	958	4	013592	013592 homo sapien	
24	174.5	7.8	906	4	013593	013593 homo sapien	
25	174.5	7.8	896	4	013594	013594 homo sapien	
26	174.5	7.8	896	4	092919	092919 homo sapien	
27	163	7.2	1093	11	070535	070535 rattus norv	
28	162	7.2	427	4	095646	095646 homo sapien	
29	159.5	7.1	383	11	088786	088786 mus musculus	

30	156.5	7.0	971	11	070458	070458 mus musculus
31	156.5	7.0	970	11	088821	088821 mus musculus
32	153.5	6.8	229	6	027950	027950 bos indicus
33	153.5	6.8	228	6	028206	028206 bos taurus
34	153.5	6.8	228	11	035228	035228 mus musculus
35	149.5	6.6	229	4	075269	075269 homo sapien
36	149	6.6	226	4	060458	060458 homo sapien
37	149	6.6	1571	4	060459	060459 homo sapien
38	143	6.6	279	11	064336	064336 rattus norv
39	143.5	6.3	86	6	018853	018853 mustela put
40	141.5	6.3	229	9	014213	014213 homo sapien
41	139.5	6.2	890	11	0921A0	0921A0 cavia porce
42	138.5	6.1	634	6	046600	046600 bos taurus
43	136.5	6.1	296	6	P79195	P79195 macaca mula
44	133	5.9	369	6	014651	014651 homo sapien
45	133	5.9	420	4	014653	014653 homo sapien

ALIGNMENTS

RESULT	1	075462	PRELIMINARY;	PRT;	422 AA.
ID	075462				
AC	075462;				
DT	01-NOV-1998 (TrEMBLrel. 08, Created)				
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)				
DT	01-MAY-1999 (TrEMBLrel. 10, Last annotation update)				
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.				
GN	CLF-1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREYNER D.,				
RA	MONOD L.N., WELLS T.N.C., KOSCO-YILIOIS M.H., GAUCHAT J.F.,				
RT	"CLF-1, a Novel Soluble Protein Shares Homology With Members of the				
RT	Cytokine Type-1 Receptor Family.",				
RT	J. Immunol.0:0-0(1998).				
DR	EMBL; AF059293; AAC28335.1; -;				
DR	PFAM; PF00041; fn3; 2.				
DR	Signal.				
FT	CHAIN	1	37	POTENTIAL.	
FT	CHAIN	38	422	CYTOKINE-LIKE FACTOR-1.	
FT	SEQUENCE.	422 AA;	46301 MW;	877F9BC9 CRC32;	

Query Match	93.18;	Score 2096;	DB 4;	Length 422;
Best Local Similarity	93.78;	Pred. No. 9.2e-177;		
Matches 388;	Conservative	7;	Mismatches 13;	Indels 6;
				Gaps 3

QY	1	MPARPPVQASARPRPLSLSPILLCLYGVPRGSGMHTVISPDPILLISGLQ	60
Db	1	MPARPPVQASARPR - PILEPIL - ILLCYGAPRAGSGMHTVISPDPILLISGLL	57
QY	61	ATCSIHDDTGATMEGIVYTLNGRRRLSEISRLINSTLALALANLNGSRQSGDNLYCH	120
Db	58	ATCSVHDDPGATREGIVYTLNGRRRLPELSRYLINSTLALALANLNGSRQSGDNLYCH	117
QY	121	ARDGSILAGSCLYVGEPPERPFNISCWRNKKDLCTWRTGAGETFLHNTSLKYLRL	180
Db	118	ARDGSILAGSCLYVGEPPERPFNISCWRNKKDLCTWRTGAGETFLHNTSLKYLRL	177
QY	181	YGDGNCEEHYVGPBSCHLPRDLAFTPEIIVEATNRGLSARSVDLTLDVLYTTDP	240
Db	178	YGDGNCEEHYVGPBSCHLPRDLAFTPEIIVEATNRGLSARSVDLTLDVLYTTDP	237
QY	241	PPVYHVSRYVGELEDOQLSVRWVSPPALKDFELQAKYQIRYVEEDSVYMKVYDVVSNOTSCH	300
Db	238	PPVYHVSRYVGELEDOQLSVRWVSPPALKDFELQAKYQIRYVEEDSVYMKVYDVVSNOTSCH	297
QY	301	LAQLKRGTYVYVQRCNPRFQIYSKKAAGINSEMSHTLAASTPRSEPRPGGVCEDERGE	360

Db 73 HECPPDKTGTGNSCYSCSKYKTSIMKMYIVITVSAINOMGISSDPLVYVYIYEPPEPVN 132
 QY 244 VHSYRSGLEDOLESMVW---SPPALD---LEQAKYQIRYVEDSDKAVVDVSNQTS 238
 Db 133 LIL-ELKHEDRPRYIMIKWSPTLITDVSGMFSIOYERLKEKATDWE-THFAPLTQ 130
 QY 299 CRLAGLKPGTYFVQVRCNPFGIYSGSKKAGIWMSESHPTAATP 342
 Db 191 LKIFNLXPGOKYLVQIRCKP-----DHGWMSEMSPESTIQIP 227

RESULT 5

ID 018880 PRELIMINARY; PRT: 296 AA.

AC 018880;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 OS PROLACTIN RECEPTOR SHORT FORM.
 DS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 RN [1]
 RN [1]
 RN [1]
 RA MEDLINE; 97375450.
 RA SCHULER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal
 tissues."
 RL Endocrinology 138:3187-3194(1997).
 DR EMBL; AF027403; AAB83999.1;
 DR PFM; PF00041; fn3; 2.
 SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 13.4%; Score 302.5; DB 6; Length 296;

Best Local Similarity 31.9%; Pred. No. 4.9e-19;

Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

QY 91 SRLNTSTLALALNINSROSGDNLVCHARDGSLAGSLYGLPPEKPNISGWSRN 150
 Db 7 SRVFIILLFVSISLNG---QS-----PPEKPLVACRSPG 40
 QY 151 MKDLTCRWTPGAGHETFLHTNYSLSKRYKRWGQDNTCEHYTVGHSCHT-PKDLATTP 209
 Db 41 KETTCWMEPCADGC--LPNTYTLTYHKEGFTLHECPDYTGFGNSCYFSKKHISIMKM 98
 QY 210 YEIWEATNRLGSARSDVLTLDVYVTTDPPDVHSRVGLEDOLSVRWY--SPPALX 267
 Db 99 YVITVNAINOMGISSDPLVYVYIYEPPEPAITL-ELKHEDRPRYIMIKWSPTPT 157
 QY 268 D-----FLFOAKYQIRYVEDSDKAVVDVSNQTSRLAGLKPGTYFVQVRCNPFGIY 322
 Db 158 DVKSGWFIIO--YEIRLKEKATDWE-THFTLKOTQLKIFNLXPGOKYLVQIRCKP----- 211
 QY 323 GSKKAGIWMSESHPTAATP 342
 Db 211 ----DHGWMSEMSPESTIQIP 227

RESULT 6

ID 093404 PRELIMINARY; PRT: 346 AA.

AC 093404;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 OS PROLACTIN RECEPTOR (FRAGMENT).
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Perciformes; Labroidae; Cichlidae; Tilapia.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-GILL;
 RA SHIRAIISHI R., MARUDA M., MORI T., TENSUYA H.;
 RT "Expression of prolactin and cortisil receptor gene in early-life
 stages of tilapia (Oreochromis mossambicus)."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF080247; AAC31825.1;
 DR PFM; PF00041; fn3; 2.
 FT NON_TER 346
 SQ SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match 11.9%; Score 268.5; DB 13; Length 346;

Best Local Similarity 33.2%; Pred. No. 5.9e-16;

Matches 71; Conservative 28; Mismatches 92; Indels 23; Gaps 9;

QY 138 PEKPNISGWSNMMDLTCRWTPGAGHETFLHTNYSLSKRYKRWGQDNTCEHYTVGPHS 197
 Db 29 PEKPEITCRSEKEKFTTCWMPGSDG--LPTIYALYRKESDVAHECPDYHTAGKNS 86
 QY 198 CHIPK-DLALFTPEIWEATNRLGSARSDVLTLDVYVTTDPPDVHSRVGLEDQ- 256
 Db 87 CFENKNDLIMWSYITVYVAINALGRTYSDPVDIVYIVXPHPEKLEVT---VMDQK 143
 QY 256 ---LSVRWSPPALD---LEQAKYQIRYVED-SDKAVVDVSNQTSRLAGLKRECT 308
 Db 144 WPELVSW-EPHPRKADTSSGWTLLYELRYLDEDESEME-NHAAGQCKMFNIFSLRSG 201
 QY 309 YFVQVRCNPFGIYSGSKKAGIWMSESHPTAATP 342
 Db 202 TYLQVRCNPFGIYSGSKKAGIWMSESHPTAATP 342
 Db 202 TYLQVRCNPFGIYSGSKKAGIWMSESHPTAATP 342

RESULT 7

ID 046386 PRELIMINARY; PRT: 217 AA.

AC 046386;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 OS PROLACTIN RECEPTOR (FRAGMENT).
 CN PRUR.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
 RN [1]
 RN [1]
 RN [1]
 RA DOUGLAS D.A., SONG J.-H., HOUE A., MURPHY B.D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF029294; AAB88899.1;
 DR PFM; PF00041; fn3; 1.
 FT NON_TER 217
 FT NON_TER 217
 SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 10.4%; Score 234.5; DB 6; Length 217;

Best Local Similarity 32.3%; Pred. No. 3.2e-13;

Matches 61; Conservative 30; Mismatches 81; Indels 17; Gaps 7;

QY 160 PGAHGEFTLNTNYSLSKRYKRWGQDNTCEHYTVGHSCHT-PKDLALFTPEIWEATN 218
 Db 2 PGEEDG--LPTKTYTLTYHKEGFTTTCPCPYITSGPNSCYFNKRKHSIMWTYITINATN 59
 QY 219 RLGASRSDVLTLDVYVTTDPPDVHSRVGLEDOLSVRWY--SPPALXDP---LFQA 273
 Db 60 EMGSSSDPRVYVYIYEPPEPAITL-ELKHEDRPRYIMIKWSPTPTLDVRSGLTL 118
 QY 274 KYQIRYVEDSDKAVVDVSNQTSRLAGLKPGTYFVQVRCNPFGIYSGSKKAGIWMSE 333
 Db 119 QYRIRLKEKATDWE-THFAGLQTKILSLVPGKYLQVRCNPFGIYSGSKKAGIWMSE 170

QY 334 SHEPASTP 342
DB 171 SPKRSTQIP 179

RESULT 8

ID 018985 PRELIMINARY; PRT; 198 AA.

AC 018985;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE SOLUBLE PROLACTIN RECEPTOR.
OS Cervus elaphus nelsoni (American elk)
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervidae;
OC Cervinae; Cervus.
RN (1)
RP SEQUENCE FROM N.A.
RA JABBOUR H.N.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y14753; CAA5048.1;
DR PFAM; PF00041; fn3; 1.
SQ SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match 10.2%; Score 230.5; DB 6; Length 198;
Best Local Similarity 33.7%; Pred. No. 6,4e-13;
Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;

QY 123 DGSILGSCLYGLVLPPEKPNISCMRNMDLCRMTPGAHGTFHTNYSLKTKRMYG 182
DB 18 NASLNGOS-----PEKPIIKCRSGPKETTCWMEPSDGG--LPTNITLYHKEGT 70
QY 183 QDNTECEHYTHVGHSHI-PKDLALFTPEIWEATNRLGSASDVLTLDVVTDP 241
DB 71 LHECPKYGKGTGNTCFKSKHSIMKIYITVNAIINQMVSSDPLVYVTVIVEEP 130
QY 242 PDVHVSNGVGLDQOLSRWVS--PPALKD--LFOAKYQIRRVESDVAKYVDVSNQ 236
DB 131 ANLTL-ELKHPEDRKPYLMKWPPTLTDVKSWMFMQYRILKPEYATDWE-HDDLHP 188
QY 297 TSCR 300
DB 189 TSSR 192

RESULT 9

ID P79203 PRELIMINARY; PRT; 335 AA.

AC P79203;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Ovis aries (Sheep)
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-M2/80; TISSUE-ANTERIOR PITUITARY;
RA TORTOISE D.T.; BROOKS J.; INGLETON P.; MCNEILLY A.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y10578; CAA71597.1;
DR PFAM; PF00041; fn3; 1.
FT NON_TER 1
FT 335
SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 10.1%; Score 226.5; DB 6; Length 335;

Best Local Similarity 31.4%; Pred. No. 2.8e-12;
Matches 58; Conservative 28; Mismatches 68; Indels 31; Gaps 7;

QY 164 GETFLHTNLSKYLKRWGQDNTECEHYTHVGHSHIPKD-LALTPYIWEATNRLGS 222
DB 8 GETLH-----ECPDKYTGKGNPCFSKRYTSIMKMYITVSAINQOI 51
QY 223 ARSDVLTLDVLTDPDPDVHVSNGVGLDQOLSRWV--SPALKDF--LFOAKYQI 277
DB 52 SSDDPLVYVTVIVEEPVNLTL-ELKHPEDRKPYLMKWPPTLTDVKSWMFMQYRIL 110
QY 278 RRVESDVAKYVDVSNQTSRNLGKRGTYFYQVRCNPGIYSGKAGIWSWSHPT 337
DB 111 RLPKPKATDWE-THRAPKLTQKIFNIXPGQKYLVOIRCKP-----DHGYWSEWSPES 162
QY 338 AASTP 342
DB 163 FTQIP 167

RESULT 10

ID 088507 PRELIMINARY; PRT; 372 AA.

AC 088507;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, last annotation update)
DE CILIARY NEUTROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
KC TISSUE-BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYUD C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RT "Mouse homolog of human ciliary neurotrophic factor receptor."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068615; AAC25711.1;
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; fn3; 1.
FT SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT 21 336 CILIARY NEUTROTROPHIC FACTOR RECEPTOR
FT CHAIN ALPHA
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 10.0%; Score 226; DB 11; Length 372;
Best Local Similarity 26.0%; Pred. No. 3.6e-12;
Matches 97; Conservative 45; Mismatches 157; Indels 74; Gaps 18;

QY 30 CYLGVPRGSGAHTAVISDPDPLILIGSSIQATCSHGDPGATAE--GLYTLNGRL 86
DB 9 CCAVLAATAAAAYVTKHSPDEAPHYOYERLGAQVTL---PCGTASDAVAVTRVNGIDL 64
QY 87 PSELSLNTSTALALANLNGRSGDNLVCHADGSLAS-CUYGLPPEKPNIS 145
DB 65 APD--LLNGSQILRLSLGLSHGLYA---CFHDSWHLRQVLHVLHGLPREV-LS 115
QY 146 CWSRNN-KDLTCRW-----TPGAGEFLHTNYSLKRYLRYVGDNTCEHYTHVGH 197
DB 116 CRSNTPKKGVCWHLPTPIYINTNVTYVLRHSHKIN-----VEKPPAL-KNR 163
QY 198 CHIPKDLAFT--PYEWEATNRLGSARSVDLTLDVLTDPDPDVHVSNGVGLDQ 255
DB 164 CHI-RYMHLESTIKYKVSISVNALGH-NTTATTFDEFITVKKDPDENVAVARVPSPNR 221
QY 256 LSVRWSPPLKD-FLEQAKYQIRRVESDVAKYVDVSNQTSRNLGKAGIWSWSHPT 314
DB 222 LEVTWQTPSTWPDSPSPPLFLRYRPLLDQOHV-ELSDGTAHTTDAVAKEXYIIIV 280


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OY 315 RCNPGCYGSKKAGIWMSEMS-----HPTAASPRSRPSPGCGV 353
DB 281 AAK-----DNEIGTWSMDSVAAHATPWTTEPRHLTTEQAQAPETTTSTSSSLAPPTTKI 334
OY 354 CEP-----RGEPSS 362
DB 335 CDPGELSGSGGGS 347

RESULT 11
OY 099665 PRELIMINARY; PRT: 862 AA.
ID 099665:
DB 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
IL 12 RECEPTOR BETA2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64198; AAB36675.1;
PFAM: PF00041; fn3: 3.
SQ SEQUENCE 862 AA; 97134 MW; 5FE4FBDS CRC32;

Query Match
Best Local Similarity 9.78; Score 217.5; DB 4; Length 862;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

OY 53 LIGSSLAQTCSHGTPGATAGLYWTL-----NGRLPSLSRL-L 94
DB 41 ILGSTVNTCSL-----KPGGCFHYSRNRKLLYKFRIRINFHGHSLNSQVTLPL 94
OY 95 NSTTALALANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPFNISCMSRNMK-D 133
DB 95 GTTLFYCKLACINSDEIQ-----ICGAEIFGVAPEQDPONLSIOKEGOGT 140
OY 154 LGCRTPGAGHETFLHTNTSLKY-----KLRWYQ--DNCEETHTVG-----PHSCHI 200
DB 141 VACVETGRGR--DTHLTETYLQSLGPKNLWQKQCDIYC-DYLDGINTLPPSPESNFT 197
OY 201 PRDLALFTYEIWEATNLSGARSVYLIDVYTTDPDPVHVSRYGGLDQLSVRY 260
DB 198 AK-----VTAVNSLIGSSSLPSTFTEFDIVRPLPPMDIRIKFKASVSRGLTYW 246
OY 261 VSPALKDPLFOAKVOIRYVEDSVDMKVVDVDSNQTSCRLAGLKGTYFYVOVRCNPGF 320
DB 247 -----RDEGLVLLNRKLRKRPSSNRSLMNNVNTKAKGRDLDLQKFTETEYFOI-SSKLH 299
OY 321 IYSGKKAGIWMSEMSHPTASTPRSERPG 348
DB 300 LY-----KGSWSDMSLSLRAGTPEEPETG 323

RESULT 12
OY 099665 PRELIMINARY; PRT: 874 AA.
ID 099665:
DB 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
IL 12 RECEPTOR BETA2.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.

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RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64199; AAB36676.1;
DR MGI: MGI:1270861; IL12RB2.
DR PFAM: PF00041; fn3: 4.
SQ SEQUENCE 874 AA; 98196 MW; 9B90EB47 CRC32;

Query Match
Best Local Similarity 9.68; Score 215.5; DB 11; Length 874;
Matches 96; Conservative 59; Mismatches 145; Indels 79; Gaps 19;

OY 9 VAGSARPPREFSLIMSPLLL-----CVLGVPRGSGAHTAVISPODPTLLGSSQAT 62
DB 1 MAQTVRECSLALFLFMILLKANIDVCKG-----TVYQPA-PVLPSSANIS 50
OY 63 CSIH-----GDTPATAT-----BELYTLNGRL-----PSLSRLINTST-LALAL 103
DB 51 CSLNPKGCGSHYPSNSNELLILKFVNDVLENLHGKRVHDHGHSTGQVNTLSIGMTLFV 110
OY 104 ANLNGSRQSGDNL-VCHARDGSLAGSLYGLPPEKPFNISCMSRNMK-DLTCRWTPG 161
DB 111 CKLNGSNOKKRPYPVC-----GVELSVGAPEPPONISCVQEGENGTYACSVNSG 161
OY 162 AHGETFLHTNYSIKYKLRWYQDN-TCE-EYHTVGPHSC-----HPRDLALFTPYEI 212
DB 162 K--VYTLKNTYTLQLS-----GPNNLQCKQCFSDNRCNRLGLGINSPLDL-ESRFIV 214
OY 213 WPEATNRLGARSBDVLTLDVLYTTDPDPVHVSRYGGLDQLSVRYWVSPALKDPLFQ 272
DB 215 RVAINDLNGSSSLPHTFTEFDIVRPLPPMDIRINFNLNAGSGSGLTQW-----EDEGV 268
OY 273 AKQIRYVEDSVDMKVVDVDSNQTSCRLAGLKGTYFYVOVRCNPGFYGSK---KAGI 329
DB 269 VNLQKXOPINSTSMNNVNTKAKRTDLDLRFTEYEFQI-----SSKHLHSGS 320
OY 330 WSEMSHPTASTPRSERPG 348
DB 321 WSNWSESLRTRTPEEPVG 339

RESULT 13
OY 016542 PRELIMINARY; PRT: 422 AA.
ID 016542:
DB 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
IL INTERLEUKIN-11 RECEPTOR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA TISSUE-MUSCLE;
RX MEDLINE: 95399754.
RA CHEREL M., SOREL M., LEBEAU B., DOBOIS S., MOREAU J.F., BATAILLE R.,
MINIVIELLE S., JACQUES Y.,
"Molecular cloning of two isoforms of a receptor for the human
hematopoietic cytokine interleukin-11.",
Blood 86:2534-2540(1995).
RN (2)
RP SEQUENCE FROM N.A.
RA VAN LEUVEN F., STAS L., HILLIER C., MIYAKE Y., GOSSIER A.,
Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 3-390 FROM N.A.
RA TISSUE-PLACENTA;
RA CHEREL M., SOREL M., DOBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
MINIVIELLE S.,
Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U32324; AAB36492.1;

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DR EMBL: Z38102; CAA86224.1; -
 DR EMBL: U32323; CAA86491.1; -
 DR EMBL: Z46595; CAA86570.1; -
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; 1g; 1.
 SQ SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 9.38; Score 209.5; DB 4; Length 422;
 Best Local Similarity 23.9%; Pred. No. 1.2e-10;
 Matches 89; Conservative 53; Mismatches 138; Indels 93; Gaps 18;

OY 43 TAVISPOPTLLI-----GSLQANGSHGDDPGANA--GGLWTNG--RLPS 88
 DB 17 TALVASSPCQAWGPVQVQGPFRSVLCC-----PGTAGPVMFNDGEPKLLQG 70
 OY 89 ELSRLNTSTALALANNGSRQSGDNLVCHARDGSLIAGSCLVVGPPKPFNISCWS 148
 DB 71 PDGGLGHELVLAGADSTDEGT-----YICOTLDGALGVTQLGYPAPRV-VSCQA 122
 OY 149 RRMKLLTCRWTPGANGFPLHNYSLKTKLRVGGDNTCEEHTVGPSSCHIPKD----- 204
 DB 123 ADYENFSCWSPSQ--ISGLPFRYLTYSRKKTIVLAGDSQRSPSTGPWPC--PODPLGAA 178
 OY 204 -----LALFPEYIWEATNRLGARSQVLTLDVLTVDPTDPPDVHVSRYGLEDDLS 257
 DB 179 RCYVGAERWQYRINTVEVNLG--ASTRLDVSLSQSLRPDPGLKVESYVGPRLRLR 237
 OY 238 VAWVSP--PALKDELFOAKYQIRYVDSYDMKVVDVSNQTSCLRLK-----PG 307
 DB 238 ASWTPASWPCQPHLL--KFRLOYRPAQHNPAMSTVEP-----AGLEEVITDAVAG 286
 OY 308 TYTFVQVRCNPGIYGSKKAGIWSMSHPTASTRSEPRPGGVCCEPRGGEPSGVR 367
 DB 287 LPHARVVSARD-----LDAGTWSTWS--PEA-----WGPSTGTGIP 321
 OY 368 RELKQFLGKXK 380
 DB 322 KEIP---AWQLH 331
 RESULT 14
 O64385 PRELIMINARY: PRT: 432 AA.
 AC O64385;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
 GN (IL11B) (IL11RA) (IL11RB)
 GN IL11RA OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE: 95045367.
 RA HILTON D.J., HILTON A.A., RAICEVIC A., BAKAR S., HARRISON-SMITH M.,
 RA GOUH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., MILLSON T.A.;
 RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for
 RT gp130 for high affinity binding and signal transduction.";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRYO;
 RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,
 RA GUENET J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6;
 RA GOSSLER A.;

RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC -1- SUBUNIT LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.
 CC -1- CONTAINS ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CAA52908.1; -
 DR EMBL: U14412; CAA53248.1; -
 DR EMBL: X94162; CAA63873.1; -
 DR EMBL: X94163; CAA63873.1; JOINED.
 DR MGD: MGI:107426; IL11RA1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; 1g; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSSEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 SQ SEQUENCE 432 AA; 46655 MW; F6583060 CRC32;

Query Match 9.38; Score 208.5; DB 11; Length 432;
 Best Local Similarity 23.9%; Pred. No. 1.5e-10;
 Matches 94; Conservative 51; Mismatches 136; Indels 113; Gaps 20;

OY 7 GPVNASARPPRLSLMSPLLCVLGVRGSGAHTAVISPOPTLLIGSSLATCSIH 66
 DB 31 GPVQVQGPGR-----PVALCCPGVSAG----- 55
 OY 67 GDTGATAGLWTLNGRLRPLSELRLN--TSTLA--LALANNGSRQSGDNLVCHAR 122
 DB 55 --TP-----VSMRBDG-----SRLLGPDGSGHRLVLAQVSDPE--GTYVOTL 97
 OY 123 DGLIAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGANGFPLHNTYSLKTKLRMYG 182
 DB 98 DVGSGWTLTKLGPPAPR--EVSCQAVDYENFSCWSPGQ--VSGLPFRYLTYSRKKTLP 154
 OY 183 QDNICEHTVGPSSCHIPKD-----LALFPEYIWEATNRLGARSQVLTLD 231
 DB 155 CAESQRESPTGFWPC--PODPLNARCVHGAERWSEYRINTVEVNLG--ASTCLDVR 211
 OY 232 VLDVTTDPPDPVHVSRYGLEDDLSYRWVSPALK--DFLFOAKYQIRYVDSYDMK 288
 DB 212 LQSLTRPDPGLVSESVGPYRRLHNSWTPASMRQPHLL--KFRLOYRPAQHNPAMS 269
 OY 289 VDDVSNQ--TSCRLAGLKPGTVTFVOYRCNPGIYGSKKAGIWSMSHPTASTRSE 346
 DB 270 TVEPIGLEEVITDAVAGLP--HAVRVSARDF-----LDAGTWSAWS--PEA----- 312
 OY 347 PGPGGVCCEPRGGEPSGVRRELKQFLGKXK 380
 DB 312 -----WGPSTGTGIPD--WSQGH 331
 RESULT 15
 P70225 PRELIMINARY: PRT: 432 AA.
 ID P70225;

AC P70225; 009074;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11BETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11RBETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RA BLINSEKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 mouse genome."
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RA MEDLINE; 96278810.
 RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11
 receptor alpha chain and a related locus."
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RA MEDLINE; 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT "Identification of a second murine interleukin-11 receptor
 alpha-chain gene (Il11ra2) with a restricted pattern of expression."
 RL Genomics 40:387-394(1997).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL; X94157; CAA63872.1;
 DR EMBL; X94158; CAA63872.1; JOINED.
 DR EMBL; X94159; CAA63872.1; JOINED.
 DR EMBL; X94160; CAA63872.1; JOINED.
 DR EMBL; X94161; CAA63872.1; JOINED.
 DR EMBL; X98519; CAA67144.1;
 DR EMBL; U69491; AAC53114.1;
 DR MGD; MGI:109123; IL11RA2.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23.
 FT CHAIN 24 432.
 FT DOMAIN 24 367.
 FT TRANSMEM 368 393.
 FT DOMAIN 394 432.
 FT DOMAIN 41 102.
 FT CARBOHYD 127 127.
 FT CARBOHYD 194 194.
 FT CONFLICT 200 200.
 FT CONFLICT 384 384.
 SO SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

Query Match 8.9%; Score 201; DB 11; Length 432;
 Best Local Similarity 24.6%; Pred. No. 7e-10;

Matches 97; Conservative 49; Mismatches 148; Indels 100; Gaps 20;

OY 7 GPVAGSARRPRPLSLMSPLLCVGLVGRGSGAHTAVASPODPTLLIGSSLAQCSTH 66
 11
 DB 31 GPGVGVYGPGR-----PVMKCPGVSNAG----- 55

OY 67 GDRPGATAGIYWTNGRLRPLSELRLN--ISTLA--LALNNGSRQSGDNLYCHAR 122
 DB 55 --TP-----VSFRDGD-----SRLOGPDGSLGHRILVLAQVDSFDE---GTYYCQTL 97
 OY 123 DGSILASCLYGLPPEKPFNISCNRNMDLRCRTPRABDEFLHTYSLKYIKMTG 182
 DB 98 DGVSQGMVTLKGLFPFAR--EYSCQAVDENFSCWSPQ--VSGLPTRYLTSRYRKTLP 154
 OY 183 QNTECEYHTVGPCHPKD-----LALFPYEIWEATNRLGSARSDVLTLD 231
 DB 155 GAEQRESPTGTPWC--PQDPLEASRCVHALEFMRSEIRINTEVNSLG-ASTCLLDVR 211
 OY 232 VLDVYTPPPPVYHVRVGGLEDQLSVKRVSPALK---DELFQAKYQIRRVEDSDVMK 288
 DB 212 LOSLRPDPQGLRVESVGPFRRLHASTWTYPASWRQPHFL--KFLQYRPAQHAPMS 269
 OY 289 VVDVSNQ--TSCRLAGLKPQVYFVOYRCNPFGLYSGKAKGINSRHPNASTP---- 343
 DB 270 TVEPIGLEVITDVTAGLP---HAKVRSARDE-----LDAGTWSAWS--PEAWGTPSTGL 319
 OY 343 -RSERP---GPGGVCEPRGGEPSGSPVREELK 371
 DB 320 LQDEIPDMSQGHQQLQEAIVAQEDSLAPRPSLQ 353

Search completed: September 16, 1999, 20:40:05
 Job time: 5556 sec

Db 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQSKHKTINODEGILPSGRGAA 420
 QY 421 RGPAG 425
 Db 421 RGPAG 425

RESULT 2

W59804
 ID W59804 standard; Protein: 425 AA.
 AC W59804:
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of the murine U4 protein.
 KW Murine; U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 OS Mus sp.
 PN MO9831611-A1.
 PD 23-JUL-1998.
 PE 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PI (GENEX) GENETICS INST INC.
 PA Collins M, Donaldson D, Neben T, Whittiers M;
 DR WPI: 98-414109/35.
 DR N-PSDB: V41688.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response for treating cancer and autoimmune disease
 PS Claim 9, Pages 26-27; 38pp; English.
 CC This is the amino acid sequence of the murine U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is used to screen for specific binding
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 425 AA;

Query Match 99.8%; Score 2313; DB 1; Length 425;
 Best Local Similarity 99.8%; Pred. No. 2, 3e-191;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGRPVPAQSAARRPRPLSLMSPLLCLVAGVPRGSGAHRAVISPDPPTLLIGSSLQ 60
 Db 1 MPAGRPVPAQSAARRPRPLSLMSPLLCLVAGVPRGSGAHRAVISPDPPTLLIGSSLQ 60
 QY 61 ATCSINGDTPGATAEGLYTLNGRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 Db 61 ATCSINGDTPGATAEGLYTLNGRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 QY 121 ARDGSIIAGSCLYVGLPEKPFNISCWSRNKMDLTCRMTPGAGETFLHTNYSLSKYLKM 180
 Db 121 ARDGSIIAGSCLYVGLPEKPFNISCWSRNKMDLTCRMTPGAGETFLHTNYSLSKYLKM 180
 QY 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 Db 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 QY 241 PPDVHVSRYVGLGLEDOLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 Db 241 PPDVHVSRYVGLGLEDOLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 QY 301 LAGLKPCTVYFYVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGERGGE 360
 Db 301 LAGLKPCTVYFYVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGERGGE 360
 QY 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQSKHKTINODEGILPSGRGAA 420

Db 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQSKHKTINODEGILPSGRGAA 420
 QY 421 RGPAG 425
 Db 421 RGPAG 425

RESULT 3

W70862
 ID W70862 standard; Protein: 425 AA.
 AC W70862:
 DT 17-MAR-1999 (first entry)
 DE Rat zcyto5 protein.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand.
 OS Rattus sp.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70896.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood.
 PS Claim 1; Page 75-76; 55pp; English.
 CC The present sequence represents a protein designated zcyto5, which is
 CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 425 AA;

Query Match 98.7%; Score 2288; DB 1; Length 425;
 Best Local Similarity 98.8%; Pred. No. 3, 3e-189;
 Matches 420; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAGRPVPAQSAARRPRPLSLMSPLLCLVAGVPRGSGAHRAVISPDPPTLLIGSSLQ 60
 Db 1 MPAGRPVPAQSAARRPRPLSLMSPLLCLVAGVPRGSGAHRAVISPDPPTLLIGSSLQ 60
 QY 61 ATCSINGDTPGATAEGLYTLNGRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 Db 61 ATCSINGDTPGATAEGLYTLNGRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 QY 121 ARDGSIIAGSCLYVGLPEKPFNISCWSRNKMDLTCRMTPGAGETFLHTNYSLSKYLKM 180
 Db 121 ARDGSIIAGSCLYVGLPEKPFNISCWSRNKMDLTCRMTPGAGETFLHTNYSLSKYLKM 180
 QY 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 Db 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 QY 241 PPDVHVSRYVGLGLEDOLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 Db 241 PPDVHVSRYVGLGLEDOLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 QY 301 LAGLKPCTVYFYVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGERGGE 360

DB 301 LAGKPGTVTFVQVRCNPFEGITGSKKAGTINSEMSHPTAASPSESRPGGVCCEPRGGE 360
 QY 361 PSSGPRRELKQFGLGKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGLTLPGRGAA 420
 DB 361 PSSGPRRELKQFGLGKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGLTLPGRGAA 420
 QY 421 RGPAG 425
 DB 421 RGPAG 425
 RESULT 4
 ID W55011 standard; Protein; 413 AA.
 AC W55011;
 DT 29-SEP-1998 (first entry)
 DE Novel haemopoietin receptor NR6.1 protein.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KM cell survival; therapeutic; neuronal proliferation; drug screening;
 KM Mouse.
 OS Mus sp.
 PN M09811225-A2.
 PF 19-MAR-1998.
 PR 11-SEP-1997; G02479.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIF/) DZIGLEMSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J;
 DR MPI: 98-260970/23.
 DR N-PSDB: V27140.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PS e.g. neuronal cells
 PS Claim 14; Page 77-81; 182pp; English.
 CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation,
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 413 AA;

Query Match 96.1%; Score 2226.5; DB 1; Length 413;
 Best Local Similarity 98.8%; Pred. No. 6.3e-184;
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MPAGRPPVNASARRPRPLSLMSPLLCVLYGVRGSGAHTAVISPODPTLLIGSSIQ 60
 DB 1 MPAGRPPVNASARRPRPLSLMSPLLCVLYGVRGSGAHTAVISPODPTLLIGSSIQ 60
 QY 61 ATGSHDDTGCATGEGLYWTLNGRRLPSELRLNTSTLALALANLNGSSROQSGDNVCH 120
 DB 61 ATGSHDDTGCATGEGLYWTLNGRRLPSELRLNTSTLALALANLNGSSROQSGDNVCH 120
 QY 121 ARODSILAGSLVYGLPPEKPFNISCWSRNKKDLTCRWTGAGHETFLHTNYSLSKYLRW 180
 DB 121 ARODSILAGSLVYGLPPEKPFNISCWSRNKKDLTCRWTGAGHETFLHTNYSLSKYLRW 180
 QY 181 YGQDNTECEHTVGPCHSPKDLALFTPEIWEATNRLGARSADVLTLDDVYVTTDP 240
 DB 181 YGQDNTECEHTVGPCHSPKDLALFTPEIWEATNRLGARSADVLTLDDVYVTTDP 240
 QY 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
 DB 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300

QY 301 LAGKPGTVTFVQVRCNPFEGITGSKKAGTINSEMSHPTAASPSESRPGGVCCEPRGGE 360
 DB 301 LAGKPGTVTFVQVRCNPFEGITGSKKAGTINSEMSHPTAASPSESRPGGVCCEPRGGE 360
 QY 361 PSSGPRRELKQFGLGKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGLTLPGRGAA 420
 DB 361 PSSGPRRELKQFGLGKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGLTLPGRGAA 420
 QY 421 RGPAG 425
 DB 421 RGPAG 425
 RESULT 5
 ID W70860 standard; Protein; 422 AA.
 AC W70860;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 protein sequence.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KM cardiac pathology; heart enlargement; zcytor5 ligand.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR MPI: 99-034662/03.
 DR N-PSDB: V70894.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
 PT down-regulating zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 66-67; 55pp; English.
 CC The present sequence represents a protein designated zcytor5, which is
 CC a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 422 AA;

Query Match 93.8%; Score 2172.5; DB 1; Length 422;
 Best Local Similarity 94.8%; Pred. No. 2.9e-179;
 Matches 401; Conservative 6; Mismatches 14; Indels 3; Gaps 2;
 QY 1 MPAGRPPVNASARRPRPLSLMSPLLCVLYGVRGSGAHTAVISPODPTLLIGSSIQ 60
 DB 1 MPAGRPPVNASARRPRPLSLMSPLLCVLYGVRGSGAHTAVISPODPTLLIGSSIQ 57
 QY 61 ATGSHDDTGCATGEGLYWTLNGRRLPSELRLNTSTLALALANLNGSSROQSGDNVCH 120
 DB 58 ATGSHDDTGCATGEGLYWTLNGRRLPSELRLNTSTLALALANLNGSSROQSGDNVCH 117
 QY 121 ARODSILAGSLVYGLPPEKPFNISCWSRNKKDLTCRWTGAGHETFLHTNYSLSKYLRW 180
 DB 118 ARODSILAGSLVYGLPPEKPFNISCWSRNKKDLTCRWTGAGHETFLHTNYSLSKYLRW 177
 QY 181 YGQDNTECEHTVGPCHSPKDLALFTPEIWEATNRLGARSADVLTLDDVYVTTDP 240
 DB 178 YGQDNTECEHTVGPCHSPKDLALFTPEIWEATNRLGARSADVLTLDDVYVTTDP 237
 QY 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
 DB 238 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 297

QY 301 LAGLPGTYEVQVRCNPFYIGSKKAGIMSESHPTASTPSERPGEVCEPGE 360
 DB 298 LAGLPGTYEVQVRCNPFYIGSKKAGIMSESHPTASTPSERPGEVCEPGE 357
 QY 361 PSSGPVRELKQFLGWLKKAAYCSNLSFRLYDQWRAMQKSHTRNDEGILSGRGAA 420
 DB 358 PSSGPVRELKQFLGWLKKAAYCSNLSFRLYDQWRAMQKSHTRNDEGILSGRGAA 417
 QY 421 RGRA 424
 DB 418 RGRA 421

RESULT 6
 W59805
 ID W59805 standard; Protein: 408 AA.
 AC W59805;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of the human U4 protein.
 KW Human: U4 protein; haematopoietin receptor superfamily;
 KM cell proliferation; immune response; antibody; cell differentiation;
 KW auto-immune disease; cancer; allergy.
 OS Homo sapiens.
 PN W09831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998; US-784863.
 PR 16-JAN-1997; US-784863.
 PA (GEMT) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR MPI: 98-414109/35.
 DR N-PDB: V41689.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and auto-immune disease
 PS Claim 9; Pages 29-30; 38pp; English.
 CC This is the amino acid sequence of the human U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is used to screen for specific binding
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 408 AA;

Query Match 91.3%; Score 2116.5; DB 1; Length 408;
 Best Local Similarity 95.1%; Pred. No. 1.8e-174;
 Matches 330; Conservative 5; Mismatches 12; Indels 3; Gaps 2;

QY 15 RPRPLSLMSPLLCVLGVRGSGAHTAVISPODPTLLIGSSLCATCSIHGDTGATA 74
 DB 1 RPR-PLPL-LLLCVLGVRGSGAHTAVISPODPTLLIGSSLCATCSIHGDTGATA 57
 QY 75 EGIYTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLYCHARDGSLIAGSLY 134
 DB 58 EGIYTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLYCHARDGSLIAGSLY 117
 QY 135 GLPEPEPNISCSRMKMDLTCRTGAGETFLHNTSLKYLKRYGQDNCEHYHYG 194
 DB 118 GLPEPEPNISCSRMKMDLTCRTGAGETFLHNTSLKYLKRYGQDNCEHYHYG 177
 QY 195 PHSCHIPKDLALTPYEIWEATNRLGSASDVLTLVDVYTTDPDPVHSRVGLED 254
 DB 178 PHSCHIPKDLALTPYEIWEATNRLGSASDVLTLVDVYTTDPDPVHSRVGLED 237
 QY 255 QLSVKNVSPALKDFLFOAKYQIRIVEDSVMKVVDVSNQTSCLAGLPGTYEVQV 314
 DB 238 QLSVKNVSPALKDFLFOAKYQIRIVEDSVMKVVDVSNQTSCLAGLPGTYEVQV 297

QY 315 RCNPFYIGSKKAGIMSESHPTASTPSERPGEVCEPGEVCEPGEVCEPGEVCEPGE 374
 DB 298 RCNPFYIGSKKAGIMSESHPTASTPSERPGEVCEPGEVCEPGEVCEPGEVCEPGE 357
 QY 375 GMLKKAAYCSNLSFRLYDQWRAMQKSHTRNDEGILSGRGAA 424
 DB 358 GMLKKAAYCSNLSFRLYDQWRAMQKSHTRNDEGILSGRGAA 407

RESULT 7
 W70841
 ID W70841 standard; Protein: 385 AA.
 AC W70841;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR MPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 83-84; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 385 AA;

Query Match 90.5%; Score 2097; DB 1; Length 385;
 Best Local Similarity 99.7%; Pred. No. 8.1e-173;
 Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 AATAVISPDDPTLLIGSSLCATCSIHGDTGATAVITLNGRRRLPSELRLNTSTLA 100
 DB 1 AATAVISPDDPTLLIGSSLCATCSIHGDTGATAVITLNGRRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRQSGDNLYCHARDGSLIAGSLYGLPEPEPNISCSRMKMDLTCRTW 160
 DB 61 LALANLNGSRQSGDNLYCHARDGSLIAGSLYGLPEPEPNISCSRMKMDLTCRTW 120
 QY 161 GAGGETFLHNTSLKYLKRYGQDNCEHYHYGHSCHIPKDLALTPYEIWEATNRL 220
 DB 121 GAGGETFLHNTSLKYLKRYGQDNCEHYHYGHSCHIPKDLALTPYEIWEATNRL 180
 QY 221 GSARDVTLVDVYTTDPDPVHSRVGLEDLSVRWSPALKDFLFOAKYQIRYR 280
 DB 161 GSARDVTLVDVYTTDPDPVHSRVGLEDLSVRWSPALKDFLFOAKYQIRYR 240
 QY 281 VEDSVDMKVVDVSNQTSCLAGLPGTYEVQVRCNPFYIGSKKAGIMSESHPTAST 340
 DB 241 VEDSVDMKVVDVSNQTSCLAGLPGTYEVQVRCNPFYIGSKKAGIMSESHPTAST 300
 QY 341 TPSERPGEVCEPGEVCEPGEVCEPGEVCEPGEVCEPGEVCEPGEVCEPGEVCEPGE 400

Db 301 TPSSRGPGCGVCEPSSGSPVREIKQFLGWLKKNAYCSNLSFRLYDQWRAMQK 360
 QY 401 SHKTRNDEGILPSGRGARGPAG 425
 Db 361 SHKTRNDEGILPSGRGARGPAG 385

RESULT 8

W70861 8
 ID W70861 standard; Protein: 425 AA.
 AC W70861;
 DT 17-MAR-1999 (first entry)
 DE Allelic variant of human zcyto5.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 cardiac pathology; heart enlargement; zcyto5 ligand; allelic variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR N-PSDB: W70895.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.,
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood.
 PS Claim 1: Page 71-72; 55pp; English.
 CC The present sequence represents an allelic variant of protein designated
 CC zcyto5, which is a cytokinin-like receptor. Soluble zcyto5 may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 425 AA;

Query Match 90.4%; Score 2094; DB 1; Length 425;
 Best Local Similarity 94.88; Pred. No. 1.7e-172;
 Matches 386; Conservative 5; Mismatches 12; Indels 4; Gaps 2;
 QY 1 MPAGRPVQASARRPRLSLMSPLLCVLYGRGSGAHTAVISPODPTLLIGSSIQ 60
 Db 1 MPAGRRPRAQASARRP-PLLP-LLLCVLYGRGSGAHTAVISPODPTLLIGSSIL 56
 QY 61 ATGCSHCDTGTGATAAGLWTLNGRRRLPSELRLNTSTLALANLNGSRQOSDNTVCH 120
 Db 57 ATGCSVHDDPGATREGILYMTLNGRRRLPSELRLNTSTLALANLNGSRQOSDNTVCH 116
 QY 121 ARGSTIAGSCLVYGLPEKPEFNISCSRNKKDLTCRWTPAHGETFLHTNYSKYLKRW 180
 Db 117 ARGSTIAGSCLVYGLPEKPEFNISCSRNKKDLTCRWTPAHGETFLHTNYSKYLKRW 176
 QY 181 YGDNCEETHTVGPSPHCHIPKDLALFTPEIWEATNRLGASASDVLTDLDVYTTDP 240
 Db 177 YGDNCEETHTVGPSPHCHIPKDLALFTPEIWEATNRLGASASDVLTDLDVYTTDP 236
 QY 241 PPDVHVSRRVGGLEDQLSVSRWVSPALADFLFOAKYQIRYVEDSVDMKVVDDVSNQSCR 300
 Db 237 PPDVHVSRRVGGLEDQLSVSRWVSPALADFLFOAKYQIRYVEDSVDMKVVDDVSNQSCR 296
 QY 301 LAGLKPCTVTFVQVRCNPFGLYSGKAGINSMSHPPTAASPRESRGPGGCGVCEPRGGE 360

Db 297 LAGLKPCTVTFVQVRCNPFGLYSGKAGINSMSHPPTAASPRESRGPGGCGVCEPRGGE 356
 QY 361 PSSGVPAREIKQFLGWLKKNAYCSNLSFRLYDQWRAMQKSHKTRNQ 407
 Db 357 PSSGVPAREIKQFLGWLKKNAYCSNLSFRLYDQWRAMQKSHKTRNQ 403

RESULT 9

W70839 9
 ID W70839 standard; Protein: 388 AA.
 AC W70839;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR N-PSDB: W70895.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.,
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood.
 PS Claim 1: Page 80-81; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 388 AA;

Query Match 88.5%; Score 2051; DB 1; Length 388;
 Best Local Similarity 96.4%; Pred. No. 7.5e-169;
 Matches 373; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 38 GSGAHTAVISPODPTLLIGSSLATCSIHGTPATAGLWTLNGRRRLPSELRLNTS 97
 Db 1 GSGAHTAVISPODPTLLIGSSLATCSVHDDPGATREGILYMTLNGRRRLPSELRLNTS 90
 QY 98 TLALANLNGSRQOSDNTVCHARDOSIAGSCLVYGLPEKPEFNISCSRNKKDLTCR 157
 Db 61 TLALANLNGSRQOSDNTVCHARDOSIAGSCLVYGLPEKPEFNISCSRNKKDLTCR 120
 QY 158 WTPAHGETFLHTNYSKYLKRWYGDNCEETHTVGPSPHCHIPKDLALFTPEIWEAT 217
 Db 121 WTPAHGETFLHTNYSKYLKRWYGDNCEETHTVGPSPHCHIPKDLALFTPEIWEAT 180
 QY 218 NRLGASASDVLTDLDVYTTDPDPPDVHVSRRVGGLEDQLSVSRWVSPALADFLFOAKYQIR 277
 Db 181 NRLGASASDVLTDLDVYTTDPDPPDVHVSRRVGGLEDQLSVSRWVSPALADFLFOAKYQIR 240
 QY 278 RYVEDSVDMKVVDDVSNQSCRAGLPGVYTFVQVRCNPFGLYSGKAGINSMSHPPT 337
 Db 241 RYVEDSVDMKVVDDVSNQSCRAGLPGVYTFVQVRCNPFGLYSGKAGINSMSHPPT 300

OY 338 AASTPSEBPGGGVCEPRGSGPVREIKOFLGMLKKHAYCSNLSFRLYDQWRAN 397
 DB 301 AASTPSEBPGGGVCEPRGSGPVREIKOFLGMLKKHAYCSNLSFRLYDQWRAN 360
 OY 398 MOKSHKTRNDEGILPSGRGAARCPA 424
 DB 361 MOKSHKTRNDEGILPSGRGAARCPA 387

RESULT 10

W70842
 ID W70842 standard; Protein: 385 AA.
 AC W70842;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc.difference 42 /note="not specified".
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 84-85; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SO Sequence 385 AA;

Query Match 87.8%; Score 2035; DB 1; Length 385;
 Best Local Similarity 96.4%; Pred. No. 1.8e-167;
 Matches 370; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 41 AHAFAVSPDPTLLIGSSLOATCSIHGDTFGATAEGILYTLNRRRLPSELRLNTSTA 100
 DB 1 AHAFAVSPDPTLLIGSSLOATCSIHGDTFGATAEGILYTLNRRRLPSELRLNTSTA 60
 OY 101 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTOR 160
 DB 61 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTOR 120
 OY 161 GAHGEFTLNTNLSLTKKRLMYGODNCEEHYTGPHSCHIPKDLAFTPEIWEATNRL 220
 DB 121 GAHGEFTLNTNLSLTKKRLMYGODNCEEHYTGPHSCHIPKDLAFTPEIWEATNRL 180
 OY 221 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 280
 DB 181 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 240
 OY 281 VEDSVDMKVVDDVSNQTSCLAGLKPQTYFFVYRCNPNPFIYSKAGIMSESHPTAS 340

DB 241 VEDSVDMKVVDDVSNQTSCLAGLKPQTYFFVYRCNPNPFIYSKAGIMSESHPTAS 300
 OY 341 TPSEBPGGGVCEPRGSGPVREIKOFLGMLKKHAYCSNLSFRLYDQWRAN 400
 DB 301 TPSEBPGGGVCEPRGSGPVREIKOFLGMLKKHAYCSNLSFRLYDQWRAN 360
 OY 401 SHKTRNDEGILPSGRGAARCPA 424
 DB 361 SHKTRNDEGILPSGRGAARCPA 384

RESULT 11

W70840
 ID W70840 standard; Protein: 392 AA.
 AC W70840;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc.difference 42 /note="not specified".
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SO Sequence 392 AA;

Query Match 85.4%; Score 1978; DB 1; Length 392;
 Best Local Similarity 97.0%; Pred. No. 1.5e-162;
 Matches 359; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 38 GGAHFAVSPDPTLLIGSSLOATCSIHGDTFGATAEGILYTLNRRRLPSELRLNTS 97
 DB 1 GGAHFAVSPDPTLLIGSSLOATCSIHGDTFGATAEGILYTLNRRRLPSELRLNTS 60
 OY 98 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTOR 157
 DB 61 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTOR 120
 OY 158 GAHGEFTLNTNLSLTKKRLMYGODNCEEHYTGPHSCHIPKDLAFTPEIWEAT 217
 DB 121 GAHGEFTLNTNLSLTKKRLMYGODNCEEHYTGPHSCHIPKDLAFTPEIWEAT 180
 OY 218 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 277
 DB 181 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 240
 OY 278 VEDSVDMKVVDDVSNQTSCLAGLKPQTYFFVYRCNPNPFIYSKAGIMSESHPT 337

Db 241 RYRVEDVDKVVYDVNSQTSCLAGLKPCTVYFVQRCNPFGIYSKKAGIMSEWSHPT 300
 QY 338 AASTPSEPPGGVCEPGEPPSSGPPVRELKQFLGWLKHAHCNSLSFRLYDQWRAAM 397
 Db 301 AASTPSEPPGGVCEPGEPPSSGPPVRELKQFLGWLKHAHCNSLSFRLYDQWRAAM 360
 QY 398 MOKSHKTRNQ 407
 Db 361 MOKSHKTRNQ 370

RESULT 12

W70850 standard; Protein: 389 AA.
 ID W70850
 AC W70850: 17-MAR-1999 (first entry)
 DE Human zcytoxin-like receptor; down-regulation; growth factor;
 KW zcytoxin; cytokinin-like receptor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytoxin ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: US-074721.
 PR 13-FEB-1998: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams R, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytoxin - useful for, e.g.
 PT down-regulating zcytoxin natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a zcytoxin variant protein. zcytoxin
 CC is a cytokinin-like receptor. Soluble zcytoxin may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytoxin could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytoxin ligands. A probe
 CC comprising zcytoxin DNA or RNA can be used to determine the presence
 CC and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytoxin and
 CC therapeutically to modify zcytoxin ligand effects.
 SQ Sequence 389 AA;

Query Match 84.7%; Score 1963; DB 1; Length 389;
 Best Local Similarity 97.3%; Pred. No. 2,9e-161;
 Matches 357; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 100
 Db 1 AHTAVISPODPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSROOSDNLVCHARDGSIILAGSLVGLPPEKPNISCSKNNKDLTCRMT 160
 Db 61 LALANLNGSROOSDNLVCHARDGSIILAGSLVGLPPEKPNISCSKNNKDLTCRMT 120
 QY 161 GAGETFLHTNYSILKYLKRWGQDNTCEHYHTVGPCHSCHKIDALFTPEIWEATNRL 220
 Db 121 GAGETFLHTNYSILKYLKRWGQDNTCEHYHTVGPCHSCHKIDALFTPEIWEATNRL 180
 QY 221 GSASDVLITLIDLVTTDPPDVHVSRLVGLDQLSVRWSPALDQLFOAKYQIRYR 280
 Db 181 GSASDVLITLIDLVTTDPPDVHVSRLVGLDQLSVRWSPALDQLFOAKYQIRYR 240
 QY 281 VEDSDMKVVDVNSQTSCLAGLKPCTVYFVQRCNPFGIYSKKAGIMSEWSHPTAAS 340
 Db 241 VEDSDMKVVDVNSQTSCLAGLKPCTVYFVQRCNPFGIYSKKAGIMSEWSHPTAAS 300

QY 341 TPSEPPGGVCEPGEPPSSGPPVRELKQFLGWLKHAHCNSLSFRLYDQWRAAM 400
 Db 301 TPSEPPGGVCEPGEPPSSGPPVRELKQFLGWLKHAHCNSLSFRLYDQWRAAM 360
 QY 401 SHKTRNQ 407
 Db 361 SHKTRNQ 367

RESULT 13

W70844 standard; Protein: 389 AA.
 ID W70844
 AC W70844: 17-MAR-1999 (first entry)
 DE Human zcytoxin-like receptor; down-regulation; growth factor;
 KW zcytoxin; cytokinin-like receptor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytoxin ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: US-074721.
 PR 13-FEB-1998: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams R, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytoxin - useful for, e.g.
 PT down-regulating zcytoxin natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a zcytoxin variant protein. zcytoxin
 CC is a cytokinin-like receptor. Soluble zcytoxin may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytoxin could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytoxin ligands. A probe
 CC comprising zcytoxin DNA or RNA can be used to determine the presence
 CC and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytoxin and
 CC therapeutically to modify zcytoxin ligand effects.
 SQ Sequence 389 AA;

Query Match 84.7%; Score 1962; DB 1; Length 389;
 Best Local Similarity 97.0%; Pred. No. 3.5e-161;
 Matches 356; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 100
 Db 1 AHTAVISPODPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSROOSDNLVCHARDGSIILAGSLVGLPPEKPNISCSKNNKDLTCRMT 160
 Db 61 LALANLNGSROOSDNLVCHARDGSIILAGSLVGLPPEKPNISCSKNNKDLTCRMT 120
 QY 161 GAGETFLHTNYSILKYLKRWGQDNTCEHYHTVGPCHSCHKIDALFTPEIWEATNRL 220
 Db 121 GAGETFLHTNYSILKYLKRWGQDNTCEHYHTVGPCHSCHKIDALFTPEIWEATNRL 180
 QY 221 GSASDVLITLIDLVTTDPPDVHVSRLVGLDQLSVRWSPALDQLFOAKYQIRYR 280
 Db 181 GSASDVLITLIDLVTTDPPDVHVSRLVGLDQLSVRWSPALDQLFOAKYQIRYR 240
 QY 281 VEDSDMKVVDVNSQTSCLAGLKPCTVYFVQRCNPFGIYSKKAGIMSEWSHPTAAS 340
 Db 241 VEDSDMKVVDVNSQTSCLAGLKPCTVYFVQRCNPFGIYSKKAGIMSEWSHPTAAS 300

QY 341 TPSEBPGGVCCEPGEPSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWRAMOK 400
 DB 301 TPSEBPGGVCCEPGEPSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWRAMOK 360
 QY 401 SHKTRNO 407
 DB 361 SHKTRNO 367

RESULT 14

ID W70851 standard; Protein: 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: 008655.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA.

Query Match 84.6%; Score 1961; DB 1; Length 389;
 Best Local Similarity 96.7%; Pred. No. 4,3e-161;
 Matches 355; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 60
 QY 101 LALANLNGRROSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRMT 160
 DB 61 LALANLNGRROSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRMT 120
 QY 161 GAHGETFLHTNYSKLYKLRWYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATRL 220
 DB 121 GAHGETFLHTNYSKLYKLRWYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATRL 180
 QY 221 GSARSDVLTLDVLTDDVTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIR 280
 DB 181 GSARSDVLTLDVLTDDVTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLPGTYVFOVRNPFGLYSGKKGINSSEHPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLPGTYVFOVRNPFGLYSGKKGINSSEHPTAAS 300
 QY 341 TPSEBPGGVCCEPGEPSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWRAMOK 400

DB 301 TPSEBPGGVCCEPGEPSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWRAMOK 360
 QY 401 SHKTRNO 407
 DB 361 SHKTRNO 367

RESULT 15

ID W70852 standard; Protein: 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: 008655.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 98-99; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA.

Query Match 84.6%; Score 1960; DB 1; Length 389;
 Best Local Similarity 96.7%; Pred. No. 5.2e-161;
 Matches 355; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 60
 QY 101 LALANLNGRROSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRMT 160
 DB 61 LALANLNGRROSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRMT 120
 QY 161 GAHGETFLHTNYSKLYKLRWYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATRL 220
 DB 121 GAHGETFLHTNYSKLYKLRWYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATRL 180
 QY 221 GSARSDVLTLDVLTDDVTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIR 280
 DB 181 GSARSDVLTLDVLTDDVTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLPGTYVFOVRNPFGLYSGKKGINSSEHPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLPGTYVFOVRNPFGLYSGKKGINSSEHPTAAS 300
 QY 341 TPSEBPGGVCCEPGEPSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWRAMOK 400

Db 301 TPRESPPGGGACEPRGCEPSSGPVRELNQFLGWLKHAACSNLSFRLYDOWRAMOK 360
OY 401 SHKTRNQ 407
Db 361 SHKTRNQ 367

Search completed: September 17, 1999, 03:08:13
Job time: 304 sec

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:06 ; Search time 53.94 Seconds

(without alignments)
77.754 Million cell updates/sec

Title: US-09-037-657-15

Sequence: 1 MPAGRPVQASARRPRPL.....NODEGILPSGRGAKAPAG 425

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

- Issued Patents, AA.*
1: /cgn2-6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2-6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2-6/ptodata/2/1aa/PCUS9.COMB.pep.*
4: /cgn2-6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	14.2	708	1 US-07-797-556-2	Sequence 2, Appl 1
2	329	14.2	708	2 US-08-308-881-2	Sequence 2, Appl 1
3	329	14.2	708	3 PCT-US95-06530-2	Sequence 2, Appl 1
4	254.5	11.0	836	1 US-07-923-976-4	Sequence 4, Appl 1
5	254.5	11.0	836	1 US-07-923-976-6	Sequence 4, Appl 1
6	254.5	11.0	836	1 US-07-923-976-8	Sequence 4, Appl 1
7	252.5	10.9	837	1 US-07-923-976-2	Sequence 8, Appl 1
8	230.5	9.5	372	1 US-07-865-878A-4	Sequence 2, Appl 1
9	230.5	9.5	372	1 US-07-676-647-2	Sequence 2, Appl 1
10	230.5	9.5	372	1 US-08-449-329-2	Sequence 2, Appl 1
11	220.5	9.5	372	1 US-08-445-073-2	Sequence 2, Appl 1
12	220.5	9.5	372	3 PCT-US91-03896-2	Sequence 2, Appl 1
13	217.5	9.4	862	2 US-08-685-118-2	Sequence 2, Appl 1
14	217.5	9.4	862	2 US-08-915-495-2	Sequence 2, Appl 1
15	216.5	9.3	602	2 US-08-419-632-6	Sequence 2, Appl 1
16	206	8.9	572	2 US-08-419-652-5	Sequence 5, Appl 1
17	192.5	8.3	635	1 US-08-184-327A-4	Sequence 4, Appl 1
18	192.5	8.3	635	1 PCT-US95-00670-4	Sequence 4, Appl 1
19	192	8.3	633	1 US-08-250-859-17	Sequence 17, Appl 1
20	192	8.3	633	1 US-08-490-803-17	Sequence 17, Appl 1
21	192	8.3	633	3 PCT-US94-08806-17	Sequence 17, Appl 1
22	192	8.3	633	3 PCT-US95-01775-17	Sequence 17, Appl 1
23	192	8.3	633	3 PCT-US95-16626-7	Sequence 7, Appl 1
24	190	8.2	1001	1 US-07-797-556-6	Sequence 6, Appl 1
25	190	8.2	1001	1 US-07-943-843-2	Sequence 2, Appl 1
26	190	8.2	1097	1 US-07-943-843-6	Sequence 2, Appl 1
27	190	8.2	1001	2 US-08-347-003-2	Sequence 6, Appl 1
28	190	8.2	1097	2 US-08-347-003-6	Sequence 6, Appl 1
29	186	8.0	626	1 US-08-184-327A-2	Sequence 2, Appl 1
30	186	8.0	482	1 US-08-184-327A-8	Sequence 8, Appl 1
31	186	8.0	626	3 PCT-US95-00670-2	Sequence 2, Appl 1
32	186	8.0	482	3 PCT-US95-00670-8	Sequence 8, Appl 1
33	185	8.0	719	1 US-07-943-843-4	Sequence 4, Appl 1
34	185	8.0	719	1 US-08-347-003-4	Sequence 4, Appl 1
35	174.5	7.5	569	1 US-08-306-231-3	Sequence 3, Appl 1
36	174.5	7.5	960	2 US-08-355-888A-8	Sequence 8, Appl 1
37	174.5	7.5	960	2 US-08-693-697-33	Sequence 33, Appl 1
38	174.5	7.5	908	2 US-08-693-697-33	Sequence 36, Appl 1
39	174.5	7.5	898	2 US-08-693-697-36	Sequence 36, Appl 1

40	173.5	7.5	908	2 US-08-588-526-3	Sequence 3, Appl 1
41	170	7.3	888	1 US-08-445-640-35	Sequence 35, Appl 1
42	169.5	7.3	960	2 US-08-588-190-3	Sequence 3, Appl 1
43	159.5	6.9	383	1 US-08-609-572-2	Sequence 2, Appl 1
44	151.5	6.5	508	2 US-08-850-293-5	Sequence 5, Appl 1
45	149.5	6.5	897	1 US-07-960-389-2	Sequence 2, Appl 1

ALIGNMENTS

RESULT 1
US-07-797-556-2
Sequence 2, Application US/07797556
Patent No. 5262522

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 37,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match 14.28; Score 329; DB 1; Length 708;
Best Local Similarity 28.64; Pred. No. 1.3e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY	46	ISPDPLILIGSSIQANCSIHG---DTPGATFAGELTYLNGRRRLPSLSLTLTSTALA	102
DB	31	ISPSPVQVLSNSTACVLEKCMDFHVANAYIVKRTNHFTHPKQDYIIINRTASVT	90
QY	103	LANNRGROSGDLYVCHARDGSLASGCLYGLPPEKPNISCSMMMDLCRWTPGA	162
DB	91	FTDIASNIQILTCILIFGQLEQVNYGITIISGLPPEKPNISCSIVGKMKCEWDGR	150
QY	163	HGETFLTNLSLKYKLKLMYGODNTCEYHATVGPSPHCHIPDLALFPEYELVETATNLGS	222
DB	151	--EHLLENFLKSEMAHFKFADCKAKRDT--PTSCVDVSTYVFVNIETVWEAKNLGK	206
QY	223	ARQVLLDLVLYVTTPPPDVHYSKRGGLLEDQLSVHWSPPALKDELPAKQIIRVE	282
DB	207	VTSIHNFDPYTKKPPPNHLSINSELSILKLTWN-PSIKSVYII-LKINIDYRTK	264
QY	283	DSYMKVY---DVSNOTSCLAGLKPGTYVFQVRCNPGIIGSKKAGIMSEMSHTPA	339

REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-676-647-2

Query Match 9.5%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDPTLL-----IGSSLOATCSIHGDTFGATAEGLYTLNGRRLPSELS 91
 15 AAAAYVYQHRSPQAPPHVOYERLGSVDYTLPCGTANMDAAVT-----WRVNGTDLAPD-- 68
 92 RLINTSTLALANLNGSRQSGDNLVCHARGSLIAGS-CLYVGLPPEKPNISCSNRN 150
 68 -LINGSOLV-----LHGELGHSGLYACFHRQSWHLRHQVLLHVGLPPEPEV-LSCRSNT 120
 151 M-KDLTCRW-----TPGAHGETFLHTNYSLKYLKRWYGODNTCEHYITVGHSHIRK 202
 121 YPRGFCYSWMLPPTIPIPTFNFTVYLGSKIM-----VCEKDPAL-KNRCHT-R 167
 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVLDVYTTDPPPVNHSRVGGLDOLSVRN 260
 168 YMHFSTIKKVSISVSNALGH-NATAITDEFITVPPDENNVANPVSNRRLLEYTW 226
 261 VSPALND-FLFOAKIQRVVEDSVWKYVDVSNQTSCLAGLKPGTYFYVQVRCPNF 319
 227 QTPSTWPDSEFPKFLRYRPLILDQOHV-ELSDGTAHTITAYAKKEITIOVAAK-- 284
 320 GIYSKKAGTSEMS-----HPTASTPSESPGPGGVCYCEPRG 358
 284 ----DNEIGTWSWVAHAHATPWTBEPNHLITTEAQAETTTSTSLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELGSG 343

RESULT 10
 US-08-449-329-2
 Sequence 2, Application US/08449329
 Patent No. 5648336
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,329

FILING DATE: 530
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/700,677
 FILING DATE: 15-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-449-329-2

Query Match 9.5%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDPTLL-----IGSSLOATCSIHGDTFGATAEGLYTLNGRRLPSELS 91
 15 AAAAYVYQHRSPQAPPHVOYERLGSVDYTLPCGTANMDAAVT-----WRVNGTDLAPD-- 68
 92 RLINTSTLALANLNGSRQSGDNLVCHARGSLIAGS-CLYVGLPPEKPNISCSNRN 150
 68 -LINGSOLV-----LHGELGHSGLYACFHRQSWHLRHQVLLHVGLPPEPEV-LSCRSNT 120
 151 M-KDLTCRW-----TPGAHGETFLHTNYSLKYLKRWYGODNTCEHYITVGHSHIRK 202
 121 YPRGFCYSWMLPPTIPIPTFNFTVYLGSKIM-----VCEKDPAL-KNRCHT-R 167
 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVLDVYTTDPPPVNHSRVGGLDOLSVRN 260
 168 YMHFSTIKKVSISVSNALGH-NATAITDEFITVPPDENNVANPVSNRRLLEYTW 226
 261 VSPALND-FLFOAKIQRVVEDSVWKYVDVSNQTSCLAGLKPGTYFYVQVRCPNF 319
 227 QTPSTWPDSEFPKFLRYRPLILDQOHV-ELSDGTAHTITAYAKKEITIOVAAK-- 284
 320 GIYSKKAGTSEMS-----HPTASTPSESPGPGGVCYCEPRG 358
 284 ----DNEIGTWSWVAHAHATPWTBEPNHLITTEAQAETTTSTSLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELGSG 343

RESULT 11
 US-08-445-073-2
 Sequence 2, Application US/08445073
 Patent No. 5849857
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/445,073
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/676,647
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mastrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-445-073-2

Query Match 9.5%; Score 220.5; DB 2; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHAVI-----SPDPTLL-----IGSSLOATCSIHGDPGATAGELWTLNGRRPSELS 91
 15 AAAAVYAAQHSPOEAPHYQERLGSVDVLLPGTAMDAAYT-----WRVNGTDLAPD-- 68
 92 RLNTSTLALANLNGSQSGDNLYCHARDGSIAGS-CLYVGLPPEKPFENISCSRN 150
 68 -LLNSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVLGPPEPV-LSGRSNT 120
 151 M-KDLTCRW-----TPAGHETFLHTNYSLSKYLKRWYGQDNTCEEYHTVGPFSCHIRK 202
 121 YPKGYCSWHLPTPIYIPFTFNTVYVLAHSGKIM-----VCEKDPAL-KNRCHI-R 167
 203 DLALT--PYEIVWEATNRLGSARSDVLLDVLVYTTDPPDVHVSRYGLEDQLSYRM 260
 168 YHMLSTIKYKYSISVSNALGH-NATATTFDEFTYKPPDPENVAVARVPSPNRRLEVTW 226
 261 VSPPALKD-FLFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPFTYVFVQVRCNPF 319
 227 QTPSTWPPDESPLKFFLRRLILDQOHV-ELSDGTAHTTIDAYAKREYIIQVAAK-- 284
 320 GIYSKKAGINSEMS-----HPTASTPSEKPGGCGVCEPRG 358
 284 ----DNEIGTMSDMSVAHAHAPWTEEPRLITTEAOAAETTTSTISLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELSG 343

RESULT 12
 PCT-US91-03896-2

Sequence 2, Application PC/TUS9103896
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furch, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/03896
 FILING DATE: 19910603

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mastrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US91-03896-2

Query Match 9.5%; Score 220.5; DB 3; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHAVI-----SPDPTLL-----IGSSLOATCSIHGDPGATAGELWTLNGRRPSELS 91
 15 AAAAVYAAQHSPOEAPHYQERLGSVDVLLPGTAMDAAYT-----WRVNGTDLAPD-- 68
 92 RLNTSTLALANLNGSQSGDNLYCHARDGSIAGS-CLYVGLPPEKPFENISCSRN 150
 68 -LLNSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVLGPPEPV-LSGRSNT 120
 151 M-KDLTCRW-----TPAGHETFLHTNYSLSKYLKRWYGQDNTCEEYHTVGPFSCHIRK 202
 121 YPKGYCSWHLPTPIYIPFTFNTVYVLAHSGKIM-----VCEKDPAL-KNRCHI-R 167
 203 DLALT--PYEIVWEATNRLGSARSDVLLDVLVYTTDPPDVHVSRYGLEDQLSYRM 260
 168 YHMLSTIKYKYSISVSNALGH-NATATTFDEFTYKPPDPENVAVARVPSPNRRLEVTW 226
 261 VSPPALKD-FLFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPFTYVFVQVRCNPF 319
 227 QTPSTWPPDESPLKFFLRRLILDQOHV-ELSDGTAHTTIDAYAKREYIIQVAAK-- 284
 320 GIYSKKAGINSEMS-----HPTASTPSEKPGGCGVCEPRG 358
 284 ----DNEIGTMSDMSVAHAHAPWTEEPRLITTEAOAAETTTSTISLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELSG 343

RESULT 13

US-08-685-118-2
 Sequence 2, Application US/08685118
 Patent No. 5840530
 GENERAL INFORMATION:
 APPLICANT: Gubler, Ulrich A
 APPLICANT: Preisky, David H
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 9.4%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.8e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 ILIGSSLOATCSIHGDTPGATAGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILIGSTVNTCSL-----KPRGCGFHSRRNKLILYKFDRIINFHGHSLNSQVTLPL 94
QY 95 NSTLALANLNGSRQSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSNMK-D 153
DB 95 GTTLFVCKLACINSDEIQ-----ICGAEIFVGAPQPNLSICIQGEQGT 140
QY 154 LCRMTPGAHGEFPLHTNYSKY-----KLRWYGO--DNCEEXHTVG-----PHSCH 200
DB 141 VACTWGR--DTHLYTETTLQSGPKNLTWQKCKDIYC-DYLDGILNLTPESESNFT 197
QY 201 PKDLALFTPEIWEATNRLGARSADVLTLVDVYTTDPPDVHVSRYGLEDQLSVRM 260
DB 198 AK-----VTAVNSLGSSSLPSTFTFLDIYRPLPMDIRIKFKQKASVRSCTLW 246
QY 261 VSPPALKDFLQAKQIQRVEDSDMKYVDVSNQTSRLAGLKGTYFYVOVRCNPFG 320
DB 247 -----RDGGLVLLNRLRPRNSRLMNNVNTKAKGRHDLDLKPFTEYEFQI-SSKLH 299
QY 321 IYGSKKAGIMSEWSHPTASTPRSERPG 348
DB 300 LY-----KGSWSDMSSESLRAQTPEEPTG 323

RESULT 14
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 9.4%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.8e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 ILIGSSLOATCSIHGDTPGATAGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILIGSTVNTCSL-----KPRGCGFHSRRNKLILYKFDRIINFHGHSLNSQVTLPL 94
QY 95 NSTLALANLNGSRQSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSNMK-D 153
DB 95 GTTLFVCKLACINSDEIQ-----ICGAEIFVGAPQPNLSICIQGEQGT 140
QY 154 LCRMTPGAHGEFPLHTNYSKY-----KLRWYGO--DNCEEXHTVG-----PHSCH 200
DB 141 VACTWGR--DTHLYTETTLQSGPKNLTWQKCKDIYC-DYLDGILNLTPESESNFT 197
QY 201 PKDLALFTPEIWEATNRLGARSADVLTLVDVYTTDPPDVHVSRYGLEDQLSVRM 260
DB 198 AK-----VTAVNSLGSSSLPSTFTFLDIYRPLPMDIRIKFKQKASVRSCTLW 246
QY 261 VSPPALKDFLQAKQIQRVEDSDMKYVDVSNQTSRLAGLKGTYFYVOVRCNPFG 320
DB 247 -----RDGGLVLLNRLRPRNSRLMNNVNTKAKGRHDLDLKPFTEYEFQI-SSKLH 299
QY 321 IYGSKKAGIMSEWSHPTASTPRSERPG 348
DB 300 LY-----KGSWSDMSSESLRAQTPEEPTG 323

RESULT 15
US-08-419-652-6
Sequence 6, Application US/08419652
Patent No. 581007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

[illegible]

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:06 / Search time 49.27 seconds

(Without alignments)
345.602 Million cell updates/sec

Title: US-09-037-657-15
Perfect score: 2317

Sequence: 1 MPAGRPGPYAQSARPPRP.....NODEGILPGRGAPAG 425

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: PIR_60:*

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331	14.3	622	2	A40144	prolactin receptor
2	329	14.2	918	2	A36337	membrane glycoprot
3	324.5	14.0	206	2	A57018	prolactin receptor
4	319.5	13.8	917	2	I49699	glycoprotein 130
5	317.5	13.7	918	2	A44257	interleukin-6 sign
6	314	13.6	830	2	I50455	prolactin receptor
7	312	13.5	610	2	A34631	lactogen receptor
8	312	13.5	610	2	A36116	prolactin receptor
9	312	13.5	412	2	A41070	prolactin receptor
10	312	13.5	310	2	A29884	prolactin receptor
11	307.5	13.3	616	2	A30304	prolactin receptor
12	307.5	13.3	303	2	I77524	prolactin receptor
13	307.5	13.3	292	2	I77525	prolactin receptor
14	307.5	13.3	608	2	I53469	prolactin receptor
15	306	13.2	831	2	J01655	prolactin receptor
16	302.5	13.1	581	2	I45971	prolactin receptor
17	261.5	11.3	630	2	I51086	prolactin receptor
18	254.5	11.0	783	2	UH0329	granulocyte colony
19	254.5	11.0	771	2	B38252	granulocyte colony
20	254.5	11.0	863	2	C38252	granulocyte colony
21	252.5	10.9	837	2	A34898	granulocyte colony
22	234	10.1	372	2	I58141	ciliary neurotroph
23	220.5	9.5	372	1	UHH0CN	ciliary neurotroph
24	209.5	9.0	422	2	I37891	interleukin-11 rec
25	208.5	9.0	432	2	I48343	interleukin-11 rec
26	208	9.0	362	2	S60614	growth promoting a
27	202.5	8.7	460	2	JL0145	interleukin-6 rece
28	200.5	8.7	468	1	A41242	interleukin-6 rece
29	199	8.6	156	2	A32668	prolactin receptor
30	194.5	8.4	440	2	JL0144	interleukin-6 rece
31	192.5	8.3	579	2	A45266	MPL-K protein prec
32	192.5	8.3	635	2	A45266	MPL-K protein prec
33	191.5	8.3	894	2	S68440	leptin receptor (v
34	191.5	8.3	900	2	S68440	leptin receptor (v
35	191.5	8.3	805	2	S68441	leptin receptor (v
36	190	8.2	1097	2	S17308	leukemia inhibitor
37	190	8.2	625	2	S35317	hematopoietic grow
38	190	8.2	150	2	B34631	lactogen receptor
39	188.5	8.1	894	2	JC4797	leptin receptor pr

40	188.5	8.1	1162	2	PC4184	leptin receptor, O
41	188.5	8.1	805	3	JC4897	leptin receptor, O
42	186	8.0	626	2	S37622	proto-oncogene - m
43	185	8.0	1092	2	JX0312	differentiation-st
44	185	8.0	719	2	JC2181	differentiation-st
45	182	7.9	895	2	S74225	leptin receptor, 1

ALIGNMENTS

RESULT 1

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C/Species: Homo sapiens (man)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C/Accession: A40144

R/Boutin, J.M.; Edey, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, D

Mol. Endocrinol 3, 1455-1461, 1989

A/Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A/Reference number: A40144, MIDID:90114212

A/Accession: A40144

A/Molecule type: mRNA

A/Residues: 1-622 <R0D>

A/Cross-references: GB:M31661, NID:q190361, PID:q190362

C/Genetics:

A/Genes: GDB:PLR

A/Cross-references: GDB:120315, OMIM:176761

A/Map position: 5p13.3-5p13.1

C/Keywords: glycoprotein, transmembrane protein

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-622/Product: prolactin receptor, long form #status predicted <MAT>

F/59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 331; DB 2; Length 622;

Best Local Similarity 37.5%; Pred. No. 3e-19; Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILASGCLYVG-LPPERFNISCSRNKDLTCMTGPGAGETPLHTNSIKYLRMYGDD 184

DB 15 LFLNTGLNLQGLRPGRLFKSPKKEFTFCWRPGTGG--LPTNYSILTYHREETLM 72

QY 185 NTEETHVTPGHSCHIPKD-LALFTPEIWEATNRLGASRSDVLTLVDVVTTPDPD 243

DB 73 HECPPDITGGPNSCHGKQYTSMTFTYIMVNTNMGSSFSDELVDVITYQPPPLE 132

QY 244 VHSRVRGLEDQSVNV--SPALDFF--LFQAKYQIRYRVEDSVMKVYDDVSNQTS 298

DB 133 LAV-EVKQPEDRKPYIMKWSPTLLIDLGTGFTLLYEIRLKRKAWE-IHFAQQTE 190

QY 299 CRLAGLKPGTVFYVQRCNPFGLYGSKKAGINSESHPTAASP 342

DB 191 FKLSLHPGOKYIVQRCR-----DHGWSAWSAPATFIQIP 227

RESULT 2

A36337

Membrane glycoprotein gp130 precursor - human

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C/Accession: A36337

R/Hibi, M.; Murekami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A/Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A/Reference number: A36337, MIDID:91084644

A/Accession: A36337

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-918 <HIB>

A/Cross-references: GB:M57230, NID:q186353, PID:q186354

C/Genetics:

A/Genes: GDB:IL6ST, GP130

A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 14.2%; Score 329; DB 2; Length 918;
 Best Local Similarity 28.6%; Pred. No. 7.4e-19;
 Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSIQATCSIHG--DTPGATAGLWTLNGRLPSELSTLNTSTLALA 102
 DB 31 ISPEFVQVQHSNFTACVLCVKEKCMDFHNAVYWKTHFTPEQYTIIRLTASVY 90
 QY 103 LANLNGSRQSDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDIASINILQTCNILLFQLEQNVYGIITISLPPKPNLCIYNKMGKMGCEMDGGR 150
 QY 163 HGETFLHTNYSKYKRLMWIGQDNTCEBYHTVGHSHCHIPDLALFTPEIWEATNRLGS 222
 DB 151 --ETHLETNETLSEWATHRFADCKAKROT--FTSCVDISTYFVNIWEVAEENALGK 206
 QY 223 ARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDPLQAKQIIRYR 282
 DB 207 VTSDFHINFDVYKVPKPPNLSVINSEELSLIKLTWN-PSIKSVII-LKYNIQYRK 264
 QY 283 DSYDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 339
 DB 265 DASWQSDIPEDASTSSSTVODLKPFTYEVFRIC-----KKEGQKQVMSSEAS 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326

RESULT 3
 A57018
 A:Protein receptor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
 C:Accession: A57018
 R:Fun, G.; Wells, J.A.
 J. Biol. Chem. 270, 13133-13137, 1995
 A:Title: prolactin receptor antagonists that inhibit the growth of breast cancer cell lines
 A:Reference number: A57018; MUID:95286597
 A:Accession: A57018
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206 <RES>
 A:Cross-references: GB:S78505; NID:9999114; PID:9999115

Query Match 14.0%; Score 324.5; DB 2; Length 206;
 Best Local Similarity 38.0%; Pred. No. 2.4e-19;
 Matches 81; Conservative 25; Mismatches 90; Indels 17; Gaps 7;

QY 136 LPPEKPNISCSMRNKKDLTCRTPGAHGETFLHTNYSKYKRLMWIGQDNTCEBYTGP 195
 DB 2 LPPEKPNISCSMRNKKDLTCRTPGAHGETFLHTNYSKYKRLMWIGQDNTCEBYTGP 195
 QY 196 HSCHIPED-LALFTPEIWEATNRLGSARSDVLTLDVLTDPDPDVVSRVSGLED 254
 DB 60 NSCHFQKQVTSMTWYIMVATNMGSSSEDELYDVYIVQDPDLPLAV-ETVQPD 118
 QY 255 QLSVRYV--SPALKDF--LEQAKQIIRKVEDSDVMKVVDVSNQTSCLAGLKPQY 309
 DB 119 RKPLWTKWSPPTLIDKTGMFLLEIRLKPKEAWE-IRFAGQOTEKFIKILSPGQK 177
 QY 310 YFVQVRCNPGIYSGSKKAGIMSEMSHPTASTP 342
 DB 178 YIVQVRCKP-----DHGYSMSKSPATFIQIP 203

RESULT 4

149699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
 C:Accession: 149699; 148370
 R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer,
 A:Reference number: 148370; MUID:92291532

QY 46 ISPODPTLLIGSSIQATCSIHG--DTPGATAGLWTLNGRLPSELSTLNTSTLALA 102
 DB 31 IYPEFVQVQHSNFTACVLCVKEKCMDFHNAVYWKTHFTPEQYTIIRLTASVY 90
 QY 103 LANLNGSRQSDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDIASINILQTCNILLFQLEQNVYGIITISLPPKPNLCIYNKMGKMGCEMDGGR 150
 QY 163 HGETFLHTNYSKYKRLMWIGQDNTCEBYHTVGHSHCHIPDLALFTPEIWEATNRLGS 222
 DB 151 --ETHLETNETLSEWATHRFADCKAKROT--FTSCVDISTYFVNIWEVAEENALGK 206
 QY 223 ARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDPLQAKQIIRYR 282
 DB 207 VTSDFHINFDVYKVPKPPNLSVINSEELSLIKLTWN-PSIKSVII-LKYNIQYRK 264
 QY 283 DSYDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 339
 DB 265 DASWQSDIPEDASTSSSTVODLKPFTYEVFRIC-----KKEGQKQVMSSEAS 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326

Query Match 13.8%; Score 319.5; DB 2; Length 917;
 Best Local Similarity 29.6%; Pred. No. 4.4e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPODPTLLIGSSIQATCSIHG--DTPGATAGLWTLNGRLPSELSTLNTSTLALA 102
 DB 31 IYPEFVQVQHSNFTACVLCVKEKCMDFHNAVYWKTHFTPEQYTIIRLTASVY 90
 QY 103 LANLNGSRQSDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDIASINILQTCNILLFQLEQNVYGIITISLPPKPNLCIYNKMGKMGCEMDGGR 150
 QY 163 HGETFLHTNYSKYKRLMWIGQDNTCEBYHTVGHSHCHIPDLALFTPEIWEATNRLGS 222
 DB 151 --ETHLETNETLSEWATHRFADCKAKROT--FTSCVDISTYFVNIWEVAEENALGK 206
 QY 223 ARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDPLQAKQIIRYR 282
 DB 207 VTSDFHINFDVYKVPKPPNLSVINSEELSLIKLTWN-PSIKSVII-LKYNIQYRK 264
 QY 283 DSYDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 339
 DB 265 DASWQSDIPEDASTSSSTVODLKPFTYEVFRIC-----KKEGQKQVMSSEAS 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326

RESULT 5
 A44257
 Interleukin-6 signal transducing molecule gp130 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C:Accession: A44257
 R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transdu
 A:Reference number: A44257; MUID:93052397
 A:Accession: A44257
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-918 <MAN>
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIF:118488)
 C:Keywords: transmembrane protein

Query Match 13.7%; Score 317.5; DB 2; Length 918;

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; 153417
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALI>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 R:O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
 A:Reference number: 153417; MUID:95014432
 A:Accession: 153417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: Nb2-11C cell line
 C:Keywords: transmembrane protein

Query Match 13.5%; Score 312; DB 2; Length 412;
 Best Local Similarity 35.4%; Pred. No. 6.2e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SLLAGSCLYVGLPPEKPFNISCWSRMKDLTCRWTPGANGELFLHNTSLKRLMYGOD 184
 15 SLLKGS-----PPGKPELHKCRSPKKEFTCWANPDTGG--LPINSLYTSKE--GK 65
 QY 185 NR--CEEYHTVGPBHSCHIRKDLAETPEYIWEATNRLGSARSADLTLDVLYVTTDP 241
 66 TYEECPDYKTSQPNSCFEFSKOYTSIKWYIITVYATNNGSSSDPLVDVYIIEPEP 125
 QY 242 PDVHVSRYVGLDGLDLSVRV--SPRLKDF--LQAKQIYRVEDSVDMKRVDDVSNQ 296
 126 RMLTL-EVQQLDKTKTYLWVKNMSPPTITVKTGWTMEYELKKEEAEME-IHFTGHQ 183
 QY 297 TSCRLAGLPGTYVYFVQVRCNPFGIYSGKAGIWMSEMSHPTAASP 342
 184 TQFKYFDLYPGQKYLQTRCKP-----DHGYSMKSSSESSVEMP 222
 Db

RESULT 10

prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A29884
 R:Boulton, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shiotto, M.; Bannville
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
 A:Reference number: A29884; MUID:86165059
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 13.5%; Score 312; DB 2; Length 310;
 Best Local Similarity 35.4%; Pred. No. 4.3e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SLLAGSCLYVGLPPEKPFNISCWSRMKDLTCRWTPGANGELFLHNTSLKRLMYGOD 184
 15 SLLKGS-----PPGKPELHKCRSPKKEFTCWANPDTGG--LPINSLYTSKE--GK 65
 QY 185 NR--CEEYHTVGPBHSCHIRKDLAETPEYIWEATNRLGSARSADLTLDVLYVTTDP 241

Db 66 TYEECPDYKTSQPNSCFEFSKOYTSIKWYIITVYATNNGSSSDPLVDVYIIEPEP 125
 QY 242 PDVHVSRYVGLDGLDLSVRV--SPRLKDF--LQAKQIYRVEDSVDMKRVDDVSNQ 296
 126 RMLTL-EVQQLDKTKTYLWVKNMSPPTITVKTGWTMEYELKKEEAEME-IHFTGHQ 183
 QY 297 TSCRLAGLPGTYVYFVQVRCNPFGIYSGKAGIWMSEMSHPTAASP 342
 184 TQFKYFDLYPGQKYLQTRCKP-----DHGYSMKSSSESSVEMP 222
 Db

RESULT 11

prolactin receptor 2 precursor - rabbit
 A:Accession: A30304
 A:Molecule type: mRNA
 A:Residues: 1-616 <EDB>
 A:Cross-references: GB:J04510; NID:g165669; PID:g165670
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rec
 A:Reference number: A60380; MUID:91146782
 A:Accession: A60380
 A:Molecule type: protein
 A:Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX'
 A:Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domain: transmembrane #status predicted <TM>
 F:59,104,132,347,389,411/Binding site: carbohydrate (asn) (covalent) #status predict

Query Match 13.3%; Score 307.5; DB 2; Length 616;
 Best Local Similarity 36.3%; Pred. No. 2.4e-17;
 Matches 77; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

QY 137 PPEKPFNISCWSRMKDLTCRWTPGANGELFLHNTSLKRLMYGODNCEHYHTVGP 196
 27 PPGKPELHKCRSPKKEFTCWANPDTGG--LPINSLYTSKEGELTHHECPDKITGPN 84
 QY 197 SCHI-PRDLAETPEYIWEATNRLGSARSADLTLDVLYVTTDPDPVHVSRYVGLDQ 255
 85 SCYRSKHTSTWITTYIITVYATNNGSSSDPLVDVYIIEPEPVLTL-EVHKHPEDR 143
 QY 256 LSVHVS--SPRLKDF--LQAKQIYRVEDSVDMKRVDDVSNQSCRAGLPGTYV 310
 144 KPYLWVKNMSPPTITVKTGWTMEYELKKEEAEME-IHFAQOQTFKLSLYPOKY 202
 QY 311 FVQVRCNPFGIYSGKAGIWMSEMSHPTAASP 342
 203 LVQVRCRP-----DHGFMSVMSPESSIQP 227
 Db

RESULT 12

prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: I57699; MUID:89261824

Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
Reference number: JQ1655; MID:93075121

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protein - protein search, using sw model

run on: September 17, 1999, 03:10:12; Search time 35.09 Seconds

(without alignments)
342.377 Million cell updates/sec

title: US-09-037-657-15

perfect score: 2317

sequence: 1 MPAGRPVAVASARPPPL.....NODEILPSGRGARGPAG 425

coring table: BLOSUM62

searched: 77977 seqs, 28268293 residues

database: SwissProt_37.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	14.3	622	1	PRLR_HUMAN
2	329	14.2	918	1	IL6B_HUMAN
3	319.5	13.8	917	1	IL6B_MOUSE
4	317.5	13.7	918	1	IL6B_RAT
5	314	13.6	830	1	PRLR_COLLI
6	312	13.5	610	1	PRLR_RAT
7	307.5	13.3	608	1	PRLR_MOUSE
8	307.5	13.3	616	1	PRLR_RABIT
9	306	13.2	831	1	PRLR_CHICK
10	305	13.2	831	1	PRLR_MELGA
11	303	13.1	581	1	PRLR_CEREL
12	302.5	13.1	581	1	PRLR_ORETI
13	261.5	11.3	630	1	PRLR_BOVIN
14	254.5	11.0	836	1	PRLR_HUMAN
15	252.5	10.9	837	1	PRLR_MOUSE
16	234	10.1	372	1	CNTR_RAT
17	222.5	9.6	372	1	CNTR_HUMAN
18	208	9.0	362	1	IL6A_MOUSE
19	202.5	8.7	468	1	IL6A_HUMAN
20	200.5	8.7	468	1	IL6A_MOUSE
21	196.5	8.5	462	1	IL6A_RAT
22	192.5	8.3	635	1	TPOR_HUMAN
23	191.5	8.3	1162	1	LEPR_MOUSE
24	190	8.2	1097	1	LEPR_HUMAN
25	190	8.2	625	1	TPOR_MOUSE
26	185	8.0	1092	1	LEPR_MOUSE
27	175	7.6	427	1	IL13_HUMAN
28	174.5	7.5	1165	1	LEPR_HUMAN
29	170	7.3	888	1	UFO_MOUSE
30	164.5	7.1	638	1	GHR_RABIT
31	158.5	6.8	508	1	EPOR_HUMAN
32	157	6.8	507	1	EPOR_MOUSE
33	156.5	6.8	507	1	EPOR_HUMAN
34	155	6.7	507	1	GHR_PIG
35	151	6.5	638	1	GHR_HUMAN
36	148.5	6.4	897	1	CYR2_HUMAN
37	147	6.3	1040	1	AXO1_RAT
38	146.5	6.3	444	1	IL13_MOUSE
39	145	6.3	634	1	GHR_SHEEP
40	143.5	6.2	380	1	IL13_HUMAN
41	143	6.2	638	1	GHR_RAT
42	140.5	6.1	650	1	GHR_MOUSE
43	140.5	6.1	297	1	GHR_MOUSE

ALIGNMENTS

RESULT	1	STANDARD	PRT	622 AA
PRLR_HUMAN				
AC	P16471;			
DT	01-AUG-1990 (REL. 15, CREATED)			
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)			
DE	PROLACTIN RECEPTOR PRECURSOR (PRL-R).			
GN	PRLR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	PRIMATE; CATARRHINI; HOMINIDAE; HOMO.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 90114212.			
RA	BOUTIN J. M., EDERY M., SHIROTA M., JOLICOEUR C., LESUEUR L.,			
RA	ALI S., GORD D., DJANE J., KELLY P. A.,			
RT	"Identification of a cDNA encoding a long form of prolactin receptor			
RT	in human hepatoma and breast cancer cells."			
RL	MOL. ENDOCRINOL. 3:1455-1461(1989).			
RN	(2)			
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.			
RX	MEDLINE; 95075462.			
RA	SOMERS W., UTSCHE M., DE VOS A. M., KOSSIAKOFF A. A.,			
RT	"The X-ray structure of a growth hormone-prolactin receptor complex."			
RL	NATURE 372:478-481(1994).			
CC	- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE			
CC	PROLACTIN.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.1sb-sib.ch/announce/			
CC	or send an email to license@1sb-sib.ch).			
CC	-----			
DR	EMBL; M31661; G190362;			
DR	PIR; A40144; A40144.			
DR	PDB; 1BP3; 23-SEP-98.			
DR	MIM; 176761;			
DR	PROSITE; PS00241; RECEPTOR_CYTOKINES_1;			
DR	PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.			
DR	PFAM; PF00041; fn3. 2			
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.			
FT	SIGNAL	1	24	
FT	CHAIN	25	622	
FT	DOMAIN	25	234	EXTRACELLULAR (POTENTIAL)
FT	DOMAIN	235	258	POTENTIAL.
FT	DOMAIN	259	622	CYTOSOLASMIC (POTENTIAL).
FT	DOMAIN	25	122	FIBRONECTIN TYPE-III.
FT	DOMAIN	123	227	FIBRONECTIN TYPE-III.
FT	DISULFID	36	46	BY SIMILARITY.
FT	DISULFID	75	86	BY SIMILARITY.
FT	CARBOHYD	59	59	POTENTIAL.
FT	CARBOHYD	104	104	POTENTIAL.
FT	CARBOHYD	233	233	POTENTIAL.
SO	SEQUENCE	622 AA;	69505 KM;	6924E155 CRC32;

Query Match: 14.3%; Score 331; DB 1; Length 622;
Best Local Similarity: 37.5%; Pred. No. 1.8e-19;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;


```

0Y      126 ILAAGSLAYG-LPPEKPFNISCNRMMKLDTGWTEGANGETFLHNNYSLKYLRNGGD 184
       : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      15 LFLNTCLNGQLPPGKRPELFCKRSPKEFTFCWRRGTGG--LPFNYSLTTHREGETIM 72
0Y      185 NTCEEHTVGVPSCHPRKD-LALFYYEILWEATENLRSARSVYLADVDVYTTPPPD 243
       : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      73 HCCPDYITGPGNSHGCRGYTSMRRIRYIMVNANTNMGSSFDGLVDTYTYIQPPPLE 132
0Y      244 VAVSRVYGLEDOLSVRW--SPPALKDF---LEQATYQIRYVEDSDVKMVDVDSNGTS 298
       : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      133 IAV-EVKOPEDKKPYLMIMWSPTLLIDLTGTFYTLLEYIRLKREKAENE-IFPAQQE 190
0Y      299 CRLAGIKPGTYEVQVRCPFGIYSGKKRGISSEMSHPNAASP 342
Db      191 FRLSLHRGAKLVQRCNP-----DHGISANSAPATFIQT 227

RESULT          2
IL6B_HUMAN      STANDARD:      PRT:    918 AA.
AC              PA0189:
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE      INTERLUKTIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLUKTIN
DE      6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATTIN M
DE      RECEPTOR) (CDM130) (CD130 ANTIGEN).
GN      IL6ST.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA.
CC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE-MYELOMA, AND PLACENTA;
RX      MEDLINE; 91084844.
RA      HIDI M., MURKAMI M., SAITO M., HIRANO T., TAGA T., KISHIMOTO T.;
RT      "Molecular cloning and expression of an IL-6 signal transducer,
RL      gp130."
RL      CELL 63:1149-1157(1990).
[2]
RN      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RP      BRAVO J., STAUTON D., HEATH J.K., JONES E.Y.;
RX      MEDLINE; 98169383.
RA      EMBO J. 17:1665-1674(1998).
RL      -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC      IL-6, LIF, OSM, CMF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC      SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC      RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
CC      AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC      EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC      -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
CC      EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC      ONE IG-LIKE DOMAIN.
CC      -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -1- DATABASE: NAME=PROX; NOTE=CD guide CD130 entry!
CC      WWW-"http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC      -----
CC      THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC      BETWEEN THE SWISS INSTITUTE OF BIOFORMATICS AND THE EMBL OUTSTATION -
CC      THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC      USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC      MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC      ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB-SDB.CH/ANNOUNCE/
CC      OR SEND AN EMAIL TO LICENSE@ISB-SDB.CH).
CC      -----
EMBL; M57230; G186354; .
PIR; A36337; A36337.

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DR	PDB:	1BQU; 26-AUG-98.
DR	MIM:	600694; -.
DR	PROSITE:	PS00340; RECEPTOR_CYTOKINES_2; 1.
DR	PFAM:	PF00041; fh3; 3.
KW	REPEAT:	TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT; 3D-STRUCTURE.
FT	SIGNAL	1 22 POTENTIAL.
FT	CHAIN	23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	DOMAIN	23 619 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	620 641 POTENTIAL.
FT	DOMAIN	642 918 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	26 120 IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124 222 FIBRONECTIN TYPE-III.
FT	DOMAIN	223 324 FIBRONECTIN TYPE-IIII.
FT	DOMAIN	325 423 FIBRONECTIN TYPE-IIII.
FT	DOMAIN	424 517 FIBRONECTIN TYPE-III.
FT	DOMAIN	518 613 FIBRONECTIN TYPE-III.
FT	DOMAIN	725 735 SER-RICH.
FT	DISULFID	134 144
FT	DISULFID	172 182
FT	CARBOHYD	43 43 POTENTIAL.
FT	CARBOHYD	83 83 POTENTIAL.
FT	CARBOHYD	131 131 POTENTIAL.
FT	CARBOHYD	157 157 POTENTIAL.
FT	CARBOHYD	227 227 POTENTIAL.
FT	CARBOHYD	379 379 POTENTIAL.
FT	CARBOHYD	383 383 POTENTIAL.
FT	CARBOHYD	390 390 POTENTIAL.
FT	CARBOHYD	553 553 POTENTIAL.
FT	CARBOHYD	564 564 POTENTIAL.
SO	SEQUENCE	918 AA; 103522 MM; 7CCG6F05 CRC32;

[illegible]

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCURIONGNATHI; MORIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR; TISSUE-MACROPHAGE;
 RX MEDLINE; 92291532.
 RA SAITO M., YOSHIDA K., HIRI M., TAGA T., KISHIMOTO T.;
 RT "Molecular cloning of a murine IL-6 receptor-associated signal
 transducer, gp130, and its regulated expression in vivo."
 J. IMMUNOL. 148:4066-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
 SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
 EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 C
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 or send an email to license@isb-sib.ch).
 C
 EMBL; X62646; G840817;
 EMBL; M83336; G193592;
 MGD; MGI:96560; IL6ST.
 PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 PFM; PF00041; fn3; 3.
 HSSP; P40189; IL6U.
 W RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 W REPEAT.
 T SIGNAL.
 T CHAIN 1 22
 T DOMAIN 23 917 POTENTIAL.
 T TRANSMEM 618 617 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 T DOMAIN 618 617 EXTRACELLULAR (POTENTIAL).
 T DOMAIN 640 917 POTENTIAL.
 T DOMAIN 26 120 CYTOPLASMIC (POTENTIAL).
 T DOMAIN 221 322 IG-LIKE C2-TYPE DOMAIN.
 T DOMAIN 323 420 FIBRONECTIN TYPE-III.
 T DOMAIN 516 611 FIBRONECTIN TYPE-III.
 T DOMAIN 723 741 FIBRONECTIN TYPE-III.
 T DISULFID 134 144 SER-RICH.
 T DISULFID 172 180 BY SIMILARITY.
 T CARBOHYD 43 43 POTENTIAL.
 T CARBOHYD 61 61 POTENTIAL.
 T CARBOHYD 83 83 POTENTIAL.
 T CARBOHYD 131 131 POTENTIAL.
 T CARBOHYD 157 157 POTENTIAL.
 T CARBOHYD 225 225 POTENTIAL.
 T CARBOHYD 388 388 POTENTIAL.
 T CARBOHYD 476 476 POTENTIAL.
 T CARBOHYD 551 551 POTENTIAL.
 T SEQUENCE 917 AA; 102452 MW; A5DCD259 CRC32;
 Query Match 13.8%; Score 319.5; DB 1; Length 917;

Best Local Similarity 29.6%; Pred. No. 2,5e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;
 QY 46 ISPODPTLLISSSIQACNSHG---DTPGATAEGLWYTLNGRRRLPSLSRLNTSTALA 102
 Db 31 IYPERPVQORSGNFTALCVLKEACLOHYVNAVSYIWMKNAAAPRQVYVINTTSSVT 90
 QY 103 LANNGSMQSGDWLVCHARDGSLIAGSLYGLPERPFRISCSWNNMDLCRWTPGA 162
 Db 91 FTDVVLSVQLTCHILSFGLEQONVGYTMISGPPKPNLTCTIVEGKMLCQMPGR 150
 QY 163 HGEFLTNLSLKRYLWYGOD-NTCEHYHVGPHSCHIPDLALFYELWVATNRGL 221
 Db 151 -ETYLENTLTKSE--WAKRFPDCKSKGT---SCWSTMPYVNIETWEAENALG 203
 QY 222 SARDVLTLDVLTVDTPPDVNVHSGLEDLSYRWVSPALKDFLQAKYQYRYR 281
 Db 204 KVSSESINFPVDVKRPTLPYKNSVTNSELSSILKSWSSG--GGLLDKSDIORYT 261
 QY 282 EDSVDKTV---DVSNOTGCRAGLAPGVYVQVNCNPFGLYSGKKAIGSEWSHPTA 338
 Db 262 KDASTWQVLEDTMSRSTFTYQDLKPFTEYFRIR---SIRDSGK-GYMSDWSEAS 316
 QY 339 ASR--PSESRP 347
 Db 317 GTTYEDRPSRP 327
 RESULT 4
 IL6B_RAT STANDARD; PRT; 918 AA.
 AC P40190;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN I30) (GP130).
 GN IL6ST.
 OS RATUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCURIONGNATHI; MORIDAE; MURINAE; RATUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 93052397.
 RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
 RT "Molecular cloning and characterization of the rat liver IL-6 signal
 transducing molecule, gp130."
 RL GENOMICS 14:666-672(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 C
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 C
 EMBL; M92340; --; NOT_ANNOTATED_CDS.

DR PIR: A44257: A44257.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 DR HSSP: P40189; 1BOU.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 REPEAT
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618
 FT TRANSMEM 619 640
 FT DOMAIN 641 918
 FT DOMAIN 26 120
 FT DOMAIN 124 221
 FT DOMAIN 222 323
 FT DOMAIN 324 422
 FT DOMAIN 423 516
 FT DOMAIN 517 612
 FT DOMAIN 724 754
 FT DISULFID 134 144
 FT DISULFID 172 181
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 205 205
 FT CARBOHYD 226 226
 FT CARBOHYD 382 382
 FT CARBOHYD 389 389
 FT CARBOHYD 477 477
 FT CARBOHYD 552 552
 SQ SEQUENCE 918 AA; 102450 MW; E6EDFCD0 CRC32;

Query Match 13.7%; Score 317.5; DB 1; Length 918;
 Best Local Similarity 29.8%; Pred. No. 3.7e-18;
 Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISQDPTLIGSLQATCSHG--DTPGATAGLYWTNGRLPSELRLNTSTLATA 102
 DB 31 IYEFVVOGSGNSMTATCYLKEKCLQVSVNATYIWKTHNVAPEQVTVIRKTSSTV 90
 QY 103 LANLNGSROOSGDNLYCHARDGSIILAGSCLYVGLPREKPNISGSRNKKDLCTRTPCA 162
 DB 91 FTVVVEQNVQNLNITLFGIEQNVYGIITLSGYPDIPNLSCLINSEKMKLCQDLPGR 150
 QY 163 HGEFTLHTNSLKYKLRMTGOD--NCEXYTVGPHSCHIPKDLALTPYEIWEATNRIG 221
 DB 151 --ETIETINTLKE--WATEKPPDRTKH--GTSSCMAGYPIIYVNIWEAENALG 204
 QY 222 SARSDVLTLDVLDVTTDPDPVHVSARGVGLDQLSVRWVSPALMDFLFOATYQIRYEV 281
 DB 205 NYSSEPIINEDPVKVPSPHNSLTNSELSSILKIAVNSGL--DSILRLKSDIQYRT 262
 QY 282 EDSVDKRV---DDVSNQISCRAGLAKPGIVYVYVRCNPFGLYSGKAKGINSMSHPA 338
 DB 263 KQNSTIQLVPLEDTVSPRSFTVQDKLPFEYVFRIR---SIKENGK--GYSDMSE--RA 316
 QY 339 ASTPRSERP 347
 DB 317 SGTTYEDRP 325

RESULT 5
 PRIR COLLI STANDARD; PRT: 830 AA.
 AC 090374:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS COLUMBA LIVIA (DOMESTIC PIGEON).

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE-CROSSAC.
 RX MEDLINE: 94283267.
 RA CHEN X., HORSEMAN N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor".
 RL ENDOCRINOLOGY 135:269-276(1994).
 CC - FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC - SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----

DR EMBL: U07694; G466382;
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFAM: PF00041; fn3; 4.
 DR HSSP: P16471; 1BP3.

KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 461 830
 FT DOMAIN 123 122
 FT DOMAIN 123 122
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SQ SEQUENCE 830 AA; 94507 MW; 5EPAD051 CRC32;

Query Match 13.6%; Score 314; DB 1; Length 830;
 Best Local Similarity 37.1%; Pred. No. 6.2e-18;
 Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PREKPNISGWRNKKDLCTRTPCAAGETPLH--INYSIKYLVNMGDNTCEETHYVCP 195
 DB 231 PREKPTLIKCRSPKEKTEFTCWKPGSDG--HPTNYTLVSKSEGEERYECPPDYKAGP 287
 QY 196 HSCHT--PRDLALFTPEYIWEATNRLGARSVDLTLDVYVTTDPDPV--HVSARGVL 252
 DB 288 NSCFDKHHTSWITINITYKATINIGSVSDPLVYDTYIQTDPVNAVITELKKYVNR 347
 QY 253 EDQLSVRWVSPALDFT---LEQATYQIRYEVSDVKRVVDVSNQTSCLAGLPGTV 309
 DB 348 KRYLVLTW--SPPLADVSSGMLTLDYELRLKDEALEMETI--FVGOQTHYKAFSLNPKK 405
 QY 310 FVVOVRCNPFGLYSGKAKGINSMS 334
 DB 406 IYVQIHCKP-----DHGGSWSEWS 424

RESULT 6
PRLR_RAT STANDARD: PRT: 610 AA.
ID PRLR_RAT P05710: 063451: 062832: 064274: 063479;
AC 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS EUTAROTIA: METAEOA: VERTEBRATA: MAMMALIA: EUTHERIA;
OC RODENTIA: SCURONGNATHI: MORIDAE: MORINAE: RATIUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91155946.
RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
EDERY M., DJIANE J., KELLY P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and
liver."
RM MOL. ENDOCRINOL. 4:1136-1143(1990).
[2]
RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RX STRAIN-SPRAGUE-DAWLEY: TISSUE-OVARY;
MEDLINE: 90241201.
RA ZHANG R., BUCCIO E., TSAI-MORRIS C.H., HU Z.Z., DUFAY M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen
receptor cDNA species."
RM BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).
[3]
RP SEQUENCE OF 281-610 FROM N.A.
RX BANVILLE D., STOCO R., MURPHY K.K., BOIE Y., KELLY P.A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RX TISSUE-LIVER;
MEDLINE: 88165059.
RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
SHIROTA M., BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of
the growth hormone/prolactin receptor gene family."
RM CELL 53:69-77(1988).
[5]
RP SEQUENCE FROM N.A. (FORM NB2).
RX TISSUE-LYMPHOMA;
MEDLINE: 92041834.
RA ALI S., PELLIGRINI I., KELLY P.A.;
RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
of prolactin receptor."
RM J. BIOL. CHEM. 266:20110-20117(1991).
[6]
RP SEQUENCE FROM N.A. (FORM NB2).
RX MEDLINE: 95014432.
RA O'NEAL K.D., YU-LEE L.Y.;
RT "Differential signal transduction of the short, Nb2, and long
prolactin receptors. Activation of interferon regulatory factor-1 and
cell proliferation."
RM J. BIOL. CHEM. 269:26076-26082(1994).
[7]
RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
[8]
RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
[9]
RP ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING OF THE PRLR GENE.
[10]
RP SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
[11]
RP SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: M57668; G206367; -
DR EMBL: M34083; G205123; -
DR EMBL: L48060; G1019651; -
DR EMBL: U34730; G1223859; -
DR EMBL: M19304; G206365; -
DR EMBL: M74152; G206380; -
DR EMBL: U07567; G641964; -
DR PIR: A29884; A29884.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 2.
DR HSSP: P16471; 1B3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
RN ALTERNATIVE SPLICING.
FT SIGNAL 1 19
FT CHAIN 20 610
FT DOMAIN 20 229
FT TRANSMEM 230 253
FT DOMAIN 254 610
FT DOMAIN 20 117
FT DOMAIN 119 222
FT DISULFID 31 41
FT DISULFID 70 81
FT CARBOHYD 54 54
FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT CARBOHYD 131 150
FT VARSPPLIC 151 610
FT VARSPPLIC 281 310
FT VARSPPLIC 311 610
FT VARSPPLIC 342 539
FT CONFLICT 236 236
FT CONFLICT 345 345
FT CONFLICT 465 465
FT CONFLICT 466 466
FT CONFLICT 469 469
FT CONFLICT 541 541
FT CONFLICT 555 555
SQ SEQUENCE 610 AA; 68599 MW; C579BC43 CRC32;

Query Match 13.5%; Score 312; DB 1; Length 610;
Best Local Similarity 35.4%; Pred. No. 6e-18;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;
QY 125 SIAGSCLYVGLPEKPEFNISSCMRNKDLGCRWTPGANGETFLHNTSLKTKLRMYGOD 184
DB 15 SILKGS-----PQKPELHKCRSPDKETFTWMNGTDG--LPTNLSLYSKE--GEK 65
QY 185 NT--CEEYTVGPHSCHIPKD-LAFTPEIWEATNRLGSASDVLTVDVYTTDP 241
DB 66 TYECPDYKTSGPSNCFSEKQYTSIMKIIITVNAITNQSSSSPLVYDVYIYEPP 125
QY 242 PPHVSRVGGLEDQLSVKNV--SPALADE--LFQARYQIYRVEDSDVMKVVYDVSNQ 296
DB 126 RNLTL-ERKQLDKTKTYLWVKWSPPTIDVKTGFTMEYELKKEALEME--HFTGHQ 183
QY 297 TSCRLAGLPGVYVVOYRQCNPFYIGSKKAGIWESEHPRASFP 342
DB 184 TQFKFDLYPGQKTYLVQTRCKP-----DHGYSRWQSESSVEVP 222

RESULT 7
PRLR_MOUSE STANDARD: PRT: 608 AA.
ID PRLR_MOUSE P062099: P15213: P15212;
AC 008501: 062099: P15213: P15212;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS MUS MUSCULUS (MOUSE).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MOS.
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN-CH3; TISSUE-MAMMARY GLAND;
RX MEDLINE: 94085788.
RA MOORE R.C., OKA T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
long-form prolactin receptor.";
RT GENE 134:263-265(1993).
RN [2]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN-SWISS WEBSTER; TISSUE-LIVER;
RX MEDLINE: 93307149.
RA CLARKE D.L., LINZER D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
mouse ovary.";
RT ENDOCRINOLOGY 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA SASAKI M.;
RN SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
RA EDERY M., PEZET A., NANDI S., KELLY P.A.;
RN SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RC STRAIN-SWISS WEBSTER; TISSUE-LIVER;
RX MEDLINE: 89261824.
RA DAVIS J.A., LINZER D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse
liver.";
RN MOL. ENDOCRINOL. 3:674-680(1989).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
(SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
GENE.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: L13593; G347842; -
DR EMBL: L14811; G283770; -
DR EMBL: D10214; G220576; -
DR EMBL: X73372; G312697; -
DR EMBL: M22959; G200482; -
DR EMBL: M22958; G200480; -
DR PIR: J06711; J06711.
DR MGI: 97763; PRLR.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE-NEG.
DR HSP: P16471; 1BP3; 2.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 608 PROLACTIN RECEPTOR.
FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 230 253 BY SIMILARITY.

FT DOMAIN 254 608 CYTOPLASMIC (BY SIMILARITY).
FT FT 20 117 FIBRONECTIN TYPE-III.
FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
FT DISULFID 31 41 BY SIMILARITY.
FT DISULFID 70 81 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 99 99 POTENTIAL.
FT CARBOHYD 127 127 POTENTIAL.
FT VARSPLIC 281 292 MISSING (IN PRL-R1).
FT VARSPLIC 293 608 MISSING (IN PRL-R2).
FT VARSPLIC 281 303 MISSING (IN PRL-R2).
FT VARSPLIC 304 608 MISSING (IN PRL-R1).
FT CONFLICT 558 558 MISSING (IN REF. 2).
SO SEQUENCE 608 AA; 68240 MR; AA401E67 CAC32.
Query Match 13.3%; Score 307.5; DB 1; Length 608;
Best Local Similarity 32.6%; Pred. No. 1,4e-17;
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;
QY 90 LSRLLNTSTALALANNGSGHSGDNLVCHARDGSLAGSCLVGLPEPEFNSICMR 149
Db 1 MSSALAYMLLYLSISLNG--OS-----PPGRPEIHKCRSP 34
QY 150 NMKDLTCRWTPGARGETFLHTNYSLKXKRLWYGODNT--CEHYTVGPHSCHIPKD-LAL 206
Db 35 DKREFTTQWNPBGSGG--LPTNLSITSKE--GKNYECEDYITSGPNSCFESKOTISI 90
QY 207 FTPEYIWEATNRLGSASRDVLTLDVYTTDPDPVHSRVGLEDOLSVRWVS--PP 264
Db 91 WKIIITVNAITNENSGSTSDPLVDYVYIYEPEPRNLTLEVKQLDKKYTLWVKMLP? 149
QY 265 ALKDF--LFOAKQIQRVEDSDVKRVDDVSNQTSCLAGLPGYVYFOVACNPGCI 321
Db 150 TITVYKGFMEYIEIRLSEADEWE-IHTGQTOFKYFDLYPGQKYLVTQCKP--- 206
QY 322 YGSKKAGIWSHPTASTP 342
Db 206 ----DRGYWKRGOEKSEIEP 222
RESULT 8
PRLR_RABIT STANDARD; PRT; 616 AA.
AC P14787;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RX MEDLINE: 89184578.
RA EDERY M., JOLICOEUR C., LEVI-MEXRUEIS C., DUSANTER-FOURT I.,
RA PETERIDOU B., BOUFIN J.M., LESUEUR L., KELLY P.A., DIJANE J.;
RT "Identification and sequence analysis of a second form of prolactin
receptor by molecular cloning of complementary DNA from rabbit
mammary gland.";
RT PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 30-228.
RX MEDLINE: 97248733.
RA HALASY D., THORAU E., DIJANE J., MORON J.P.;
RT "homology modeling of rabbit prolactin hormone complexed with its
receptor.";
RT PROTEINS 27:459-468(1997).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.

```

-1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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or send an email to license@isb-sib.ch).
-----
EMBL: J04510; G165670; .
DR PIR: A30304; A30304.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 2.
RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 616
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 239 258
FT DOMAIN 25 122
FT DOMAIN 124 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 104 104
FT CARBOHYD 132 132
SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;

Query Match 13.3%; Score 307.5; DB 1; Length 616;
Best Local Similarity 36.3%; Pred. No. 1.4e-17;
Matches 77; Conservative 28; Mismatches 90; Indels 17; Gaps 7;

137 PEKPPNISGWSNMMDLCRWTPGAHGEFTLHNTSLKRLKRYGQDNTCEHYHTVGP 196
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
27 PEKPPITICRSPKSEKFTTCWMPGADG--LPTNTLLTHKSGEITTHCPCPYKTGSPN 84
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
197 SCHI-PKDLAFTPEIWEATNRLGSARSDVLTLDVLTDTTPDPDVAVSRGLEDQ 255
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
85 SCVFSKSHSIYIITVATNMGSSVSDPYVDTYIVEDDPVNLTL-EKKHEDR 143
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
256 LSVRWVS--PALKDF--LFOAKYQIRYVEDSVKVVVDVSNQTSCLAGLKPGTV 310
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
144 KYLWTKMLPPLVDVRSGLTLLEYELRLKPEKAEME-THFAGQGTQFRLSLYPGKY 202
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
311 FYOVRCNPFGIYSKAKGWSHPTAATP 342
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
203 LVQVRCKP-----DHGWSVSWSPSSIQIP 227
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 9
RBLR_CHICK STANDARD: PRT; 831 AA.
C 004594;
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
PRLR.
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALIFORMES; PHASINIDAE; PHASININAE; GALLUS.
[1]
SEQUENCE FROM N.A.
STRAIN-WHITE LEIGHORN; TISSUE-KIDNEY;
MEDLINE: 93075121.
TANKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
"Double antenna structure of chicken prolactin receptor deduced from

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RT the cDNA sequence.
RL BLOCHM. BIOPHYS. RES. COMMUN. 188:490-496(1992).
-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
-1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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-----
EMBL: D13154; G222849; .
DR PIR: J01655; J01655.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PFAM: PF00041; fn3; 4.
DR HSSP: P16471; 1BP3.
RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SEQUENCE 831 AA; 94102 MW; B977BF07 CRC32;

Query Match 13.2%; Score 306; DB 1; Length 831;
Best Local Similarity 35.0%; Pred. No. 2.8e-17;
Matches 76; Conservative 27; Mismatches 96; Indels 18; Gaps 8;

137 PEKPPNISGWSNMMDLCRWTPGAHGEFTLH-TNYSIKYLRKRYGQDNTCEHYHTVGP 195
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
230 PEKPPITICRSPKSEKFTTCWMPGADG--HPTNTLLYSKEGEEOYECDDYRTAGP 286
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
196 HSCHI-PKDLAFTPEIWEATNRLGSARSDVLTLDVLTDTTPDPDV--HVSNGSL 252
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
287 NSCYFDKHTSTMTIINIVRAATNMGSSSDPHYVDTYIQPDPVAVTLELKKPIVR 346
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
253 EQLSVRWVS--PALKDF--LFOAKYQIRYVEDSVKVVVDVSNQTSCLAGLKPGTV 309
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
347 KYLVLTW--SPPLADVRSGLTLLEYELRLKPEGEEMETL-FVGGQGTQYKNFSLNPGKX 404
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
310 FYOVRCNPFGIYSKAKGWSHPTAATP 346
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
405 IYIQLHCKP-----DHGWSWSSSENTIQTIPNDR 435
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 10
RBLR_MELGA STANDARD: PRT; 831 AA.
AC 091094; 091091; 091092;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR).
GN PRLR.
OS EULAGRIS GALLOPADO (COMMON TURKEY).
OC EULAGRIS GALLOPADO; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; MELEAGRIDAE; MELEAGRIS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA ZHOU J.F., ZADWORYN D., GUENENE D., KUNHEIN U.;
RN SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
[2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE-Ovary;
RA PITTS G.R., YOO S.K., FOSTER D.N., EL HALAMANI M.E.;
RN SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC EMBL: L76587; G1345365; -
DR EMBL: U22947; G973165; -
DR EMBL: U22947; G973165; -
DR PROSITE: P500241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE: P500340; RECEPTOR_CYTOKINES_2; 2.
DR PFM: P500041; fn3; 4.
DR HSSP: P16471; 1BP3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT DISULFID 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; F8715C98 CRC32;
Query Match 13.2%; Score 305; DB 1; Length 831;
Best Local Similarity 35.5%; Pred. No. 3.3e-17;
Matches 77; Conservative 25; Mismatches 97; Indels 18; Gaps 8;

253 EDOLSVRWYSPALADFE---LFQANYQIRRYEDSVDMKVVVDVSNQISCRLAGKPGTV 309
DB 347 KPYLMILM-SPPPLADVRSGMTLTDVELKREGEEMETV-FVGQOTQYKMFSLNPKK 404
QY 310 YFVQVRCNPFQYIGSKKAGINSESHPTAASPRSR 346
DB 405 YIVQIHCRP-----DHGSMSESENIEIIPNDR 435
RESULT 11
PRLR_CEREL
ID PRLR_CEREL STANDARD; PRT; 581 AA.
AC 028235;
DE 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS CERUUS ELAPHUS (RED DEER).
OC EURKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLIA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
OC CERUUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 96030711.
RA CLARKE L.A., EDERY M., LONDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
RA KELLY P.A., JABBOUR H.N.;
RT "Expression of the prolactin receptor gene during the breeding and non-breeding seasons in red deer (Cervus elaphus): evidence for the expression of two forms in the testis".
RL J. ENDOCRINOL. 146:313-321(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC EMBL: X94953; E218406; -
DR PROSITE: P500241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: P500340; RECEPTOR_CYTOKINES_2; 1.
DR PFM: P500041; fn3; 2.
DR HSSP: P164787; 1AN3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT DISULFID 59 59
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 581 AA; 65159 MW; 721F0366 CRC32;
Query Match 13.1%; Score 303; DB 1; Length 581;
Best Local Similarity 33.6%; Pred. No. 3.1e-17;
Matches 76; Conservative 36; Mismatches 92; Indels 22; Gaps 8;

DB 18 NASLNGOS-----PPGKPKIKCSPGKETFTCWEPGSDG--LPNTYTLTYHNEGRT 70

OY 183 ODNTEEEHTVPSCHT-PKDLALFTPEIWEATNRLGSARSDVLTLDVLTDTDP 241

DB 71 LIHECPDYKGTGPNCTFSKHTSIWKIYIVTNAINONGVSSDPLYDYVYIEPEEP 130

OY 242 PDVHVSFRVGLDOLSVRWV--PALADF--LFOAKQIYIRVEDSVDMKRVVDVSNQ 296

DB 131 ANLTL-ELKHPEDRPYLWIKWFPPLTLDVKSQGMFMIOYERIKRPETADWE-IHFAAKQ 188

OY 297 TSCRLAGLPGTVYFVQVRCNPFGLYSGSKAGIEMSHPTASTP 342

DB 189 TOLKFSLYPGOKYLVQVRCP-----DHGTWSEMPSESSIOIP 227

RESULT 12

PRLR_BOVIN STANDARD: PRT: 581 AA.

AC 028172:

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS BOS TAURUS (BOVINE).

OC EURAKOTR; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC ANTIDACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.

RN [1]

SEQUENCE FROM N.A.

RP RP

RC TISSUE-ENDOMETRIUM.

RX MEDLINE: 93246019.

RA SCOTT P., KESSLER M.A., SCHULER L.A.;

RT "Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues."

RL MOL. CELL. ENDOCRINOL. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC CC

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CC EMBL: L02549; G163618; -

CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

CC PFAM: PF00041; fn3; 2.

CC HSSP: P14787; IAN3.

CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

CC SIGNAL 1 24

CC CHAIN 1 24

CC DOMAIN 25 581

CC TRANSMEM 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DISULFID 36 46

CC DISULFID 36 46

CC CARBOHYD 59 59

CC CARBOHYD 59 59

CC SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 13.1%; Score 302.5; DB 1; Length 581;

Best Local Similarity 31.9%; Pred. No. 3.4e-17;

Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

OY 91 SLLNTLTALALANLNGSRGDNLYCHARDGSLAGSLYGLPEKPFNISCWERN 150

DB 7 SHVFTLLFLTSVSLNG--OS-----PEKRLVXCRSPG 40

OY 151 MEDLCRTPGARGETFEHTNYSLKTKLWYGODWTCCEHTVPSCHT-PKDLALFTP 209

DB 41 KETFTCWEPGADG--LPNTYTLTYHNEGRTLIHECPDYKGTGPNCTFSKHTSIWKI 98

OY 210 YEIWEATNRLGSARSDVLTLDVLTDTDPDPVHVSFRVGLDOLSVRWV--SPALK 267

DB 99 YIIVTNAINONGISSDPLYHYVYIEPEEPANLTL-ELKHPEDRPYLWIKWSPPTMT 157

OY 268 D-----LFOAKQIYIRVEDSVDMKRVVDVSNQTSCLAGLPGTVYFVQVRCNPFGLY 322

DB 158 DVKSGWFTIO--YEIRLPEKATDWE-THTLKQTLQKIFNLVQGVQVIRKRP----- 211

OY 323 GSKAGIEMSHPTASTP 342

DB 211 ---DHGTWSEMPSESSIOIP 227

RESULT 13

PRLR_ORENI STANDARD: PRT: 630 AA.

AC 091513:

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS OREOCROKIS NILOTIUS (NILE TIPIPIA) (TIPIPIA NILOTICA).

OC EURAKOTR; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;

OC LABROIDEI; CICHLIDAE; TIPIPIA.

RN [1]

SEQUENCE FROM N.A.

RP RP

RC TISSUE-KIDNEY;

RX MEDLINE: 95320210.

RA SANDRA O., SOHN F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;

RT "Expression cloning of a cDNA encoding a fish prolactin receptor."

RL PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC CC

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CC EMBL: L34783; G903847; -

CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

CC PFAM: PF00041; fn3; 2.

CC HSSP: P16471; IBP3.

CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

CC SIGNAL 1 23

CC CHAIN 1 23

CC DOMAIN 24 630

CC TRANSMEM 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DOMAIN 23 234

CC DISULFID 37 47

CC DISULFID 37 47

CC CARBOHYD 92 92

CC CARBOHYD 92 92

CC SEQUENCE 101

SQ SEQUENCE 630 AA; 70810 MW; E9A4E553 CRC32;
 Query Match 11.38; Score 261.5; DB 1; Length 630;
 Best Local Similarity 33.28; Pred. No. 8.1e-14;
 Matches 71; Conservative 26; Mismatches 94; Indels 23; Gaps 9;
 QY 138 PERPNISCSRNKMDLTCMTGAGHETFLHNSKYLKRYGQDNCEHYHYPHS 197
 DB 29 PGKPELKRSPEKETTCMKKQSDG--LPTTLYALYKESGDVYHECPDYHTAGKNS 86
 QY 198 CHIPKDAL-FTPEYIWEATNRLGSASDVLDTVDVYTPDPDVHSRYGGLDQ- 256
 DB 87 CFENKNTLWISYINIVATNLGKRYSDPDIDVYIYQPPPELVT---YAKDQ 143
 QY 256 ---LSRWSPALKDF---LFOAKYQIRKVED-SYDMKVVDDVSNGTSCRLAGLPGT 308
 DB 144 WPLRLYSW-EPKPKADTRSGMITLILRYKLEDESEME-NNAAGQCKNFJSLRS 201
 QY 309 VFEVQVRCNPFYIGSKAGISGEMSHPTASTP 342
 DB 202 TYLIQVRCR-----DHGFNEMSTSYKVP 228
 RESULT 14
 GCSR_HUMAN
 ID GCSR_HUMAN STANDARD: PRT; 836 AA.
 AC 09062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 DE (CD114 ANTIGEN)
 GN CSFR OR GCSR.
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMPEL S., SIMS J.E., COSMAN D.,
 RA PARK L., SORESENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein.";
 RL J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor.";
 RL J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RX MEDLINE: 92007729.
 RA FUKUNAGA R., ISHIZAKA-IREDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor.";
 RL EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RX MEDLINE: 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WXXWS

RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELLING OF 125-331.
 RX MEDLINE: 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis.";
 RL J. BIOL. CHEM. 272:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
 CC EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC MELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSR-1 (SHOWN UNDER),
 CC GCSR-2, GCSR-3 AND GCSR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN CSFR ARE A CAUSE OF KOSTMANN SYNDROME;
 CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD114 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X55721; G31697; -
 DR EMBL; X55720; G31699; -
 DR EMBL; S71484; G240884; -
 DR EMBL; M59818; G183047; -
 DR EMBL; M59819; G485364; -
 DR EMBL; M59820; G183049; -
 DR PIR; JH0329; JH0329; -
 DR PIR; JH0330; JH0330; -
 DR PIR; A38252; A38252; -
 DR PDB; 1A27; 28-JAN-96.
 DR MIM; 138971; -
 DR MIM; 202700; -
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM; PF00041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT; ALTERNATIVE SPLICING; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 836
 FT DOMAIN 25 627
 FT TRANSMEM 628 630
 FT DOMAIN 651 836
 FT DOMAIN 121 227
 FT DOMAIN 228 332
 FT DOMAIN 333 428
 FT DOMAIN 429 525
 FT DOMAIN 526 621
 FT DISULFID 131 142
 GRANULOCYTE COLONY STIMULATING FACTOR
 RECEPTOR
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE DOMAIN.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 BY SIMILARITY.

Query Match	11.08;	Score 254.5;	DB 1;	Length 836;
Best Local Similarity	28.98;	Pred. No. 4,4e-13;		
Matches 97; Conservative	48;	Mismatches 148;	Indels 43;	Gaps 16

Query Match 10.9% ; Score 252.5 ; DB 1; Length 837;
Best Local Similarity 27.8%; Pred. NO. 6.3e-13;
Matches 107. Conservative 56. WtMatrix

```
RA FUKUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;  
RT "Expression cloning of a receptor for murine granulocyte colony-stimulating factor." RT  
RN CMLL 61:341-350(1990).  
[2]  
RP STRUCTURE BY NMR OF 225-333.  
RX MEDLINE; 97331327.  
RY YAMASAWI K., NAITO S., ANAGUCHI H., OKUBO T., OTA Y.;  
RT "Solution structure of an extracellular domain containing the wswms motif of the granulocyte colony stimulating factor receptor and its interaction with ligand." RT  
RL NAT. STRUCT. BIOL. 4:498-504(1997).  
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.  
CCC  
CCC -1- SUBUNIT: DIMER (PROBABLE).  
CCC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CCC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.  
CCC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.  
CCC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CCC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
```

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EMBL; M58288; G193455; .
PIR; A34898; A34898.
PDB; 1GCF; 22-OCT-97.
PDB; 1CFO; 22-OCT-97.
MDP; MG188533; CSFRG.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CITOKINES_2; 1.
PFAM; PF00041; fn3; 3.
REPEAT; TRANSMEMBRANE; GLYCOPROTEIN; IMMUGLOBLULIN FOLD; SIGNAL;
REPEAT; 3D-STRUCTURE
FT CHAIN 1 25
FT 26 837

DOMAIN 26 626 POTENTIAL,
TRANSSEM 627 650 GRANDUCYTE COLONY STIMULATING FACTOR
DOMAIN 651 837 RECEPTOR.
DOMAIN 26 118 EXTRACELLULAR (POTENTIAL).
DOMAIN 122 228 CTROPALASIC (POTENTIAL).
DOMAIN 229 333 IG-LIKE C2-TYPE DOMAIN.
DOMAIN 334 431 FIBRONECTIN TYPE-III.
DOMAIN 432 528 FIBRONECTIN TYPE-III.
DOMAIN 529 624 FIBRONECTIN TYPE-III.
DISUFLID 132 143 BY SIMILARITY.
DISUFLID 249 296 BY SIMILARITY.
DISUFLID 267 310 BY SIMILARITY.
CARBOHYD 51 51 POTENTIAL.
CARBOHYD 94 94 POTENTIAL.
CARBOHYD 129 129 POTENTIAL.
CARBOHYD 186 186 POTENTIAL.
CARBOHYD 279 279 POTENTIAL.
CARBOHYD 392 392 POTENTIAL.
CARBOHYD 408 408 POTENTIAL.
CARBOHYD 474 474 POTENTIAL.
CARBOHYD 487 487 POTENTIAL.
CARBOHYD 582 582 POTENTIAL.
CARBOHYD 613 613 POTENTIAL.
SEQUENCE AA: 837 AA: 93406 MW; D55E84D4 CRC32;

```

QY 29 LCVLSVPRGSGAHNAVISPQDPTLIGSSLAATCSIHGDTPEATAG-LYITLNGRL- 87
Db 14 LIFLLPRLESCGHIISP--PVYRLGDPVLASCTISPNCSNLDQAKILWRLDEPIQ 71
QY 87 PSELRL--NTSTLALANNGSROGSDNLVCHARDSILAGSCLVYGLPREKPMI 144
Db 72 PDROHHLPDGTOESLITLPHLNT-QAFLFCIVPVEDSVQLDDQELHAGIPPAFSPNL 130
QY 145 SCMSR-NMKDLTCRMTPGAHGETFLNTNYSK-YKLR--WYGODNTCEYHTVGRSCH 199
Db 131 SCIMHLTNSLVQMEPBP--ETHLPTSLKSFRRADQYOGDIIPCVAKKRNNGS 188
QY 200 IP-KDLATFYEIWEATNRUGSANSVLTLDVDTVTTPP-----PDVHVSRYG 250
Db 189 IPRKNLLIYQYMAIWQANMLSSSESPKLCIDPMQVYKLEPPMLQALDIGPDVYVSHQPG 248
QY 251 GLEDOLSVRWVS-PAKDLFOAKYQIRYVE-DSVDMKYVDY-SNOTSCLAGLKPG 307
Db 249 CL-----WLSKPKPKPSEIYMEQECELRYOPOLKANNTLVFHLPSXDOFELGGLHOA 301
QY 308 TVYFVQVRGNPFGIYGSKRAGIWEVS-----HPT-ASTPRSERGPGGVCPEPGRGP 361
Db 302 PYTLOMRC-----IRSSLPGFWSPPSGLOLRPTMKAPTIRLDT-----WCQKKQIDP 350
QY 362 SS-----GPVRELKQIFLWL 377
Db 351 GTVSVOLEWKPFLQEDSGQIQGYL 375

```

Search completed: September 17, 1999, 03:10:12
 Job time: 292 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:05 ; Search time 68.96 Seconds
(without alignments)
379.293 Million cell updates/sec

Title: US-09-037-657-15

Perfect score: 2317
Sequence: 1 MPAGRPGVPAQSAARRPPRL.....NODEGILPSGRGAARPGAG 425

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :

- 1: SP:REMBL_10:*
- 2: sp.archaea:*
- 3: sp.bacteria:*
- 4: sp.fungi:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.protoct:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2176.5	93.9	422	4	075462	075462 homo sapien
2	355.5	15.3	881	13	057519	057519 xenopus lae
3	324.5	14.0	206	4	016354	016354 homo sapien
4	306	13.2	581	6	046561	046561 ovls aries
5	302.5	13.1	296	6	018880	018880 bos taurus
6	268.5	11.6	346	13	093404	093404 oreochromis
7	234.5	10.1	217	6	046386	046386 mustela vis
8	230.5	9.9	198	6	018985	018985 cervus elap
9	226.5	9.8	335	6	P79203	P79203 ovls aries
10	226	9.8	372	11	088507	088507 mus muscullu
11	217.5	9.4	862	4	099665	099665 homo sapien
12	215.5	9.3	874	11	P97378	P97378 mus muscullu
13	209.5	9.0	422	4	016542	016542 homo sapien
14	208.5	9.0	432	11	064385	064385 mus muscullu
15	201	8.7	432	11	P70225	P70225 mus muscullu
16	194.5	8.4	440	11	000343	000343 mus muscullu
17	193.5	8.4	710	13	057520	057520 xenopus lae
18	187.5	8.1	1165	6	002671	002671 sus scrofa
19	182	7.9	895	11	062960	062960 rattus norv
20	177	7.6	316	11	035545	035545 rattus norv
21	174.5	7.5	958	4	092920	092920 homo sapien
22	174.5	7.5	1165	4	092921	092921 homo sapien
23	174.5	7.5	958	4	013592	013592 homo sapien
24	174.5	7.5	906	4	013593	013593 homo sapien
25	174.5	7.5	896	4	013594	013594 homo sapien
26	174.5	7.5	896	4	029219	029219 mus muscullu
27	163	7.0	1093	11	070535	070535 rattus norv
28	162	7.0	427	4	095646	095646 homo sapien
29	159.5	6.9	383	11	088786	088786 mus muscullu

ALIGNMENTS

30	156.5	6.8	971	11	070458	070458 mus muscullu
31	156.5	6.8	970	11	088821	088821 mus muscullu
32	153.5	6.6	229	6	027950	027950 bos indicus
33	153.5	6.6	229	6	028206	028206 bos taurus
34	153.5	6.6	228	11	035228	035228 mus muscullu
35	149.5	6.5	229	4	075269	075269 homo sapien
36	149	6.4	1896	4	060468	060468 homo sapien
37	149	6.4	1571	4	060469	060469 homo sapien
38	149	6.4	890	11	092140	092140 cavia porce
39	143	6.2	279	11	064236	064236 rattus norv
40	142.5	6.2	86	6	018853	018853 mustela put
41	141.5	6.1	229	4	014213	014213 homo sapien
42	136.5	5.9	634	6	046600	046600 bos taurus
43	136.5	5.9	269	6	P79195	P79195 macaca mula
44	133	5.7	396	4	014631	014631 homo sapien
45	133	5.7	420	4	014633	014633 homo sapien

RESULT 1	PRELIMINARY:	PRT:	422 AA.
ID 075462			
AC 075462:			
DT 01-NOV-1998 (TREMBLrel. 08, Created)			
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.			
GN CLF-1.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN [1]			
RP SEQUENCE FROM N.A.			
RA ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREYNER D.,			
RA MENUD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.,			
RT CLF-1, a Novel Soluble Protein Shares Homology with Members of the			
RT Cytokine Type-I Receptor Family."			
RL J. Immunol. 0:0-0(1998).			
DR EMBL: AF059293; AAC28335.1;			
DR PFM: PF00041; fn3; 2.			
KW Signal.			
FT SIGNAL.			
FT CHAIN			
SQ SEQUENCE 422 AA; 46301 MW; 877F9BC9 CRC32;			

Query Match 93.9%; Score 2176.5; DB 4; Length 422;
Best Local Similarity 94.8%; Pred. No. 4.6e-184;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1	MPAGRPGVPAQSAARRPPPLSLMSPILLCLVGRGSGAHTAVISQDDPLLIGSSIQ 60
DB 1	MPAGRPGVPAQSAARRPP-PLPL--LLLCVAGPARAGSGAHTAVISQDDPLLIGSSIL 57
QY 61	ATCSIHGDTPTAGTGLWTNGRLPELSRLNTSTLALALANLNSROOSGDNVCH 120
DB 58	ATCSVHGDPPTAGTGLWTNGRLPELSRLNTSTLALALANLNSROOSGDNVCH 117
QY 121	ARDGSLIAGSCLVGLPEKPKPNISCSWNNKDLTCRTPGAHGFTPLHTNYSLEKYLKW 180
DB 118	ARDGSLIAGSCLVGLPEKPKPNISCSWNNKDLTCRTPGAHGFTPLHTNYSLEKYLKW 177
QY 181	YGQDWTCEHYTHVGHSHIPKDLALFTPEIWEATNRLSASNDVLTLDVLYVTTDP 240
DB 178	YGQDWTCEHYTHVGHSHIPKDLALFTPEIWEATNRLSASNDVLTLDVLYVTTDP 237
QY 241	PPDVAVSVAGLEDDLSRTWSPPALKDFLFOAKYQIYRVDSVDKVVYDVDSNOTSCR 300
DB 228	PPDVAVSVAGLEDDLSRTWSPPALKDFLFOAKYQIYRVDSVDKVVYDVDSNOTSCR 297
QY 301	LAGLKGTVTVVQVRCNPFGLYSGKAGIMSEWSHPTAASIPRSEBPGGVCPEPRGE 360

DB 298 LAGKPGTVEYVGRCPFGIYSGKAGIEMSHPRATPSERPGGCGE 357
 QY 361 PSSGPRRELKOTLGMLKKAAYCSNLSFRLYDQWRAMQSRHTRNODEGILPSGRGAA 420
 DB 358 PSSGPRRELKOTLGMLKKAAYCSNLSFRLYDQWRAMQSRHTRNODEGILPSGRGAA 417
 QY 421 RGA 424
 DB 418 RGA 421

RESULT 2

057519 PRELIMINARY; PRT; 881 AA.
 AC 057519;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DE GP130P1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHEN J., GRACE A., CHIEN K.R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041845; AAC03531.1;
 DR PFIAM; PF00041; fn3; 4.
 SQ SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

Query Match 15.3%; Score 355.5; DB 13; Length 881;
 Best Local Similarity 30.5%; Pred. No. 4,2e-23;
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;

QY 50 DFTLLIGS-SLOATCSIHGDTGATAGLTYLNGRRRLPSELRLNTSTLALANING 108
 DB 33 DGTGIVGERPFTAYCVINOTCRDASRIYWKGVKPEYELINOTTSVTEPNTLT 92
 QY 109 SFGQSGDNLVCHARDGSLAGSCLVGLPBEKFNISCSRMKMLTGTWPGANGETFL 168
 DB 93 LNSPLTCLNMGAGVANTLYGFFFLGDPDPFTMLTCLVYNQDMLTCTWPGR--PNTL 150
 QY 169 HTNLSLKYKLRW-----YQDNTCEHYHTVGPBSCHIPKDLALFPYEIWTATNRL 220
 DB 151 PNTYLSH--RWAHFGANVCRGANNSC-----TIHSP-GPGFYIDTFOVATNEL 198
 QY 221 GSABSDVLTLDVLYTTDPPDVHVSRYGLEDQLSVRWVSPPLAKDFLQAKYQINR 280
 DB 199 GLOKSETLTIDPVNIVKPNPOLSLSLELPNALKIEMKNPT--NAFLKYNINR 255
 QY 281 VEDSVDMKVY--DDVSNOTSCLAGLKGTYFPYQVNCNPGIYSGKAGIEMSHPT 337
 DB 256 PKTIDWEMVPEEDASHSDFTLDDLPNTYEVYSIRC-----IHKDGHGFWSDMSLX 310
 QY 338 AASTRSEPRPGGCGVCEPRGSGPSSGP 365
 DB 311 KQVTP-EAP-----PGRGP 323

RESULT 3

016354 PRELIMINARY; PRT; 206 AA.
 AC 016354;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95286597.
 RA FUD G., WELLS J.A.;
 RT "Prolactin receptor antagonists that inhibit the growth of breast
 cancer cell lines."
 RT J. Biol. Chem. 270:13133-13137(1995).
 RL EMBL; S78505; AAB34470.1;
 DR PFIAM; PF00041; fn3; 2.
 FT NON-TER
 SQ SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match 14.0%; Score 324.5; DB 4; Length 206;
 Best Local Similarity 38.0%; Pred. No. 3,4e-21;
 Matches 81; Conservative 25; Mismatches 90; Indels 17; Gaps 7;

QY 136 LPPEKFNISCSRMKDLCTRWTPGANGETFLHTNLSLKYKLRWYGODNTCEHYHTVGP 195
 DB 2 LPPEKFNISCSRMKDLCTRWTPGANGETFLHTNLSLKYKLRWYGODNTCEHYHTVGP 59
 QY 196 HSCHPKD-LALFTYEIWEATNRLSGASDVLTLVDVYTTDPPDVHVSRYGLED 254
 DB 60 NSCHGKQYTSWMTYIMVATNMGSSFSDELVDVYTYIQPDPLEAV-EVKQPED 118
 QY 255 QLSVRW--SPPAKDF--LFOAKYQIRVEDSVDMKVYDDVSNOTSCLAGIEMSHPT 309
 DB 119 KPYIMINWSPPTLIDLTGWFLLYELTRLEKNAEWE-IHFAQOQTEFRILSLHPGOK 177
 QY 310 YFVGRCPFGIYSGKAGIEMSHPTASTP 342
 DB 178 YLVGRCKP-----DHGYWSAMSPATFIQIP 203

RESULT 4

046561 PRELIMINARY; PRT; 581 AA.
 AC 046561;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Caprinae; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BIGNON C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,
 RA BIGNON C.,
 RA DIANE J.;
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
 and genomic analysis reveal that the two forms arise by different
 alternative splicing mechanisms in ruminants and in rodents."
 RT J. Mol. Endocrinol. 19:109-120(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BIGNON C., DIANE J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041257; AAB96795.1;
 DR PFIAM; PF00041; fn3; 2.
 KW Signal.
 FT SIGNAL.
 FT CHAIN
 SQ SEQUENCE 581 AA; 65235 MW; 6792A7C7 CRC32;

Query Match 13.2%; Score 306; DB 6; Length 581;
 Best Local Similarity 34.8%; Pred. No. 5,6e-19;
 Matches 78; Conservative 32; Mismatches 92; Indels 22; Gaps 8;

QY 125 SIAGSCLYGLPPEKFNISCSRMKDLCTRWTPGANGETFLHTNLSLKYKLRWYGGD 184

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Db 20 SLNMQS-----PPKPKLRCRSPGKETFTCMWEPGADG--LPTNYTLTYRKGETLI 72
QY 185 MTCEHYHTVGHSPCHIPD-LALFTPEIWEATRLGASRSDVLTLDVDTTDPD 243
Db 73 HECDDYKGTGNSCYFSKRYTSMKMYITVSALNQMISSSDPLVTVYVEPEPN 132
QY 244 VHSRVGGLDQLSVRMV--SPALKDF--LFOAKYQIRYVEDSVMKVVDVSNOTS 298
Db 133 LTL-ELKHPEDRKRYLTKMSPPPLTDVKSQWFSIQYIRLKPENATWE--THFAPKLTQ 190
QY 299 CRLAGLPGTYFYQVRCNPGYIGSKAGIWSWSHPTAASP 342
Db 191 LKIFNLXPGRKYLVQIRKP-----DHGYWSEMSPESTIQIP 227

RESULT 5
ID 018880 PRELIMINARY; PRT; 296 AA.
AC 018880;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
Bovinae; Bos.
[1]
RP SEQUENCE FROM N.A.
RP MEDLINE: 97375450.
RA SCHULER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues."
RT Endocrinology 138:3187-3194(1997).
DR EMBL: AF027403; AAB8399.1; -.
DR PFAM: PF00041; fn3; 2.
SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 13.18; Score 302.5; DB 6; Length 296;
Best Local Similarity 31.98; Pred. No. 4.7e-19;
Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

2Y 91 SRLNTSTLALANLNGSQSGDNLYCHAROSIAGSLYGLPPEKPNISCSRN 150
Db 7 SRVYFILLFLSLNG--QS-----PPKPKLYKCRSPG 40
2Y 151 MKDLTCRWTPGAGETFLHTNYSILKYLRYMGODNTCEHYHTVGHSPCHIPD 209
Db 41 KEFTCMWEPGADG--LPTNYTLTYRKGETLIHECPDYKGTGNSCYFSKRYTSMK 98
2Y 210 YELVWATNRLGASRSDVLTLDVDTTDPDPPDVHVSRYVGLDQLSVRMV--SP 267
Db 99 YATVAINQMGISSSDPLVTVYVEPEPNALTL-ELKHPEDRKRYLTKMSPP 157
2Y 268 D-----FLFOAKYQIRYVEDSVMKVVDVSNOTSRLGLPGTYFYQVRCNPG 322
Db 158 DVKSGFIIO--YELKPEKADWE--THFTLKOTOLKIFNLXPGRKYLVQIRKP 211
2Y 323 GSKKAGIWSWSHPTAASP 342
Db 211 ---DHGYWSEMSPESTIQIP 227

RESULT 6
ID 093404 PRELIMINARY; PRT; 346 AA.
AC 093404;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).

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OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica);
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
[1]
RP SEQUENCE FROM N.A.
RP TISSUE-GILL.
RA SHIRAIASHI K., MATSUDA M., MORI T., TENGUYA H.;
RT "Expression of prolactin and cortisol receptor gene in early-life
RT stages of tilapia (Oreochromis mossambicus).";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF080247; AAC31825.1; -.
DR PFAM: PF00041; fn3; 2.
FT NON_TER 346
SQ SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match 11.64; Score 268.5; DB 13; Length 346;
Best Local Similarity 33.28; Pred. No. 5.0e-16;
Matches 71; Conservative 28; Mismatches 92; Indels 23; Gaps 9;

QY 138 PEKPNISCSNRNKKDLTCRWTPGAGETFLHTNYSILKYLRYMGODNTCEHYHTV 197
Db 29 PKRPEITCRSPKERTFTCMWEPGSDG--LPTTYALTYRKESDVTYHECPDYHTACKNS 86
QY 198 CHIRK-DLALFTPEIWEATNRLGASRSDVLTLDVDTTDPDPPDVHVSRYVGLDQ 256
Db 87 CFENKNDTLTWVSYNITVAVNMGKYSDDVIDVYIYKPHPEKLEVT--VMDQG 143
QY 256 ---LSVRWSPPLKDF--LFOAKYQIRYVED-SVDMKVVDVSNOTSRLAGLKPRT 308
Db 144 WPLRYVSW--EPKPADRSMTITLYELRYKLEDESEWE--NHAAGQKXNFISLNSG 201
QY 309 VYFQVRCNPGYIGSKAGIWSWSHPTAASP 342
Db 202 TYLIQVRCR-----DHGFWSMSSTSYVXP 228

RESULT 7
ID 046386 PRELIMINARY; PRT; 217 AA.
AC 046386;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
GN PRLR.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
[1]
RP SEQUENCE FROM N.A.
RP TISSUE-TESTIS;
RA DOUGLAS D.A., SONG J.-H., HOUDE A., MURPHY B.D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF028294; AAB88899.1; -.
DR PFAM: PF00041; fn3; 1.
FT NON_TER 217
SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 10.18; Score 234.5; DB 6; Length 217;
Best Local Similarity 32.38; Pred. No. 3.1e-13;
Matches 61; Conservative 30; Mismatches 81; Indels 17; Gaps 7;

QY 160 PGAGETFLHTNYSILKYLRYMGODNTCEHYHTVGHSPCHIPD-LALFTPEIWEATN 218
Db 2 PGSDG--LPTKTYLHYHNEGTTTTCPCDYITSGPNSCYFNKHTSIWYITINATN 59
QY 219 RLGSARSDVLTLDVDTTDPDPPDVHVSRYVGLDQLSVRMV--SPALKDF--LFOA 273
Db 60 EMQSSSDPRYVTVYVEPEPNLTL-ELKHPEDRKRYLTKMSPPPLTDVDSRGWLT 118

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QY 274 KTOIRYEDSDYDMKVVDDVNSQTSRLAGLPGTYVYQVACNPFIGSKAGIWSM 333
 DB 119 QYKIRKPKKATEME-THEAGLOTOFKILSLYPGOKYLYQVACRP-----DHGFWSEM 170
 QY 334 SHPTAASP 342
 DB 171 SPKRSIQIP 179

RESULT 8
 O18985 PRELIMINARY: PRT: 198 AA.
 AC O18985;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE SOLUBLE PROLACTIN RECEPTOR.
 OS Cervus elaphus nelsoni (American elk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA JABOUR H.N.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Y14753; CAA75048.1;
 DR PFAM: PF00041; fn3; 1.
 SQ SEQUENCE 198 AA; 22652 MW; COABBA0 CRC32;

Query Match
 Best Local Similarity 9.9%; Score 230.5; DB 6; Length 198;
 Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;

QY 123 DGSIIAGSLYGLPPEKPFNISCNRNKKDLTCMTPEAGHETFLHNTSKYIKRWG 182
 DB 18 NASLNGOS-----PQKPKIKRSPGKFTFCWMEPSDGS--LPITYTLTHHEGRT 70
 QY 183 QNTCEHYHTVGPSPCHI-PKDLALFTPEIWEATNRLGSAVDLTLDVYTTDPP 241
 DB 71 LHCEPDYITGPNPTCYESKHTSIKIYITVNAIINGVSSDPLDYVITYVEPEPP 130
 QY 242 PVHVSRRVGLDQLSVRWVS--PPALKDF--LFOAKYQIRYEDSDYDMKVVDDVNSQ 296
 DB 131 AHLTL-ELKHPRDKRYLTIKNEPPLITGVKSGFMIOYEILKPKRTATDWE-HDDLHP 188
 QY 297 TSCR 300
 DB 189 TSSR 192

RESULT 9
 P79203 PRELIMINARY: PRT: 335 AA.
 AC P79203;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-422/80; TISSUE-ANTERIOR PITUITARY;
 RA TORONTO D.T.; BROOKS J.; INGLETON P.; MCNEILLY A.S.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Y10578; CAA71597.1;
 DR PFAM: PF00041; fn3; 1.
 FT NON_TER 1 1
 FT NON_TER 335 335

SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;
 Query Match
 Best Local Similarity 9.8%; Score 226.5; DB 6; Length 335;
 Matches 58; Conservative 28; Mismatches 68; Indels 31; Gaps 7;

QY 164 GETFLHTNYSIKYLRWYGQDNTCEHYHTVGPSPCHIPKD-LALFTPEIWEATNRLGS 222
 DB 8 GETLIH-----ECPDYITGPNPTCYESKHTSIKIYITVNAIINGV 51
 QY 223 ARSDVLTLDVYTTDPPPVHVSRRVGLDQLSVRWVS--SPALKDF--LFOAKYQI 277
 DB 52 SSDDPLDYVITYVEPEPPVNLTL-ELKHPRDKRYLTIKNEPPLITGVKSGFMIOYEI 110
 QY 278 KRYVEDSDYDMKVVDDVNSQTSRLAGLPGTYVYQVACNPFIGSKAGIWSM 337
 DB 111 RUKPERATDWE-THEAPRLTQIKIFNLPGOKYLYQVACRP-----DHGFWSEMSPES 162
 QY 338 AASTP 342
 DB 163 FIQIP 167

RESULT 10
 O88507 PRELIMINARY: PRT: 372 AA.
 AC O88507;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
 GN CNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-BRAIN, SKELETAL MUSCLE;
 RA MADDA M.; YACUCHI N.; HANYU C.; MAKATA Y.; ONODA N.; TULIN E.E.;
 RA KOJIMA T.; HASEGAWA M.; KIRUCHI Y.; NOMURA H.;
 RL "Mouse homolog of human ciliary neurotrophic factor receptor."
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF068615; AAC25711.1;
 DR PFAM: PF00041; fn3; 1.
 DR PFAM: PF00047; 19; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT ALPHA.
 SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match
 Best Local Similarity 9.8%; Score 226; DB 11; Length 372;
 Matches 97; Conservative 45; Mismatches 157; Indels 74; Gaps 18;

QY 30 CYLSVPRGSGAHNVISPODPTLIGSSLOATCISHDTPRATF--GLYTLNGRRL 86
 DB 9 CCAYIAAAAVYTKHSPQEPAPHYERLGDVTL----PGTASWDAAVATWRNGTDL 64
 QY 87 PSELRLNTSTIALALANLNGSRQSGDNTVCHRDGSIILAGS-CLVYGLPPEKPFNIS 145
 DB 65 APD--LNGSOLILRSLELHSGSLYA-----CFHRDSMHLRHQVLLHGLPPEPPV-LS 115
 QY 146 CWSRNM-FDLRCRW-----TPGAHGETFLHTNYSIKYLRWYGQDNTCEHYHTVGPS 197
 DB 116 CSNSTYPRGFCYCWMLPPTIYPTNFNTVYLGSKRIM-----VCEKDPAL-KNR 163
 QY 198 CHIPDALLFT--PEIWEATNRLGSAKSDVLTLDVYTTDPPPVHVSRRVGLDQ 255
 DB 164 CHI-RYMLFSTIKYKVSISVSMAGH-NTAITEFDEITIVKPPPEPVAVAPPSNDR 221

256 LSVRWSPALAKD-FLFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLPGTVYFQV 314
222 LEVYMQTPSPWDESEFPLKFLRYRPLLDQNGHV-ELSDGNAHTTDAKREYIIV 280
315 RCPNPFYISKRGKISSENS-----HPTAATPSEBPGGCV 353
281 AAK-----DNEIGTWSVSAHAATPTEPRHLTTEAQAPEITTSLSLAPPTKI 334
354 CEP-----RGCEPS 362
335 CDPGLSGSGGGS 347

ESULT 11
199665
D 099665 PRELIMINARY: PRT: 862 AA.
01-MAY-1997 (TREMBLrel. 03, Created)
01-NOV-1998 (TREMBLrel. 03, Last sequence update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
IL-12 RECEPTOR BETA2.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.R., GUBLER U.,
Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
EMBL: U64198; AAB36675.1;
PFAM: PF00041; fn3; 3.
SEQUENCE 862 AA; 97134 MW; 5FE4FBD5 CRC32;

Query Match 9.4%; Score 217.5; DB 4; Length 862;
Best Local Similarity 25.6%; Pred. No. 6e-11;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

53 LLIGSLONTGSHDDTGATAGLYWTL-----NGRRLSELRL-L 94
41 ILIGSTVITSL-----KPKQGCHSRNKKLILYKFRDIRINHHGSLNSOVYGLPL 94
95 NTSTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPPEKPFNISQMSRNMK-D 153
95 GTTFVYCKLACINSEIQ-----ICGAEIVGVAPEQPONLSCTIQKEQGT 140
154 LTCRTPCAHGETFLHNYSLKY---KLRYGQ--DMTCEYHYVG-----PSSCHI 200
141 VACTWENGR--DTHLYETYLQLSGPKMLTQKCKDIYC-DYLDGILVLPESPESNFT 197
201 PKDALTFPEYELWENATRLGSAKSDVLTLDVLYTTDPPPDVHVSRYGLEDOLSVRW 260
198 AK-----VTAVNSLGSLSSTPFTFLDIYRPLPPMDIRIKFQKASVSCITLYW 246
261 VSPALAKDFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLPGTVYFQVQCNPPG 320
247 -----RDEGLVNLRLKRYRPSNSLMMVNTAKAGRHDLDLKPFTEYEFQI--SSKLH 299
321 IYSGKKGAGIWMSEWHPAATPSEBPG 348
300 LY-----KGSWSDWSESLRAQTPPEEPGT 323

ESULT 12
97378
D 97378 PRELIMINARY: PRT: 874 AA.
01-MAY-1997 (TREMBLrel. 03, Created)
01-MAY-1997 (TREMBLrel. 03, Last sequence update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
RA GATELY M.R., GUBLER U.,
Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
EMBL: U64199; AAB36676.1;
DR MGD; MGI:1270861; IL12RB2.
DR PFAM; PF00041; fn3; 4.
SEQUENCE 874 AA; 98196 MW; 9890EB47 CRC32;

Query Match 9.3%; Score 215.5; DB 11; Length 874;
Best Local Similarity 25.3%; Pred. No. 9.1e-11;
Matches 96; Conservative 59; Mismatches 145; Indels 79; Gaps 19;

QY 9 VAOSARPPRPLSLMSPLL-----CYLGPFGSGAHNAVISPQDPTLLIGSLQAT 62
DB 1 MGVYBECSLALFLFMWLLIRANIDVCKLG-----TVYQPA-PVPLGSAANIS 50
QY 63 CSIH-----GDPFGATA-----EGLYTLNGRRL-----PSELRLNTST-LATAL 103
DB 51 CSUNPQSGSHYPSSELILLKFNVDVLYENHGGKVDHGTGHSSTFOYTNLSLGTFLFV 110
QY 104 AALNGSRQSGDNL-VCHARDGSIAGSLYGLPPEKPFNISQMSRNMK-DLTCRWTPG 161
DB 111 CKLNGSNQCKRPVPC-----GVEISGVAPPEPPQNSCVOEGENGVAQSWMSG 161
QY 162 ANGTEFLHNTYSLAKYKRLRYGQDN-TCE-EHTVGPSC-----HFKDLATLPPEI 212
DB 162 K--VYLLKNTVYLOLS---GPNLTCQKQCFSDNRONCRDLGINSPLDA-ESRFIV 214
QY 213 WYEATNRLGSAKSDVLTLDVLYTTDPPPDVHVSRYGLEDOLSVRWSPALAKDFLQ 272
DB 215 RYTAINDLNGSSLSHTFTFLDIYRPLPPMDIRINFVLAAGSGRLQW-----EDGCV 268
QY 273 AKYQIRYVEDSVDMKVVDVSNQTSCLAGLPGTVYFQVQCNPFYISK---KAGI 329
DB 269 VLNQRLYQPLNSTSWNMVNAATYAKGYDLRLRPTEYEFQI-----SSKHLSSGS 320
QY 330 WSEWHPAATPSEBPG 348
DB 321 WSNWSESLRTPTPEEPVG 339

RESULT 13
016542
ID 016542 PRELIMINARY: PRT: 422 AA.
AC 016542; 014626;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RX MEDLINE; 95399754.
RA CHEREL M., SOREL M., LEBEAU B., DOBOIS S., MOREAU J.F., BATAILLE R.,
RA MINVIELLE S., JACOUES Y.,
RT "Molecular cloning of two isoforms of a receptor for the human
hematopoietic cytokine Interleukin-11.";
RL Blood 86:2534-2540(1995).
[2]
RP SEQUENCE FROM N.A.
RA VAN LIEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSLER A.,
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE-PLACENTA;

RA CHEREL M., SOREL M., DUBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
 RA MINVILLE S.,
 RA Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U32324; AAB36492.1; -
 DR EMBL; Z38102; CAAB6224.1; -
 DR EMBL; U32323; AAB36491.1; -
 DR EMBL; Z46595; CAAB6570.1; -
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; 19; 1.
 SO SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 9.0%; Score 209.5; DB 4; Length 422;
 Best Local Similarity 23.9%; Pred. No. 1.2e-10;
 Matches 89; Conservative 53; Mismatches 136; Indels 93; Gaps 18;

QY 43 TAVISPODPTLLI-----GSSLOATCSINGDPGATA-EGLYWTNG--RLUPS 88
 DB 17 TALVASASPCPOAMGPPEVQKGPGRSVKLC-----PGYADDPVWFMDGEPKLLQG 70
 QY 89 ELRLNLTALALANANGSROSGDNLVCHARDGSLAGSCLYGLPPKPRNIGWS 148
 DB 71 PDGSGHLLVLAQADSTDEGT-----YIQTLIDGALGTYTQLGYPAPRPV-VSCOA 122
 QY 149 RNMKDLTCRTPGAAGETFLHTNTSLKYLWYGODNTCEYHMGPSCHIPRO----- 204
 DB 123 ADYENFSCITWSPSQ--ISGLPTRYITSTRKTYLGADSQRSPTSGPFC--PDDPLGA 178
 QY 204 -----LALFTPYEIWEATNRLSARSVDLTLDLVYTTDPPDVHVSRYGLEQDLS 257
 DB 179 RCYVGAFFWQYRINTVEVNPGL-ASTRLDVSLSQSLRDPDGLVESEVPGPRRLR 237
 QY 258 VRWVSP---PALKDELPOAKQIRRVESVDWKVYVDVSNQTSCLAGL-----PG 307
 DB 238 ASWYTPASWPCQPHLL--KRLDYRPAQHAWSTVEP-----AGLEEVTTDAVAG 286
 QY 308 TVYFQVACNPFYIGSKAGIMSEMSHPTASTPRSPRPGGVCPEPGCESSGPVR 367
 DB 287 LPHAVRVSARDP-----LDAGTWSWS-PEA-----WGTSTGTITP 321
 QY 368 RELKOFGLWLNKH 380
 DB 322 KEIP---AMGOLH 331

RESULT 14
 Q64385 PRELIMINARY; PRT; 432 AA.
 AC Q64385;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NRL1) (ETL2)
 DE (IL-11RALPHA) (IL11RA1).
 GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE; 95045367.
 RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
 RA GONGG N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;
 RA "Cloning of a murine IL-11 receptor alpha-chain; requirement for
 RA gp130 for high affinity binding and signal transduction.";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRO;
 RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAOTTES D.,
 RA GUDNET J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6;
 RA GOSSLER A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed Interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- CONTAINS ONE IG-LIKE DOMAIN.
 DR EMBL; X74953; CAAS2908.1; -
 DR EMBL; U14412; AAAS3248.1; -
 DR EMBL; X94162; CAAG3873.1; -
 DR EMBL; X94163; CAAG3873.1; JOINED.
 DR MCD; MG1:107426; IL11RA1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; 19; 1.
 KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNLF 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT POTENTIAL.
 SO SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

Query Match 9.0%; Score 208.5; DB 11; Length 432;
 Best Local Similarity 23.9%; Pred. No. 1.5e-10;
 Matches 94; Conservative 51; Mismatches 136; Indels 113; Gaps 20;

QY 7 GPVAGSARRPRPLSLMSPLLCLVLPVPGSGAHTAVISPODPTLLIGSSLOATCSIH 66
 DB 31 GPVGVYQGGGR-----PYMLCCPEVSAG----- 55
 QY 67 GDIPGATAEGLYWTNGRLRLPSELRLN--TSTLA--LALANINGSRQSGDNLVCHAR 122
 DB 55 --TP-----VSWFRDSD-----SRLLQGPDSGLGRLVLAQVSDPE---GTYVQOTL 97
 QY 123 DGSILAGSCLYGLPPKPRNIGWSNMMDLTCRTPGAAGETFLHTNTSLKYLWYG 182
 DB 98 DGVSGGVNTLKLGPFRAP--EVSCQAVDYENFCTWSPGQ--VSGLTRFLTSRKRTLP 154
 QY 183 QDNTCEHYHVGPSCHIPRO-----LALFTPYEIWEATNRLSARSADVTLTD 231
 DB 155 GASQQRSPSTGWPFC--PDDPLEASRCVHGAEFWSEYRINTVEVNPGL-ASGCLLDVR 211
 QY 232 VLQVYTTDPPDVHVSRYGLEQDLSRYVSPALK---DFLFOAKQIRRVEDSVDK 288
 DB 212 LQSLIRDDPDQGRVSEVSPYPRLLHASTYTPASWRQPHFL--KRLDYRPAQHAWMS 269
 QY 289 VVDVSNQ--TSCRLAGLKRGTYFQVQVNRNPGIYSKAGIMSEMSHPTASTPRSER 346
 DB 270 TVEIGLEEVTTDAVAGLP---HAYVVSARDP-----LDAGTWSAWS-PEA----- 312
 QY 347 PGPGGVCEPRGGEPSGYPVRELKQFLWLNKH 380
 DB 312 -----WGTSTGTITPQDEIIPD---WSQGH 331

RESULT 15
 ID P70225 PRELIMINARY; PRT: 432 AA.
 AC P70225: 009074:
 DT 01-FEB-1997 (TREMBLERel. 02, Created)
 DT 01-FEB-1997 (TREMBLERel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLERel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11RETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11RETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (1)
 SEQUENCE FROM N.A.
 RC STRAIN-CD1: TISSUE-TESTIS;
 MEDLINE: 9712900.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RA "Two differentially expressed Interleukin-11 receptor genes in the
 mouse genome.";
 RA Biochem. J. 320:359-363(1996).
 (2)
 SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 MEDLINE: 96278810.
 RA ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G.;
 RA "Structural analysis of the gene encoding the murine Interleukin-11
 receptor alpha-chain and a related locus.";
 RA J. Biol. Chem. 271:13754-13761(1996).
 (3)
 SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 MEDLINE: 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RA "Identification of a second murine Interleukin-11 receptor
 alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RA Genomics 40:387-394(1997).
 C -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN-11.
 C -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 C -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 C -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 C -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 C -1- CONTAINS ONE IG-LIKE DOMAIN.
 C -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 EMBL: X94157; CAA63872.1; -
 EMBL: X94158; CAA63872.1; JOINED.
 EMBL: X94159; CAA63872.1; JOINED.
 EMBL: X94160; CAA63872.1; JOINED.
 EMBL: X94161; CAA63872.1; JOINED.
 EMBL: X98519; CAA67144.1; -
 EMBL: 069491; AAC53114.1; -
 MGD: MGI:109123; IL11RA2.
 PFM: PFM0041; fn3; 2.
 PFM: PFM0047; lg; 1.
 W Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 T SIGNAL 1 23
 T CHAIN 1 23
 T DOMAIN 24 432
 T TRANSMEM 367 393
 T DOMAIN 368 432
 T DOMAIN 394 432
 T DOMAIN 41 102
 T CARBOHYD 127 127
 T CARBOHYD 194 194
 T CONFLICT 200 200
 T CONFLICT 384 384
 Q SEQUENCE 432 AA: 46721 MW: C4FD7DEC CRC32;

QY 7 GPVQASARRPPRLSSLSKSPILLCLVLPVPGSGAHTAVISPODPTILLIGSSLOATCSIH 66
 Db 31 GPPEVOYGOPGR-----PYMLCCPGVSAG----- 55
 QY 67 GDTFGATAEGLYTLNGLRRLPSELRLN--TSTLA--LALANLNGSRQSGDNLVCHAR 122
 Db 55 --TF-----VSRDD--SRLLOGPSGLGRVLAQVDSDE--GRYVQTL 97
 QY 123 DGIILAGSCLYVGLPPEKPPNISCSNRMDLCRTWPGAHGETFLHTNYSKTKLWYG 182
 Db 98 DGVSQGVTLKGLPPARP--EVSCQAVDYENFSGTWSPG--VSGLTRILTSYRKTLP 154
 QY 183 QDNTCEETHVGPESHCHIPD-----LALFTPEIWEATNRLGARSADVLTLD 231
 Db 155 GAEQRESPESTGPPFC--PODPLEASRCVHGAEFSEYRINVTENVSLG--ASTCLLDVR 211
 QY 232 VLQVYTTDPDPDVHVSNGLELOLSVRYSPFALK--DFLQAKYQIRYREDSDYDK 288
 Db 212 LQSLIRDPDPOGLVESVPPYPRLLHNSWTYPASWRQPHLL--KRLQYRPAOHFAMS 269
 QY 289 VVDVSNQ--TSCRLAGLKGTYFYVQVRCNPFGIYSKKGAGINSESHPTASTP--- 343
 Db 270 TVEPIGLEEYITDTVAGLP---HAYVSAEDF-----LDAGTWSAMS--PEAWGTPTSTGL 319
 QY 343 -RSERP---GPGGVCCEPRGSGPSSGPPVRELEK 371
 Db 320 LQDEIPDWSQHGQOLEAVVAQEDSLAPAPPSIQ 353

Search completed: September 16, 1999, 20:40:05
 Job time: 5556 sec

Query Match 8.7%; Score 201; DB 11; Length 432;
 Best Local Similarity 24.6%; Pred. No. 6,9e-10;
 Matches 97; Conservative 49; Mismatches 148; Indels 100; Gaps 20;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:13; Search time 64.1 Seconds

(without alignments)
57.275 Million cell updates/sec

Title: US-09-037-657-17

Perfect score: 864

Sequence: 1 GIVYFVQVRCNPFQIGYSKR.....RTSGCRADGVREVRGSG 155

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	864	100.0	155	1 W55013	Novel haemopoietin
2	631.5	73.1	350	1 W55015	Amino acid sequenc
3	631.5	73.1	389	1 W70846	Human zcytores vari
4	631.5	73.1	389	1 W70847	Human zcytores vari
5	631.5	73.1	389	1 W70848	Human zcytores vari
6	631.5	73.1	389	1 W70849	Human zcytores vari
7	631.5	73.1	389	1 W70850	Human zcytores vari
8	631.5	73.1	389	1 W70851	Human zcytores vari
9	631.5	73.1	389	1 W70852	Human zcytores vari
10	631.5	73.1	389	1 W70853	Human zcytores vari
11	631.5	73.1	392	1 W70840	Human zcytores vari
12	631.5	73.1	389	1 W70844	Human zcytores vari
13	631.5	73.1	425	1 W55011	Novel haemopoietin
14	577	66.8	413	1 W55012	Novel haemopoietin
15	573	66.3	425	1 W55012	Novel haemopoietin
16	573	66.3	425	1 W55012	Novel haemopoietin
17	573	66.3	385	1 W55804	Nucleotide sequenc
18	573	66.3	425	1 W70841	Human zcytores vari
19	569	65.9	408	1 W70862	Rat zcytores protel
20	569	65.9	388	1 W70839	Amino acid sequenc
21	569	65.9	385	1 W70842	Human zcytores vari
22	569	65.9	422	1 W70860	Human zcytores vari
23	209	24.2	303	1 W70843	Human zcytores vari
24	209	24.2	303	1 W70845	Human zcytores vari
25	166	19.2	31	1 W70858	Human zcytores vari
26	121	14.0	278	1 W55014	Human zcytores vari
27	84	9.7	2237	1 R33550	Sequence of the al
28	78.5	9.1	500	1 R33550	Sequence of the al
29	78	9.0	1931	1 W36847	Human fusion polyp
30	78	9.0	2339	1 R27649	Human calcium chan
31	78	9.0	2339	1 R33549	Sequence of the al
32	78	9.0	2337	1 R71005	Human neuronal cal
33	78	9.0	2337	1 R71006	Human neuronal cal
34	78	9.0	434	1 R66420	Peptide fragment o
35	78	9.0	2337	1 W37878	Human calcium chan
36	78	9.0	2337	1 W63141	Human calcium chan
37	75	8.7	2237	1 P93284	Sequence of clone
38	74	8.6	267	1 W56293	Babesia microti BM
39	73.5	8.5	712	1 R07094	Protein having imm
40	73.5	8.5	240	1 R22597	Foetal oncogene pe
41	72.5	8.4	211	1 R24273	Truncated human pr
42	72.5	8.4	630	1 R93120	Tilapia prolactin
43	72.5	8.4	606	1 R93121	Tilapia prolactin

ALIGNMENTS

44	72	8.3	525	1 W36846	Human fusion polyp
45	72	8.3	304	1 W2155	Human endonuclease
RESULT 1					
W55013	1				
W55013	standard; Protein; 155 AA.				
AC	W55013				
DT	29-SEP-1998 (first entry)				
DE	Novel haemopoietin receptor NR6.3 protein.				
KW	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;				
KW	cell survival; therapeutic; neuronal proliferation; drug screening;				
KW	Mouse.				
OS	Mus sp.				
PN	W09811225-A2.				
PD	19-MAR-1998.				
PF	11-SEP-1997; G02479.				
PR	11-SEP-1996; AU-002246.				
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.				
PA	(DIE/) DIELEWSKA H E.				
PI	Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,				
PI	Kojima T, Maeda M, Nash A, Nicola NA, Nakar S, Willison T,				
PI	Zhang J.				
DR	WPI: 98-260970/23.				
DR	N-PSDE: V27142.				
PT	New isolated haemopoietin receptor - used for developing products				
PT	for modulating proliferation, differentiation and survival of cells,				
PT	e.g. neuronal cells				
PS	Claim 16; Page 90-92; 182pp; English.				
CC	The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6.				
CC	Interaction between the novel HR and a ligand facilitates proliferation,				
CC	differentiation and survival of a wide variety of cells. The HR and its				
CC	derivatives can be used for modulating the activity of the receptors e.g.				
CC	to regulate development, maintenance or regeneration in an array of				
CC	different cells and tissues in vitro and in vivo. They can be present in				
CC	therapeutics used for modulating neuronal proliferation, differentiation				
CC	and survival. The products can also be used for detection and diagnosis,				
CC	e.g. for cancers or predisposition to cancers, or for drug screening.				
SQ	Sequence 155 AA.				
Query Match					
Best Local Similarity 100.0%; Score 864; DB 1; Length 155;					
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 GIVYFVQVRCNPFQIGYSKRKAGIWSMSHPTAASPPRSPGPGGVCPEPRGESSGPV 60				
DB	1 GIVYFVQVRCNPFQIGYSKRKAGIWSMSHPTAASPPRSPGPGGVCPEPRGESSGPV 60				
OY	61 RELKQFLGMLKKHAYCSLFRLDQWRAAMQXSHKTRNOYKLGACVGGAGEERD 120				
DB	61 RELKQFLGMLKKHAYCSLFRLDQWRAAMQXSHKTRNOYKLGACVGGAGEERD 120				
OY	121 PEOPOHRTLLSKHRTGSCPRADGVREVRGSG 155				
DB	121 PEOPOHRTLLSKHRTGSCPRADGVREVRGSG 155				
RESULT 2					
W55015					
ID	W55015 standard; Protein; 350 AA.				
AC	W55015				
DT	29-SEP-1998 (first entry)				
DE	Amino acid sequence of clone HFR-66 encoding human NR6.				
KW	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;				
KW	cell survival; therapeutic; neuronal proliferation; drug screening;				
KW	Human.				
OS	Homo sapiens.				
PN	W09811225-A2.				
PD	19-MAR-1998.				

PF 11-SEP-1997: G02479.
 PR (AMRA-) AMRAD OPERATIONS PVT LTD.
 PA (DZIE/) DZIEGLESKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR N-PSDB: V27144.
 PT New isolated haemopoietin receptor - used for developing products
 for modulating proliferation, differentiation and survival of cells,
 e.g. neuronal cells
 PS Claim 18: Page 102-104: 182pp; English.
 CC The NR6 protein is a novel haemopoietin receptor (HR). Interaction
 between the novel HR and a ligand facilitates proliferation.
 CC differentiation and survival of a wide variety of cells. The HR and its
 derivatives can be used for modulating the activity of the receptors e.g.
 to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 therapeutics used for modulating neuronal proliferation, differentiation
 and survival. The products can also be used for detection and diagnosis,
 e.g. for cancers or predisposition to cancers, or for drug screening.
 SO Sequence 350 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 350;
 Best Local Similarity 76.8%; Pred. No. 1.5e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 60
 DB 228 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 287
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGKAEERD 120
 DB 288 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNQ----- 329
 QY 121 PGEOPQHRTLSKHRTGSCPRADGVREV 151
 DB 329 -----HRTGSCPRADGVREV 345

RESULT 3
 W70846
 ID W70846 standard; Protein: 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human zcytores variant.
 KW zcytores; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytores ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: U08865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytores - useful for, e.g.
 PT down-regulating zcytores natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 89-90: 55pp; English.
 CC The present sequence represents a zcytores variant protein. zcytores
 is a cytokinin-like receptor. Soluble zcytores may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytores could be used to detect cardiostrophin-1 in the

CC blood, and to discover other possible zcytores ligands. A probe
 CC comprising zcytores DNA or RNA can be used to determine the presence
 CC and integrity of the zcytores gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytores and
 CC therapeutically to modify zcytores ligand effects.
 SO Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
 Best Local Similarity 76.8%; Pred. No. 1.5e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 60
 DB 267 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 326
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGKAEERD 120
 DB 327 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNQ----- 368
 QY 121 PGEOPQHRTLSKHRTGSCPRADGVREV 151
 DB 368 -----HRTGSCPRADGVREV 384

RESULT 4
 W70847
 ID W70847 standard; Protein: 389 AA.
 AC W70847;
 DT 17-MAR-1999 (first entry)
 DE Human zcytores variant.
 KW zcytores; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytores ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: U08865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytores - useful for, e.g.
 PT down-regulating zcytores natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 91-92: 55pp; English.
 CC The present sequence represents a zcytores variant protein. zcytores
 is a cytokinin-like receptor. Soluble zcytores may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytores could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcytores ligands. A probe
 CC comprising zcytores DNA or RNA can be used to determine the presence
 CC and integrity of the zcytores gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytores and
 CC therapeutically to modify zcytores ligand effects.
 SO Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
 Best Local Similarity 76.8%; Pred. No. 1.5e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 60
 DB 267 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGESSGPV 326
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGKAEERD 120

DB 327 RRELKQFLGMLKKHAYCNSLSPRLDQWRAMQKSHKTRNQ----- 368

OY 121 PGEOPPOHRTLLSKHRTGSCPRADGVREV 151

DB 368 -----HRTGSCPRADGARREV 384

RESULT 5

W70848 standard; Protein; 389 AA.

ID W70848;

AC W70848;

DT 17-MAR-1999 (first entry)

DE Human Zcyto5 variant.

KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;

KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;

OS Homo sapiens.

PN MO9849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

PI WPI: 99-034662/03.

PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.

PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1

PT in blood

PS Claim 1; Page 92-93; 55pp; English.

CC The present sequence represents a Zcyto5 variant protein. Zcyto5

CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to

CC down-regulate the effects of a growth and/or maintenance factor in

CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotoxin-1 on cardiac pathologies, so preventing heart

CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the

CC blood, and to discover other possible Zcyto5 ligands. A probe

CC comprising Zcyto5 DNA or RNA can be used to determine the presence

CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify Zcyto5 and the

CC therapeutically to modify Zcyto5 ligand effects.

CC Sequence 389 AA.

SO

Query Match 73.1%; Score 631.5; DB 1; Length 389;

Best Local Similarity 76.8%; Pred. No. 1.5e-58;

Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

OY 1 GTVYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPBGCGVCPRGEPSSGPV 60

DB 267 GTVYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPBGCGVCPRGEPSSGPV 326

OY 61 RRELKQFLGMLKKHAYCNSLSPRLDQWRAMQKSHKTRNQ----- 368

DB 327 RRELKQFLGMLKKHAYCNSLSPRLDQWRAMQKSHKTRNQ----- 368

OY 121 PGEOPPOHRTLLSKHRTGSCPRADGVREV 151

DB 368 -----HRTGSCPRADGARREV 384

RESULT 6

W70849 standard; Protein; 389 AA.

ID W70849;

AC W70849;

DT 17-MAR-1999 (first entry)

DE Human Zcyto5 variant.

KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;

KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;

KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.

OS Homo sapiens.

PN MO9849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

PI WPI: 99-034662/03.

PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.

PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1

PT in blood

PS Claim 1; Page 94-95; 55pp; English.

CC The present sequence represents a Zcyto5 variant protein. Zcyto5

CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to

CC down-regulate the effects of a growth and/or maintenance factor in

CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotoxin-1 on cardiac pathologies, so preventing heart

CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the

CC blood, and to discover other possible Zcyto5 ligands. A probe

CC comprising Zcyto5 DNA or RNA can be used to determine the presence

CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify Zcyto5 and

CC therapeutically to modify Zcyto5 ligand effects.

CC Sequence 389 AA.

SO

Query Match 73.1%; Score 631.5; DB 1; Length 389;

Best Local Similarity 76.8%; Pred. No. 1.5e-58;

Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

OY 1 GTVYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPBGCGVCPRGEPSSGPV 60

DB 267 GTVYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPBGCGVCPRGEPSSGPV 326

OY 61 RRELKQFLGMLKKHAYCNSLSPRLDQWRAMQKSHKTRNQ----- 368

DB 327 RRELKQFLGMLKKHAYCNSLSPRLDQWRAMQKSHKTRNQ----- 368

OY 121 PGEOPPOHRTLLSKHRTGSCPRADGVREV 151

DB 368 -----HRTGSCPRADGARREV 384

RESULT 7

W70850 standard; Protein; 389 AA.

ID W70850;

AC W70850;

DT 17-MAR-1999 (first entry)

DE Human Zcyto5 variant.

KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;

KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;

KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.

OS Homo sapiens.

PN MO9849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

PI WPI: 99-034662/03.

PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.

PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1

PT in blood

PS Claim 1; Page 95-96; 55pp; English.

CC The present sequence represents a Zcyto5 variant protein. Zcyto5

CC is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 60
DB 267 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 368
QY 121 PGEQPOHRTLKSHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 8

ID W70851 standard; Protein: 389 AA.

AC W70851; 17-MAR-1999 (first entry)
DE Human Zcytors variant.
KW Zcytors; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytors ligand; variant.
OS Homo sapiens.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
PI WPI; 99-034662/03.
PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g. down-regulating Zcytors natural ligands or detecting cardiotrophin-1 in blood
PS Claim 1; Page 96-97; 55pp; English.
CC The present sequence represents a Zcytors variant protein. Zcytors is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 60
DB 267 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 368
QY 121 PGEQPOHRTLKSHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 9

ID W70852 standard; Protein: 389 AA.

AC W70852; 17-MAR-1999 (first entry)
DE Human Zcytors variant.
KW Zcytors; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytors ligand; variant.
OS Homo sapiens.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
PI WPI; 99-034662/03.
PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g. down-regulating Zcytors natural ligands or detecting cardiotrophin-1 in blood
PS Claim 1; Page 98-99; 55pp; English.
CC The present sequence represents a Zcytors variant protein. Zcytors is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 60
DB 267 GTTFFVQVRCNPFGIYSGKAGIWSHPTASTPRSERPGGVCPEGPSSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGACVGGAGEERD 368
QY 121 PGEQPOHRTLKSHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 10

ID W70853 standard; Protein: 389 AA.

Accession	Result	11
W70840	standard; Protein; 392 AA.	
W70840.		
AC		
DD1	17-MAR-1999 (first entry)	
DE	Human Zcytors variant.	
DDX	Zcytors; cytokinin-like receptor; down-regulation; growth factor	
DDX	maintenance factor; thyroid; heart; skeletal muscle; cardiotor	
DDX	cardiac pathology; heart enlargement; Zcytors ligand; variant	
DDX	Homologs.	
DDX	W09849307.A1.	
DDX	05-NOV-1998.	
DDX	01-MAY-1998; U08865.	
DDX	13-FEB-1998; US-074721.	
DDX	01-MAY-1997; US-045287.	
DDX	01-MAY-1997; US-850030.	
DDX	13-FEB-1998; US-023890.	
DDX	(ZYMO) ZYMOGENETICS INC.	
DDX	Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,	
DDX	Lok S, Presnell SR, Whitmore TE;	
DDX	WPI; 99-034662/03.	

RESULT 12
 W70844 standard; Protein; 389 AA.
 W70844; 17-MAR-1999 (first entry)
 Human Zcytor5 variant.
 Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
 Homo sapiens.
 MO9849307-A1.
 05-NOV-1998.
 01-MAY-1998; 008665.
 13-FEB-1998; US-074721.
 01-MAY-1997; US-045287.
 01-MAY-1997; US-850030.
 13-FEB-1998; US-023890.
 (ZIMO) ZYMOGENETICS INC.
 Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 Lok S, Presnell SR, Whitmore TE,
 WPI; 99-034662/03.
 New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 in blood
 Claim 1; Page 87-88; 55pp; English.
 The present sequence represents a Zcytor5 variant protein. Zcytor5
 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 down-regulate the effects of a growth and/or maintenance factor in
 thyroid, heart, and skeletal muscle for example to lessen the effect
 of cardiostrophin-1 on cardiac pathologies, so preventing heart
 enlargement. To discover other possible Zcytor5 ligands. A probe
 blood, and to discover could be used to detect cardiostrophin-1 in the
 and compensing Zcytor5 DNA or RNA can be used to determine the presence
 and integrity of the Zcytor5 gene on chromosome 19. Antibodies and thyr
 anti-Idiotypic antibody could be used to purify Zcytor5 and thyr
 therapeutically to modify Zcytor5 ligand effects.
 Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. No. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 267 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 326
QY 61 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOVKLGACVGGAGAEEND 120
DB 327 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOVKLGACVGGAGAEEND 368
QY 121 PGQPPQHTLSKHKTRSCPRADGVREV 151
DB 368 -----HRTGSCPRADGVREV 384

RESULT 13
W70861
ID W70861 standard; Protein: 425 AA.
AC W70861;
DT 17-MAR-1999 (first entry)
DE Allelic variant of human zcytors.
KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
OS cardiac pathology; heart enlargement; zcytors ligand; allelic variant.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Velmerberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI: 99-034662/03.
DR N-PSDB: V70895.
PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.,
PT down-regulating zcytors natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 71-72; 55pp; English.
CC The present sequence represents an allelic variant of protein designated
CC zcytors, which is a cytokinin-like receptor. Soluble zcytors may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcytors could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcytors ligands. A probe
CC comprising zcytors DNA or RNA can be used to determine the presence
CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytors and
CC therapeutically to modify zcytors ligand effects.
SQ Sequence 425 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 425;
Best Local Similarity 76.8%; Pred. No. 1.6e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 303 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 362
QY 61 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOVKLGACVGGAGAEEND 120
DB 363 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOVKLGACVGGAGAEEND 404
QY 121 PGQPPQHTLSKHKTRSCPRADGVREV 151
DB 404 -----HRTGSCPRADGVREV 420

RESULT 14

W55011
ID W55011 standard; Protein: 413 AA.

AC W55011;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
OS Mouse.
PN Mus SP.
PD W09811225-A2.
PF 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Raker S, Willson T,
PI Zhang J;
DR WPI: 98-260970/23.
DR N-PSDB: V27140.

PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PS e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 66.8%; Score 577; DB 1; Length 413;
Best Local Similarity 100.0%; Pred. No. 8.2e-53;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 307 GTVYFVQVNCNPGIGYSGKAGIWMSESHPTASTPSPRSPGGGVCCEPRGEPSSGPV 366
QY 61 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOV 102
DB 367 RRELKQFLGWLKHAHCNSLSPFLYDQWRAMQKSHKTRNOV 408

RESULT 15

W55012
ID W55012 standard; Protein: 425 AA.

AC W55012;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
OS Mouse.
PN Mus SP.
PD W09811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Raker S, Willson T,
PI Zhang J;
DR WPI: 98-260970/23.
DR N-PSDB: V27141.

PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PS e.g. neuronal cells
 PS Claim 15; Page 84-87; 182pp; English.
 CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 425 AA;

Query Match 66.3%; Score 573; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 2.2e-52;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTVYFVQVRCNPFQIGSKKAGIMSEWHPPTAASPRSPRPGGVCCEPRGSSGPV 60
 DB 307 GTVYFVQVRCNPFQIGSKKAGIMSEWHPPTAASPRSPRPGGVCCEPRGSSGPV 366
 QY 61 RRELKQFLGWLKHAHCNSLSEFLYDQWRAMQKSHKTRNQ 101
 DB 367 RRELKQFLGWLKHAHCNSLSEFLYDQWRAMQKSHKTRNQ 407

Search completed: September 17, 1999, 03:08:14
 Job time: 305 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:07 ; Search time 53.94 Seconds
(without alignments)
28.357 Million cell updates/sec

Title: US-09-037-657-17

Perfect score: 864
Sequence: 1 GVTYFQVQVNCNPGIYGSK.....RTGSCPRADVREVRS 155

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database:

Issued_Patents_AA.*
1: /cgn2.6/prodata/2/laa/5A.COMB.pep.*
2: /cgn2.6/prodata/2/laa/5B.COMB.pep.*
3: /cgn2.6/prodata/2/laa/PCTUS9.COMB.pep.*
4: /cgn2.6/prodata/2/laa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	9.8	501	2	US-08-660-963-13	Sequence 13, Appl
2	78	9.0	434	1	US-08-337-602-3	Sequence 3, Appl1
3	78	9.0	2339	2	US-08-455-543A-47	Sequence 47, Appl
4	78	9.0	2237	2	US-08-455-543A-48	Sequence 48, Appl
5	78	9.0	2239	2	US-08-223-305C-47	Sequence 47, Appl
6	78	9.0	2237	2	US-08-223-305C-48	Sequence 48, Appl
7	72.5	8.4	245	2	US-08-438-439C-17	Sequence 17, Appl
8	72	8.3	304	2	US-08-808-550-2	Sequence 2, Appl1
9	71	8.2	297	2	US-08-808-550-42	Sequence 42, Appl
10	70.5	8.2	1339	1	US-08-026-138E-3	Sequence 3, Appl1
11	68.5	7.9	709	1	US-07-814-964-7	Sequence 7, Appl1
12	68.5	7.9	1754	1	US-07-745-206A-13	Sequence 13, Appl1
13	68.5	7.9	709	1	US-08-258-442-7	Sequence 7, Appl1
14	68.5	7.9	709	1	US-08-328-809-2	Sequence 2, Appl1
15	68.5	7.9	1754	2	US-08-311-363-13	Sequence 13, Appl1
16	68.5	7.9	709	3	PCT-US92-11107-7	Sequence 7, Appl1
17	68.5	7.9	224	2	PCT-US95-04971-10	Sequence 10, Appl1
18	68	7.9	623	2	US-08-653-740-7	Sequence 7, Appl1
19	67.5	7.8	372	1	US-07-865-878A-4	Sequence 4, Appl1
20	67.5	7.8	372	1	US-07-676-647-2	Sequence 2, Appl1
21	67.5	7.8	372	1	US-08-449-329-2	Sequence 2, Appl1
22	67.5	7.8	245	1	US-08-439-725A-11	Sequence 11, Appl1
23	67.5	7.8	183	2	US-08-441-629-15	Sequence 15, Appl1
24	67.5	7.8	232	2	US-08-485-721-2	Sequence 2, Appl1
25	67.5	7.8	232	2	US-08-392-935-2	Sequence 2, Appl1
26	67.5	7.8	372	2	US-08-445-073-2	Sequence 2, Appl1
27	67.5	7.8	245	2	US-08-867-471-11	Sequence 11, Appl1
28	67.5	7.8	245	2	US-08-438-439C-7	Sequence 7, Appl1
29	67.5	7.8	372	3	PCT-US91-03896-2	Sequence 2, Appl1
30	67.5	7.8	232	3	PCT-US93-08326-2	Sequence 2, Appl1
31	67.5	7.8	183	3	PCT-US95-09172-15	Sequence 15, Appl1
32	67	7.8	655	1	US-08-148-910-12	Sequence 12, Appl1
33	67	7.8	655	1	US-08-448-937A-12	Sequence 12, Appl1
34	67	7.8	467	2	US-08-727-548-2	Sequence 2, Appl1
35	66.5	7.7	1001	1	US-07-797-556-6	Sequence 6, Appl1
36	66.5	7.7	1001	1	US-07-943-843-2	Sequence 2, Appl1
37	66.5	7.7	1097	1	US-07-943-843-6	Sequence 6, Appl1
38	66.5	7.7	635	1	US-08-184-327A-4	Sequence 4, Appl1
39	66.5	7.7	1001	2	US-08-347-003-2	Sequence 2, Appl1

40	66.5	7.7	1097	2	US-08-347-003-6	Sequence 6, Appl1
41	66.5	7.7	620	2	US-08-419-652-7	Sequence 7, Appl1
42	66.5	7.7	126	2	US-08-822-262-1	Sequence 1, Appl1
43	66.5	7.7	635	3	PCT-US95-00670-4	Sequence 4, Appl1
44	66	7.6	668	1	US-08-205-018-2	Sequence 2, Appl1
45	66	7.6	859	1	US-08-395-580-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-08-660-963-13
Sequence 13, Application US/08660963

Patent No. 5852187
GENERAL INFORMATION:

APPLICANT: Thorne, Michael O.
APPLICANT: Gaylin, Bruce D.

APPLICANT: Horikawa, Reiko
APPLICANT: Lyons Jr., Charles E.

TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: POPHAM, HARK, SCHNOBICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450

STREET: G. Street
CITY: Washington

STATE: D.C.
COUNTRY: USA

ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,963

FILING DATE: 12-JUN-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: O'Shaughnessy, Brian P.

REGISTRATION NUMBER: 32,747
REFERENCE/DOCKET NUMBER: 18046, 036

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-824-8000

TELEFAX: 202-824-8199
TELEX: 248516

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 501 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-660-963-13

Query Match
Best Local Similarity 26.0%; Pred. No. 0.2;

Matches 38; Conservative 13; Mismatches 47; Indels 48; Gaps 8;

29 HP---TAATPREFRPPG-----GGVCEPRGSPSS---GPVRELKQFLGMLK 74

DB 194 HPRSGEALPLPOLHHPVNHILXPGGSCVPEGRHPLSPGHEHPLQ-----LHCPVQ 247

QY 75 AYCNSIFLLIQWRAWAKS-----HRTNQVGR--GEACVGGKAEER-----120

DB 248 GFCDRLSFDHQLAAGRSQVPLPLSLHIAQHREGLVAVGSRGLASLHQRVGL 307

QY 120 -----DPGPPQPHHTLSK 136

DB 308 QVGLRCVILGPRQLP-----LLVDHQ 329

RESULT 2
US-08-337-602-3
Sequence 3, Application US/08337602
Patent No. 5623051
GENERAL INFORMATION:
APPLICANT: Catterall, William A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: FOR PRESYNAPTIC CALCIUM CHANNEL BLOCKERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98042-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,602
FILING DATE: 10-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010, 602
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-337-602-3

Query Match 9.0%; Score 78; DB 1; Length 434;
Best Local Similarity 23.2%; Pred. No. 0.92;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPRGSPSSGPVRRLEKQFLGWLKHAHCSNLS 81
DB 182 SHKEAAGPEPARSERGSGRGGRRHHRGSPPEAAREP-----RRH----- 227
QY 82 FLYLDQWAMWOKSHKTRNOVGKLGACVGGK-----AEEERDPCEOPPOHR 129
DB 227 -----RAHRHQP-----SKECAGANGERARRHGRGPRAGPRAEAGEEPAR-- 269
QY 130 TLISKRTGSC-PRADGVRR 150
DB 269 ---RHRARRKQAPAEAVEKE 286

RESULT 3
US-08-455-543A-47
Sequence 47, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-47

Query Match 9.0%; Score 78; DB 2; Length 2339;
Best Local Similarity 23.2%; Pred. No. 7.2;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPRGSPSSGPVRRLEKQFLGWLKHAHCSNLS 81
DB 891 SHKEAAGPEPARSERGSGRGGRRHHRGSPPEAAREP-----RRH----- 936
QY 82 FLYLDQWAMWOKSHKTRNOVGKLGACVGGK-----AEEERDPCEOPPOHR 129
DB 936 -----RAHRHQP-----SKECAGANGERARRHGRGPRAGPRAEAGEEPAR-- 978
QY 130 TLISKRTGSC-PRADGVRR 150

Db 978 ----RHRARHKAQPAHEAVEKE 995

RESULT 4

US-08-455-543A-48
Sequence 48, Application US/08455543A
Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

US-08-455-543A-48

Query Match 9.0%; Score 78; DB 2; Length 2237;
Best Local Similarity 23.2%; Pred. No. 6.8;
Matches 33; Conservative 15; Mismatches 39; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSEF---PQGGGYCEPGEPSGYPVRELKQFLGWLKRAYCSNLS 81

DB 891 SSKENAGPEPSESRGPGGEGRRHRRGSPERAEAREP-----RRH----- 936

QY 82 FLYDQWRAMWOKSHRTNRQVGLGACVCGSG-----AEEPRDGEQPPQHR 129

DB 936 -----RAHRHDP-----STECAGAGERRARRRGGRAGPRAESEDEPAR-- 978

QY 130 TILSKHRTGSC-PRADGVRR 150
DB 978 ----RHRARHKAQPAHEAVEKE 995

RESULT 5

US-08-223-305C-47
Sequence 47, Application US/08223305C
Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2339 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-223-305C-47

Query Match 9.0%; Score 78; DB 2; Length 2339;
 Best Local Similarity 23.2%; Pred. No. 7.2;
 Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSEK---PGPGGVCPEPGSGPVRRELKQFLGMLKKAHCNLS 81
 DB 891 SHSEKAGPPEARSERGRGPGGRRHHRGSPFEAAERP-----RRH----- 936
 QY 82 FRLYDQRAWMOKSHKTRNOVGKIGACVCGKG-----AAEERDPGEOPQHR 129
 DB 936 -----RAHRHQDP-----SKECAGAKGERARHRGPRAGPREASEGSEPAR-- 978
 QY 130 TLSKHRTGSC-PRADGVARE 150
 DB 978 ----RRARRKQAPAEHAEVEKE 995

RESULT 6
 US-08-223-305C-48
 Sequence 48, Application US/08223305C
 Patent No. 5851824
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSO Version 1.5
 CURRENT APPLICATION DATA:
 FILING DATE: April 4, 1994
 APPLICATION NUMBER: US/08/223,305C
 PRIOR APPLICATION DATA:
 FILING DATE: April 10, 1992
 APPLICATION NUMBER: 07/868,354
 PRIOR APPLICATION DATA:
 FILING DATE: 15-AUG-1991
 APPLICATION NUMBER: US 07/745,206
 PRIOR APPLICATION DATA:
 FILING DATE: 30-NOV-1990
 APPLICATION NUMBER: US 07/620,250
 PRIOR APPLICATION DATA: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 52516 (P519739)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2237 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-223-305C-48

Query Match 9.0%; Score 78; DB 2; Length 2237;
 Best Local Similarity 23.2%; Pred. No. 6.8;
 Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSEK---PGPGGVCPEPGSGPVRRELKQFLGMLKKAHCNLS 81
 DB 891 SHSEKAGPPEARSERGRGPGGRRHHRGSPFEAAERP-----RRH----- 936
 QY 82 FRLYDQRAWMOKSHKTRNOVGKIGACVCGKG-----AAEERDPGEOPQHR 129
 DB 936 -----RAHRHQDP-----SKECAGAKGERARHRGPRAGPREASEGSEPAR-- 978
 QY 130 TLSKHRTGSC-PRADGVARE 150
 DB 978 ----RRARRKQAPAEHAEVEKE 995

RESULT 7
 US-08-438-439C-17
 Sequence 17, Application US/08438439C
 Patent No. 5876967
 GENERAL INFORMATION:
 APPLICANT: Nathans, Jeremy
 APPLICANT: Macke, Jennifer P.
 TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent' Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: May 12, 1995
 APPLICATION NUMBER: US/08/438,439C
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Haller, Lisa A.
 REGISTRATION NUMBER: 38,347

DB 4 RRSISGPGAG---PRGCEEEEPGLRR-----EAAAEAKSH 37
QY 97 KTRNOVGKIGACVGGKGAEEERDGPQP 125
DB 38 SPVKPRRAQRLRVAEEGSDSEKGEAGP 66

RESULT 10
US-08-026-138E-3
; Sequence 3, Application US/08026138E
; Patent No. 5502166
; GENERAL INFORMATION:
; APPLICANT: Masayoshi MISHINA
; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nishiohata Residence 1-107
; STREET: 5214, Nishiohata-machi
; CITY: Niigata-shi
; STATE: Niigata-ken
; COUNTRY: JAPAN
; ZIP: 951
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS v.5
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026/138E
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 39563/1992
; FILING DATE: 26-FEB-1992
; APPLICATION NUMBER: JP 173155/1992
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: JP 215017/1992
; FILING DATE: 12-AUG-1992
; APPLICATION NUMBER: JP 303878/1992
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamburg, C. Bruce
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-4551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-2340
; TELEFAX: (212) 953-7733
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: mouse
; TISSUE TYPE: brain
; PUBLICATION INFORMATION:
; AUTHORS: Masayoshi MISHINA
; TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
; US-08-026-138E-3

Query Match 8 2%; Score 70.5; DB 1; Length 1239;

Best Local Similarity 26.1%; Pred. No. 21;
Matches 35; Conservative 10; Mismatches 42; Indels 47; Gaps 7;

QY 30 PTAATPSEPRPSPGCGVPEPRGEPSSG---PVREELKQFLGLMKKAYCSNLSFRLXD 86
DB 932 PT-TSGPRSTCTPPGPQP-SFSGWRPFGGGRFTLAPRAP----- 969
QY 87 QWRAMQSKHTRNOVGKIGEAC-----VGGKGAEE---RDPEQPPQ-----HRTL 131

DB 969 -----QPARPGRQRLSTCPHAPGLGKGGCGESGIRNRTSRPPERRALPERSL 1022
QY 132 LSKHRTGSCPRAD 145
DB 1023 LHAHCYSSFPRAE 1036

RESULT 11
US-07-814-964-7
; Sequence 7, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey R.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pfl, Peter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellelt, Patl
; APPLICANT: Essigmann, John M.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Millia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,964
; FILING DATE: 19911226
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4/87AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human SSR (predicted)
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..496
; OTHER INFORMATION: /label= Acidic
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 512..534
; OTHER INFORMATION: /label= Basic I
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 539..614
; OTHER INFORMATION: /label= HMG-box
; FEATURE:
; NAME/KEY: Domain

LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-07-814-964-7

Query Match
Best Local Similarity 21.98; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGVCEPGEPSGPPVRELKOFGLW-----KKHAYCS--NLSFLYD 86
DB 529 RKSRRKP-----VEVKKGKDPNAP-KRPMAYMLNLSREKISDHPGISTDLSKRAE 563
QY 87 QNRA-----WMQSKHTRNQVGLGACVGGKGAEEERDPGEPPQHRLLSKHRT- 138
DB 584 IWGMSKEKKEEDRKADRDYERAMKEYEGGRGSSKRSKKKKYKVMKKSTP 643
QY 138 -RGSCDRA 144
DB 644 SRGSSSKS 651

RESULT 12
US-07-745-206A-13
Sequence 13, Application US/07745206A
Patent No. 5429921

GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McGue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-13

Query Match 7.98; Score 68.5; DB 1; Length 1754;
Best Local Similarity 22.08; Pred. No. 52;
Matches 33; Conservative 13; Mismatches 45; Indels 59; Gaps 6;

QY 30 PTASTRSERPPGGVCEPGEPSG--PYRELKOFGLKKHAYCSNLSFLYD 87
DB 816 PLVYELRGDAGRGVGGKAPAEAAPEGVDPPIRRHR----- 854
QY 88 WRAMQSKHTRNQVGLGE-----ACVGGKGAEEERDPGEQ-----PPQHRLL 131
DB 854 -----HRDKDTPAGQDRAEAPRAESGEPGAREERPRADRSKSKENAGPPPARTS 905

QY 132 LSKHR-----TRGSCPRADGVREVRGS 154
DB 906 AAQAQAPRAAGCTTGAPR-----RRRPSGS 931

RESULT 13
US-08-258-442-7
Sequence 7, Application US/08258442
Patent No. 5670621

GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Patrl
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,442
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human SSRP (predicted)

FEATURE:
NAME/KEY: Domain
LOCATION: 440..496
OTHER INFORMATION: /label- Acidic
NAME/KEY: Domain
LOCATION: 512..534
OTHER INFORMATION: /label- Basic I

FEATURE:
NAME/KEY: Domain
LOCATION: 539..614
OTHER INFORMATION: /label- HMG-box
FEATURE:
NAME/KEY: Domain
LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-08-258-442-7

Query Match
Best Local Similarity 21.9%; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGGVCPEPGEPSGVPRLKQFLGWL-----KKHAYCS--NLSEFLYD 86
DB 529 RSRKKRP---VEYKKCKDNPAP-KRPMASVYMLNLSREKIKSDHPGISITDLSKAGE 583
QY 87 QWRA-----WMQSKHTRNOVGKLGACVGGKGAEEERDPGEGPPQHRTILSKHRT- 138
DB 584 IMKGMSEKKEEMDRKADARRDYEKAMKEYEGGREGSSKRDSSKKKKVYKMEKSTP 643
QY 138 -RSCCPRA 144
DB 644 SRGSSSKS 651

RESULT 14
US-08-328-809-2
Sequence 2, Application US/08328809

GENERAL INFORMATION:
APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Peter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIR-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human SSRP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 440..496
OTHER INFORMATION: /label- Acidic
FEATURE:
NAME/KEY: Domain
LOCATION: 512..534
OTHER INFORMATION: /label- Basic I
FEATURE:
NAME/KEY: Domain
LOCATION: 539..614
OTHER INFORMATION: /label- HMG
FEATURE:
NAME/KEY: Domain
LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-08-328-809-2

Query Match
Best Local Similarity 21.9%; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGGVCPEPGEPSGVPRLKQFLGWL-----KKHAYCS--NLSEFLYD 86
DB 529 RSRKKRP---VEYKKCKDNPAP-KRPMASVYMLNLSREKIKSDHPGISITDLSKAGE 583
QY 87 QWRA-----WMQSKHTRNOVGKLGACVGGKGAEEERDPGEGPPQHRTILSKHRT- 138
DB 584 IMKGMSEKKEEMDRKADARRDYEKAMKEYEGGREGSSKRDSSKKKKVYKMEKSTP 643
QY 138 -RSCCPRA 144
DB 644 SRGSSSKS 651

RESULT 15
US-08-311-363-13
Sequence 13, Application US/08311363

GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McGue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/311,363
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-51506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1754 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-311-363-13

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Query Match 7.9%; Score 68.5; DB 2; Length 1754;
Best Local Similarity 22.0%; Pred. No. 52;
Matches 33; Conservative 13; Mismatches 45; Indels 59; Gaps 6;

QY 30 PTASTPRSEPRPGGVCCEPRGGEPSG--PVRELKQFLGWLKKAHYCSNLSFRLYDQ 87
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 816 PLVELGHDGARGVGGKARPEAAEAPGVDPPRRHR----- 854

QY 88 WRAWMOKSHKTRNOVGKLG-----ACVGGKGAEEERDQEQ-----PQHRTL 131
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 854 -----HRDKDTPAAGDDDRAPKAESGEGPAREERPPRADSHSKKAAGPPEARTS 905

QY 132 LSKHR-----TRGSCPRADGVRRREVNGS 154
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 906 AAFAQAPRAAGTGAAPR---RRRPSGS 931

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Search completed: September 16, 1999, 20:41:08
 Job time: 5437 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:07 ; Search time 49.27 Seconds

(without alignments)
126.043 Million cell updates/sec

Title: US-09-037-657-17
Perfect score: 864

Sequence: 1 GTVFVGVRCNPFQIGYSKK.....RTRGSCPRADGVRRVRSRG 155

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: 1: PIR60:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	10.9	416	2	homeotic protein H
2	92.5	10.7	533	2	59 protein, brain
3	84	9.7	577	2	cleavage stimulat
4	83	9.6	485	2	finger protein KZF
5	82.5	9.5	488	2	cellulase (EC 3.2.
6	80.5	9.3	816	2	hypothetical prote
7	78	9.0	1386	2	serine/threonine-s
8	78	9.0	2339	2	omega-conotoxin-se
9	78	9.0	1309	2	probable RNA-direc
10	78	9.0	593	2	B71323
11	77.5	9.0	174	1	BOIC1T
12	77.5	8.9	554	2	AS6730
13	76.5	8.9	1325	2	S16129
14	76	8.8	691	2	A25704
15	75	8.7	336	2	JC4102
16	74.5	8.6	990	2	T02309
17	74	8.6	303	2	S28147
18	74	8.6	756	2	T00367
19	73.5	8.5	712	2	A45638
20	73	8.4	3164	1	KMBEH6
21	72.5	8.4	444	2	D26421
22	72.5	8.4	2111	2	A70668
23	72.5	8.4	2110	2	B41110
24	72.5	8.4	725	2	JC1300
25	72.5	8.4	630	2	I51086
26	72	8.3	431	1	WJH26
27	72	8.3	433	2	S20963
28	72	8.3	1027	2	S28774
29	72	8.3	437	2	S04020
30	71.5	8.3	1537	2	JC4172
31	71.5	8.3	660	1	OCBE3
32	71.5	8.3	372	2	I58141
33	71.5	8.3	417	2	S47539
34	71.5	8.3	411	2	S31664
35	71	8.2	1106	2	J00405
36	71	8.2	1872	2	S36152
37	70.5	8.2	1870	2	S37671
38	70.5	8.2	411	2	PC2061
39	70.5	8.2	1522	2	T00028

40 70.5 8.2 984 2 T00326
41 70.5 8.2 705 2 A35363
42 70.5 8.2 668 2 B35363
43 70.5 8.2 581 2 I45971
44 70.5 8.2 706 2 E30411
45 70.5 8.2 670 2 F30411

hypothetical prote
synapsin I splice
synapsin Ib - huma
prolactin receptor
synapsin Ia - bovi
synapsin Ib - bovi

ALIGNMENTS

RESULT 1
S27198
homeotic protein Hox D3 - human
N/Alternative names: homeotic protein Hox 4A
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Sep-1997
C/Accession: S27198
R/Taniguchi, Y.; Fujii, A.; Moriyoshi, T.
Biochim. Biophys. Acta 1132, 332-334, 1992
A/Title: Cloning and sequencing of the human homeobox gene HOXA4.
A/Reference number: S27198; MUID:93041940
A/Accession: S27198
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-416 <TAN>
A/Cross-References: EMBL:D11117; NID:g219879; PID:d1002368; PID:g219880
C/Genetics:
A/Introns: 165/1
C/Superfamily: homeotic protein Hox B3; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:179-235/Domain: homeobox homology <HOX>

Query Match 10.9% Score 94; DB 2; Length 416;
Best Local Similarity 25.8%; Pred. No. 0.11;
Matches 31; Conservative 16; Mismatches 43; Indels 30; Gaps 4;

QY 17 GSKKAGIEMSHPTAATPRSERP---GPGGV--CEPRGERSGVRRELKQFLGM 70
DB 88 GSGPELNEQGPPOPPPPPTLPSCPTNPGGVPAKPKGPPAASSSATISQIFPM 147
QY 71 LKHAVCNLSFRLIDQWRAMQKSHKTRNOVGKLEACVGGKAEERDPGQPOHRT 130
DB 148 MKE-----SRNSKQKNSCATAGESC-----EDKSPPAKSRVRT 183

QY Hoxb-Luv

RESULT 2
A49364
59 protein, brain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Sep-1998
C/Accession: A49364
R/Shaw, D.J.; McCurrach, M.; Rundie, S.A.; Harley, H.G.; Crow, S.R.; Sohn, R.; Thirio
Genomics 18, 673-679, 1993
A/Title: Genomic organization and transcriptional units at the myotonic dystrophy loc
A/Reference number: A49364; MUID:94140369
A/Accession: A49364
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-533 <SHA>
A/Cross-References: GB:L19267; NID:g306711; PID:g306712

Query Match 10.7% Score 92.5; DB 2; Length 553;
Best Local Similarity 25.8%; Pred. No. 0.21;
Matches 34; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 30 PTAATPSSERPGP-----GGVCEPRGERSGSP-VARE-----LKQFLGWLK 73
DB 349 PPAASSSGGEPGPPLRLSRNSLPHPAGGKAGAGPVAALGCTFTSGRF----- 403
QY 74 HAYCNSLFRLLDQWRAMQKSHKTRNOVGKLEACVGGKAEERDPGQPOHRTLLS 133

Db 403 -----ATLQERDRGAKEKRYHSIGNISRGSGSGSGGEGEPSPV---RSRD 453
 QY 134 KHRTRGS--CPR 143
 Db 454 PAKVLGTALCPR 465

RESULT 3

AA0220

cleavage stimulation factor 64k chain - human
 N/Alternate names: 64k polyadenylation factor

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Sep-1998

C/Accession: AA0220

R/Takagaki, Y.; MacDonald, C.C.; Shenk, T.; Manley, J.L.

Proc. Natl. Acad. Sci. U.S.A. 89, 1403-1407, 1992

A/Title: The human 64-kDa polyadenylation factor contains a ribonucleoprotein-type RNA

A/Reference number: AA0220; MUID: 92159058

A/Accession: AA0220

A/Molecule type: mRNA

A/Residues: 1-577 <TAK>

A/Cross-references: GB:M85085; NID:9181138; PID:9181139

A/Note: Sequence extracted from NCBI Backbone (NCBIN:82408, NCBI:82414)

C/Genetics:

A/Genes: GDB:CTF2

A/Cross-references: GDB:137080; OMIM:600368

A/Map position: 21q22.3-21q22.3

C/Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

C/Keywords: heterotrimer; phosphoprotein; RNA binding

F/17-84/Domain: ribonucleoprotein repeat homology <RMA>

F/414-464/Region: 5-residue repeats (M-E-A-R-A/G)

Query Match 9.7%; Score 84; DB 2; Length 577;

Best Local Similarity 27.2%; Pred. No. 1.4;

Matches 41; Conservative 15; Mismatches 55; Indels 40; Gaps 8;

QY 18 SKKAGIMSEMSHPTAATSRSEPRGCGVCEPRGEGSPGVRRELKQFLGMLKKHAYC 77
 Db 249 SMGGVPAAGCMRAVATGCGPSLAPGGM-OAQMGPSSGVSHEKRG----- 297
 QY 78 SNLSFRLYDQWRAMQKSHKTRN---QVGLGEA-----CVGKGKLEER---DPG 122
 Db 297 ---VPMQDP-RAAMQRGSLPANVPFRGLGDAPNDPRGTLTAVTGEVERGTLGPRH 351
 QY 123 EDPQGHRTLSKTRTSGCPRADGVAREYRG 153
 Db 352 QGPPMH--VPGHESKGRPP-----HELRG 374

RESULT 4

AA0751

finger protein MZF1 - human

C/Species: Homo sapiens (man)

C/Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 24-Sep-1998

C/Accession: AA0751

R/Hromas, R.; Collins, S.J.; Hlckstein, D.; Raskind, W.; Deaven, L.L.; O'Hara, P.; Hager

J. Biol. Chem. 266, 14183-14187, 1991

A/Title: A retinoid acid-responsive human zinc finger gene, MZF-1, preferentially expres

A/Reference number: AA0751; MUID: 91317761

A/Accession: AA0751

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-485 <HRO>

A/Cross-references: GB:M58297; NID:9189043; PID:9189044

C/Genetics:

A/Genes: GDB:ZNF42; MZF-1

A/Cross-references: GDB:125898; OMIM:194550

A/Map position: 19q13.2-19q13.4

C/Keywords: DNA binding; transcription regulation; zinc finger

Query Match 9.6%; Score 83; DB 2; Length 485;
 Best Local Similarity 27.9%; Pred. No. 1.5;
 Matches 43; Conservative 8; Mismatches 63; Indels 40; Gaps 8;

QY 17 GSKKAGIMSEMSHPTAATSRSEPRGCGVCEPRGEGSPGVRRELKQFLGMLKKHA 75
 Db 76 GVGPALITTRMSRGRS---NGRSTGCGV--RGACDVGCKVFSQRSNLTNRKXHT 130
 QY 76 -----YCSNLSFRLYDQWRAMQKSHKTRNOV-----GRIGACVGGKGAEEER- 120
 Db 131 GERPVCSGCG-----RSFSRSSHLRHQITHTERPFVCGDCGCFVSARLEHRR 183
 QY 120 -DPGEP-----POHRTLSKTRTSCRP 142
 Db 184 VHTGQPFRCACGCGSFQSRNLTQHORIHGDP 217

RESULT 5

A25156

cellulase (EC 3.2.1.4) 1 - Bacillus sp.

N/Alternate names: endo-1,4-beta-glucanase

C/Species: Bacillus sp.

C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Mar-1998

C/Accession: A25156

R/Fukumori, F.; Sashihara, N.; Kudo, T.; Horikoshi, K.

J. Bacteriol. 168, 479-485, 1986

A/Title: Nucleotide sequences of two cellulase genes from alkalophilic Bacillus sp.

A/Reference number: A91825; MUID: 87056924

A/Accession: A25156

A/Molecule type: DNA

A/Residues: 1-488 <FRK>

A/Cross-references: GB:M44781; GB:X53449; NID:9142659; PID:9142660

A/Experimental source: strain N-4, plasmid pNK1

C/Function:

A/Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such a

A/Pathway: cellulose degradation

C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 9.5%; Score 82.5; DB 2; Length 488;
 Best Local Similarity 22.8%; Pred. No. 1.7;
 Matches 34; Conservative 14; Mismatches 50; Indels 51; Gaps 7;

QY 24 MSEMS-----HPT-----AATPRSEPRGCGV 47
 Db 283 WANMSLTKDESSAALMPGANPTGWTAEISPSGAFVREKIRISASIPSDPTPPS--- 340
 QY 48 CEPNGEPPSGPVARELKQFLGMLKKHAYCSNLSFRLYDQWR--WMQKSHKTRNOV-- 104
 Db 340 -DPDGEPTPTP-PSDGEIYAMPDNOIYTIETIYHNGQLMOKAKWWTQNOEPGANQIGPW 397

RESULT 6

S64439

hypothetical protein YGR130C - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein G6382

C/Species: Saccharomyces cerevisiae

C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 14-Nov-1997

R/van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talia, E.; Nawrocki, A.;

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64428

A/Accession: S64439

A/Molecule type: DNA

A/Residues: 1-816 <VAN>

A/Cross-references: EMBL:Z72915; NID:91323214; PID:e243523; PID:91323215; MFS:YGR13

A/Experimental source: strain S288C

C/Genetics:

A/Map position: 7R

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 17, 1999, 03:10:12 ; Search time 35.09 Seconds

(without alignments)
124.867 Million cell updates/sec

Title: US-09-037-657-17

Sequence: 1 GYVYFQVQVNCNPGITGSKK.....RTGSCPADGVREVRGSG 155

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	10.9	416	1	HXD3_HUMAN
2	92.5	10.7	553	1	DMR3_HUMAN
3	84	9.7	577	1	CST2_HUMAN
4	83	9.6	485	1	ZN42_HUMAN
5	82.5	9.5	488	1	GUNI_BAC54
6	81	9.4	1181	1	HAIR_RAT
7	80.5	9.3	816	1	YGA3_YEAST
8	79	9.1	1027	1	CARF_RTEPA
9	78	9.0	2339	1	CIC5_HUMAN
10	77.5	9.0	174	1	BAR1_CHITE
11	77	8.9	554	1	PEX2_PODAN
12	73	8.4	3164	1	TEGU_HSV11
13	72.5	8.4	725	1	GUNG_CLOCE
14	72.5	8.4	2110	1	MCAS_MYCBO
15	72.5	8.4	630	1	PRLR_ORENI
16	72.5	8.4	444	1	SHU4_ECOLI
17	72	8.3	431	1	HXB3_HUMAN
18	72	8.3	437	1	NBR3_STRCT
19	71.5	8.3	372	1	CNTR_RAT
20	71.5	8.3	417	1	HXD3_MOUSE
21	71.5	8.3	581	1	PRLR_CEREL
22	71.5	8.3	660	1	YHL1_EBV
23	71	8.2	1043	1	NNP1_HUMAN
24	70.5	8.2	461	1	CSH2_PARRR
25	70.5	8.2	2547	1	FAFX_MOUSE
26	70.5	8.2	2559	1	FAF_MOUSE
27	70.5	8.2	581	1	PRLR_BOVIN
28	70.5	8.2	706	1	SYN1_BOVIN
29	70.5	8.2	705	1	SYN1_HUMAN
30	70.5	8.2	238	1	YW15_MYCTU
31	70	8.1	2142	1	BAT2_HUMAN
32	70	8.1	1919	1	KARI_RAT
33	70	8.1	431	1	UL61_HCMVA
34	69.5	8.0	372	1	CNTR_HUMAN
35	69.5	8.0	2555	1	FAFY_HUMAN
36	69.5	8.0	199	1	SRP_MOUSE
37	69.5	8.0	708	1	HSR2_HUMAN
38	69.5	8.0	514	1	VE2_HPV05
39	69	8.0	860	1	AREA_PENRO
40	69	8.0	1182	1	HAIR_MOUSE
41	69	8.0	252	1	ICP3_HSV1D
42	69	8.0	1227	1	LAF4_HUMAN
43	69	8.0	128	1	YPRR_ECOLI

ALIGNMENTS

44 68.5 7.9 436 1 GDF6_BOVIN P55106 bos taurus
45 68.5 7.9 865 1 NRFA_PENRO Q92269 penicillium

RESULT 1

HXD3_HUMAN STANDARD; PRT; 416 AA.
AC P31249;
DT 01-JUL-1993 (REL. 26, CREATED)
DE 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DE 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE HOMEBOX PROTEIN HOX-D3 (HOX-4A).
GN HOXD3 OR HOX4A.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93041940.
RA TANIGUCHI Y., FUJII A., MORIUCHI T.;
RT Cloning and sequencing of the human homebox gene HOX4A.;
RL BIOCHIM. BIOPHYS. ACTA 1132:332-334(1992).
RN [2]
RP SEQUENCE OF 178-243 FROM N.A.
RX MEDLINE; 90215256.
RA BONCINELLI E., ACAMPORA D., PANNESSE M., D'ESPOSITO M., SOMMA R.,
GAUDINO G., STORNIATOLO A., CARIERO M., FAIELLA A., STIMONE A.;
RT Organization of human class I homeobox genes.;
RL GENOME 31:745-756(1989).
CC - FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
A SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC - SUBCELLULAR LOCATION: NUCLEAR.
CC - SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL, D1117; G219880;
DR PIR, S27198; S27198.
DR PIR, S15548; S15548.
DR MIN, 142980;
DR PROSITE, PS00027; HOMEBOX_1; 1.
DR PROSITE, PS00032; ANTEENAPEDIA_1.
DR PROSITE, PS00071; HOMEBOX_2; 1.
DR PFM: PF00046; homebox; 1.
DR HSSP: P02833; 1SN.
KW HOMEBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
KW TRANSCRIPTION REGULATION.
FT DOMAIN 84
FT DOMAIN 100 108 POLY-GLY.
FT DOMAIN 134 137 POLY-PRO.
FT DOMAIN 144 149 POLY-SER.
FT DNABIND 178 237 ANTP-TYPE HEXAPEPTIDE.
FT CONFLICT 241 241 G -> A (IN REF. 2).
SQ SEQUENCE 416 AA; 43927 MW; 6FD1F6B2 CRC32;

Query Match 10.94; Score 94; DB 1; Length 416;
Best Local Similarity 25.84; Pred. No. 0.09;
Matches 31; Conservative 16; Mismatches 43; Indels 30; Gaps 4;

QY 17 GSKRAGIMSEWSHPTASTRSERP-----GPGGV--CEPRGEPSSGVPVRELKQFLGW 70
DB 88 GSQPGNLSNQPPQPPPTLPSCSPINFGGVPKPKRGKGNASSSATISKQIFPW 147

[illegible]

FT	REPEAT	440	444	7.
FT	REPEAT	445	449	8.
FT	REPEAT	450	454	9.
FT	REPEAT	455	459	10. (APPROXIMATE).
FT	REPEAT	460	464	11.
FT	REPEAT	465	469	12. (APPROXIMATE).
FT	DOMAIN	470	526	GLY/PRO-RICH.
FT	MOD. RES	83	83	PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT	MOD. RES	364	364	PHOSPHORYLATION (BY CGPK) (POTENTIAL).
FT	MOD. RES	498	498	PHOSPHORYLATION (BY CGPK) (POTENTIAL).
SEQUENCE		577 AA:	60959 NM:	9868DCBD CRC32;

Query Match 9.7%; Score 84; DB 1; Length 577;
Best Local Similarity 27.2%; Pred. NO. 1.1;
Matches 41; Conservative 15; Mismatches 55; Indels 40; Gaps 8

18 SKKAGIWSHPTASTPRSEPPGGVCEPGEPSGPGVRRKQFLGMLKKHAYC 77
123 EOPPOHRTLLSKHRTGSCPRADGVAREVVG 153
297 ---VPMOP-RAAQRGSLPANVPTPRLGLDAPNDPRGTLTSTGVEPRGYLGP 351
78 SNLSRLYDQWRAAMQSKRTNR---QVGLGEA-----CVGKGAEEER---DPG 122
123 EOPPOHRTLLSKHRTGSCPRADGVAREVVG 153
352 QGPRMHH--VPGHESRGPP-----HELRG 374
RESULT 4
D ZN42_HUMAN STANDARD: PRT: 485 AA.
C P28698:
01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).
ZNF42.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
SEQUENCE FROM N.A.
MEDLINE: 91317761.
O'HARA P., COLLINS S.J., HICKSTEIN D., RASKIND W., DEAVEN L.L.,
"A retinoic acid-responsive human zinc finger gene, MZF-1,
preferentially expressed in myeloid cells."
J. BIOL. CHEM. 266:14183-14187(1991).
J. BIOL. CHEM. 266:14183-14187(1991).
- FUNCTION: MAY BE ONE REGULATOR OF TRANSCRIPTIONAL EVENTS DURING
HEMOPOIETIC DEVELOPMENT.
- SUBCELLULAR LOCATION: NUCLEAR.
- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN DIFFERENTIATING
MYELOID CELLS.
- INDUCTION: BY RETINOIC ACID.
- SIMILARITY: BELONGS TO THE KRUPEL SUBFAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.

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EMBL: M58297; G189044;
PIR: A40751; A40751.
MIM: 194550;
PROSITE: PS00028; ZINC_FINGER_C2H2; 13.
PFAM: PF00096; zf-C2H2; 13.
HSSP: P25490; 12NM.
TRANSFAC: T00529;
TRANSCRIPTION REGULATION: ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
DOMAIN 61 72 ASP/GLU-RICH (ACIDIC).
DOMAIN 107 213 4 C2H2-TYPE ZINC-FINGERS.
DOMAIN 214 235 GLY/PRO-RICH.
DOMAIN 236 482 9 C2H2-TYPE ZINC-FINGERS.
ZN_FING 107 129 C2H2-TYPE.
ZN_FING 135 157 C2H2-TYPE.
ZN_FING 163 185 C2H2-TYPE.
ZN_FING 191 213 C2H2-TYPE.
ZN_FING 236 258 C2H2-TYPE.
ZN_FING 264 286 C2H2-TYPE.
ZN_FING 292 314 C2H2-TYPE.
ZN_FING 320 342 C2H2-TYPE.
ZN_FING 348 370 C2H2-TYPE.
ZN_FING 376 398 C2H2-TYPE.

FT ZN_FING 404 426 C2H2-TYPE.
FT ZN_FING 432 454 C2H2-TYPE.
FT ZN_FING 460 482 C2H2-TYPE.
SQ SEQUENCE 485 AA; 54463 MW; 908B33F1 CRC32;
Query Match
Best Local Similarity 9.6%; Score 83; DB 1; Length 485;
Matches 43; Conservative 8; Mismatches 63; Indels 40; Gaps 8;
QY 17 GSKKAGIWSHPTASTPRSEPPGGVCEPGEPSGPGVRRKQFLGMLKKHAYC 75
DB 76 GVGPAALITRMSPPGRS---KGRSTGGGV--KGRCDVCGKVFQSRNLLRQKTH 130
QY 76 ---YCSNLSRLYDQWRAAMQSKRTNRQV-----GKLGECVCGKGAEEER- 120
DB 131 GERPFVCEGC-----RSFGRSHLLHQLTHEERPFVCGDGGGVRRARLEHR 183
QY 120 -DPGROP-----FOHRTLLSKHRTGSCP 142
DB 184 VHTGQPPRCACGGGSGFRNSNLLQHORIHGDP 217
RESULT 5
GN1_BACS4 STANDARD: PRT: 488 AA.
ID GN1_BACS4
AC P06566;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE ENDOGLUCANASE A (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE)
(CLONE PN1).
GN CELA.
OS BACILLUS SP. (STRAIN N-4).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87056924.
RA FUKUMORI F., SASHIHARA N., KUDO T., HORIKOSHI K.;
"Nucleotide sequences of two cellulase genes from alkalophilic
Bacillus sp. strain N-4 and their strong homology."
J. BACTERIOL. 168:479-485(1986).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
LINKAGES IN CELLULOSE.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).

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EMBL: M14781; G142660;
PIR: A25156; A25156.
DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; 1.
DR PRAM: PR00150; CELLULOSE; 1.
KW CELLULOSE DEGRADATION; HYDROLASE; GLYCOSIDASE.
FT ACT_SITE 163 163 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 252 252 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 488 AA; 54264 MW; 1C1ABCB CRC32;
Query Match
Best Local Similarity 9.5%; Score 82.5; DB 1; Length 488;
Matches 34; Conservative 14; Mismatches 50; Indels 51; Gaps 7;
QY 24 MSEM-----HPT-----ASTPSEPPGGGGV 47
DB 283 WANNSLTHDESSAALMPGNTAALSPSGAFVREKIREASIPSPDTPPS--- 340

CN		FUN(S&S9IC); S&S9IC.
KM		EXTRACELLULAR MATRIX; CONNECTIVE TISSUE; REPEAT; HYDROXYLATION
KW		GLYCOPROTEIN; COLLAGEN.
FT	DNAIN	NONHELICAL REGION (N-TERMINAL). 1 12

FT	DOMAIN	13	1023	TRIPLE-HELICAL REGION.
FT	MOD_RES	1024	1027	NONHELICAL REGION (C-TERMINAL).
FT	MOD_RES	21	21	HYDROXYLATION (PARTIAL).
FT	MOD_RES	24	24	HYDROXYLATION (PARTIAL).
FT	MOD_RES	27	27	HYDROXYLATION (PARTIAL).
FT	MOD_RES	39	39	HYDROXYLATION (PARTIAL).
FT	MOD_RES	53	53	HYDROXYLATION (PARTIAL).
FT	MOD_RES	54	54	HYDROXYLATION (PARTIAL).
FT	MOD_RES	72	72	HYDROXYLATION (PARTIAL).
FT	MOD_RES	90	90	HYDROXYLATION (PARTIAL).
FT	MOD_RES	93	93	HYDROXYLATION (PARTIAL).
FT	MOD_RES	123	123	HYDROXYLATION (PARTIAL).
FT	MOD_RES	128	128	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	255	255	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	285	285	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	306	306	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	327	327	HYDROXYLATION (PARTIAL).
FT	MOD_RES	339	339	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	366	366	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	540	540	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	551	551	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	561	561	HYDROXYLATION (PARTIAL).
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FT	MOD_RES	610	610	HYDROXYLATION (PARTIAL).
FT	MOD_RES	621	621	HYDROXYLATION (PARTIAL).
FT	MOD_RES	627	627	HYDROXYLATION (PARTIAL).
FT	MOD_RES	645	645	HYDROXYLATION (PARTIAL).

FT	MOD_RES	647	647	HYDROXYLATION (PARTIAL).
FT	MOD_RES	648	648	HYDROXYLATION (PARTIAL).
FT	MOD_RES	663	663	HYDROXYLATION (PARTIAL).
FT	MOD_RES	708	708	HYDROXYLATION (PARTIAL).
FT	MOD_RES	711	711	HYDROXYLATION (PARTIAL).
FT	MOD_RES	714	714	HYDROXYLATION (PARTIAL).
FT	MOD_RES	717	717	HYDROXYLATION (PARTIAL).
FT	MOD_RES	723	723	HYDROXYLATION (PARTIAL).
FT	MOD_RES	744	744	HYDROXYLATION (PARTIAL).
FT	MOD_RES	759	759	HYDROXYLATION (PARTIAL).
FT	MOD_RES	773	773	HYDROXYLATION (PARTIAL).
FT	MOD_RES	774	774	HYDROXYLATION (PARTIAL).
FT	MOD_RES	783	783	HYDROXYLATION (PARTIAL).
FT	MOD_RES	792	792	HYDROXYLATION (PARTIAL).
FT	MOD_RES	815	815	HYDROXYLATION (PARTIAL).
FT	MOD_RES	816	816	HYDROXYLATION (PARTIAL).
FT	MOD_RES	843	843	HYDROXYLATION (PARTIAL).
FT	MOD_RES	849	849	HYDROXYLATION (PARTIAL).
FT	MOD_RES	855	855	HYDROXYLATION (PARTIAL).
FT	MOD_RES	861	861	HYDROXYLATION (PARTIAL).
FT	MOD_RES	867	867	HYDROXYLATION (PARTIAL).
FT	MOD_RES	888	888	HYDROXYLATION (PARTIAL).
FT	MOD_RES	894	894	HYDROXYLATION (PARTIAL).
FT	MOD_RES	903	903	HYDROXYLATION (PARTIAL).
FT	MOD_RES	915	915	HYDROXYLATION (PARTIAL).
FT	MOD_RES	933	933	HYDROXYLATION (PARTIAL).
FT	MOD_RES	939	939	HYDROXYLATION (PARTIAL).
FT	MOD_RES	945	945	HYDROXYLATION (PARTIAL).
FT	MOD_RES	954	954	HYDROXYLATION (PARTIAL).
FT	MOD_RES	963	963	HYDROXYLATION (PARTIAL).
FT	MOD_RES	966	966	HYDROXYLATION (PARTIAL).
FT	MOD_RES	984	984	HYDROXYLATION (PARTIAL).
FT	MOD_RES	990	990	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1010	1010	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1011	1011	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1013	1013	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1014	1014	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1016	1016	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1017	1017	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1019	1019	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1020	1020	HYDROXYLATION (PARTIAL).
SO	SEQUENCE	1027 AA; 94353 MW; 95940NC4 CRC32;		

Query Match 9.1%; Score 79; DB 1; Length 1027;
Best local similarity 27.5%; Pred. No. 5.9;
Matches 39; Conservative 5; Mismatches 50; Indels 48; Gaps 5;

QY	21	AGIWSMSHPYASTP--RSERPGCG-GVCEPRGEPSSGPFVRELKQFLGWLKKHAYC 77
DB	879	AGIMGGRLPGAAGPGDGEHGEHGGVGVGPAFGSGRA----- 922
QY	78	SNLSFLYQWAMQKSKTKNQVKLGECVCGKGAEEED---PGEOPPHRTLLS 133
DB	922	-----GIMGMGEA--GGKAGXGDGMGLPELQGLQGPGRS 957
QY	134	KHRTGSCPRADGVRRVNGSG 155
DB	958	GESGPPGAPGPRGAGEAGRG 979

RESULT 9
CIC5_HUMAN STANDARD; PRT: 2339 AA.
AC 000975; ID 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-
DE TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT)
GN CACULI15.
OS HOMO SAPIENS (HUMAN).

	FT	CARBOHYD	751	751	POTENTIAL.
	FT	CARBOHYD	1063	1063	POTENTIAL.
	FT	CARBOHYD	1563	1563	POTENTIAL.
	FT	CARBOHYD	1675	1675	POTENTIAL.
	FT	CARBOHYD	1867	1867	POTENTIAL.
	FT	CARBOHYD	2169	2169	POTENTIAL.
	FT	CARBOHYD	2207	2207	POTENTIAL.
	FT	CARBOHYD	2169	2169	POTENTIAL.
	FT	CARBOHYD	2207	2207	POTENTIAL.
	FT	VANOSPLIC	2164	2226	MISSING (IN ALPHA-1B-2).
	FT	VANOSPLIC	2227	2339	RUSGSEHNALLORDPISPLAGSRIGSDPYLGO RLDSGLSHVHALPEDTLFEESAVATNSGRSSTSVYS
	SO	SEQUENCE	2339 AA;	262494 MW;	166FF9780 CRC32; LAAPGLEPTCP (IN ALPHA-1B-2).
		Query Match	9.08;	Score 78;	DB 1; Length 2339;
		Best Local Similarity	23.28;	Pred. No. 17;	
		Matches 33;	Conservative 15;	Mismatches 38;	Indels 56; Gaps 8;
OY		28 SHPAASP----	RSER-----PGGGVCCEPRGEGSPGVRRRELKOFLOMKKHACSNLS	81	
Dd		891 SHSENAMOPPARSGRGPEGEGRHHRHSPEEAAREP-----	RRH-----	936	
OY		82 FRLDYOWRAMQSKSHKTNOVGKLGAECVGKG-----	AEEEDPDGEPPQH	129	
Dd		936 -----RAHRHDDP-----	SKECAAKGERARRAHNRGRAGRAPAEAGEEPAR--	978	
OY		130 TLISKHRTRGSC-PRADGVRR	E	150	
Dd		978 ----RHRARKAPOAHEAVEKE	995		
		RESULT 10			
BARI_CHITE	ID	BARI_CHITE	STANDARD;	PRT;	174 NA.
AC	AC	P02849;			
DT	DT	21-JUL-1986 (REL. 01,	CREATED)		
DT	DT	21-JUL-1986 (REL. 01,	LAST SEQUENCE UPDATE)		
DT	DT	01-FEB-1994 (REL. 28,	LAST ANNOTATION UPDATE)		
DE	DE	BALBIANI RING PROTEIN I (GIANT SECRETORY PROTEIN I-A) (GSP-IA)			
GN	GN	BRI.			
OC	OC	CHIRONOMUS TENTANS (MIDGE).			
OC	OC	EUKAROTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INsectA;			
OC	OC	PERICOTA; DIPTERA; NEMATOCERA; CHIRONOMOIDEA; CHIRONOMIDAE;			
OC	OC	CHIRONOMINAE; CHIRONOMUS.			
RN	RN	[1]			
RP	RP	SEQUENCE OF 1-116 FROM N.A. (CLONE PCTBR1-1).			
RC	RC	TISSUE-SALIIVARY GLAND;			
RX	RX	MEDLINE; 83238361.			
RA	RA	CASE S.T., BYERS M.R.;			
RT	RT	"Repeated nucleotide sequence arrays in Balbiani ring 1 of Chironomus tentans contain internally nonrepeating and subrepeating elements.";			
RT	RT	J. BIOL. CHEM. 258:7793-7799(1983).			
RN	RN	[2]			
RP	RP	SEQUENCE OF 7-174 FROM N.A. (CLONE PCT21).			
RC	RC	TISSUE-SALIIVARY GLAND;			
RA	RA	WIESLANDER L., SUMEGI J., DANEHOLT B.;			
RT	RT	"Evidence for a common ancestor sequence for the Balbiani ring 1 and Balbiani ring 2 genes in Chironomus tentans.";			
RT	RT	PROC. NATL. ACAD. SCI. U.S.A. 73:6956-6960(1982).			
CC	CC	-I- FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR			
CC	CC	STRUCTURE, THE LARVAL TUBE.			
CC	CC	-SUBCELLULAR LOCATION: SECRETED.			
CC	CC	-TISSUE SPECIFICITY: SALIVARY GLAND.			
CC	CC	-----			
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	CC	the European Bioinformatics Institute. There are no restrictions on its			

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DR EMBL; K00447; G156531; -
 DR EMBL; J01055; G552075; -
 DR PIR; A03339; BQICIT.

REPEAT.
 FT NON-TER 1 1
 FT DOMAIN 42 85 4 X 11 AA TANDEM REPEATS.
 FT REPEAT 42 52 1-1.
 FT REPEAT 53 63 1-2.
 FT REPEAT 64 74 1-3.
 FT REPEAT 75 85 1-4.
 FT DOMAIN 124 167 4 X 11 AA TANDEM REPEATS.
 FT REPEAT 124 134 2-1.
 FT REPEAT 135 145 2-2.
 FT REPEAT 146 156 2-3.
 FT REPEAT 157 167 2-4.
 FT VARIANT 40 40 N -> K (IN CLONE PCT21).
 FT VARIANT 57 57 G -> E (IN CLONE PCT21).
 FT VARIANT 72 72 K -> R (IN CLONE PCT21).
 FT VARIANT 86 86 R -> G (IN CLONE PCT21).
 FT NON-TER 174 174
 SO SEQUENCE 174 AA; 18920 MW; E9720893 CRC32;

Query Match 9.0%; Score 77.5; DB 1; Length 174;
 Best Local Similarity 23.9%; Pred. No. 1.3; Matches 37; Conservative 20; Mismatches 61; Indels 37; Gaps 6;

21 AGTWSMHTAATSPRSEPPGCGVCEPRGSGPYRRELKQFLGMLKHAACSNL 80
 34 AGPFSHNSPEKSKSRPEKPSKGS--KPRPEKPSKSKPRPEKPSKSRPEKPSK 90
 81 SFRLYQWRAWMOK--SHKTRNOVGKLEA-----CVGGAEEERPGSOP-PQHTLL 132
 91 -----NKAERKCARNGRGNMAKCRCTSGAKSPKSEPSKSKPRPEKPSKE 139

133 SKHR-----TRGSCPRADGVRRVR 152
 140 SKRPEKPSKSKPRPEKPSKSKPRPEKPSKSKPRPEKPSKSKPRPEKPSK 174

RESULT 11
 EX2_PODAN STANDARD; PRT; 554 AA.
 C P51021:
 D 01-OCT-1996 (REL. 34, CREATED)
 T 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 T 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 T PEROXISOME ASSEMBLY PROTEIN CARL (PEROXIN-2).
 T PEX2 OR CARL
 T PODOSPORA ANSERINA.
 T EURARITIA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
 T SORDARIALES; SORDARIACEAE; PODOSPORA.
 T [1]
 T SEQUENCE FROM N.A.
 C STRAIN-S:
 C MEDLINE; 95323960.
 C BERTEAUX-DECELLIER V., PICARD M., THOMSON-COFFE C., ZICKLER D.,
 C PAVIER-ABOUE A., SIMONET J.-M.;
 C "A nonmammalian homolog of the Pex1 gene (Zellweger syndrome)
 C discovered as a gene involved in caryogamy in the fungus Podospora
 C anserina";
 C CELL 81:1043-1051(1995).
 C -1- FUNCTION: INVOLVED IN CARYOGAMY (NUCLEAR FUSION), A PROCESS
 C REQUIRED FOR SEXUAL SPOROGATION.
 C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
 C -1- SIMILARITY: CONTAINS A CHHC4-CLASS ZINC FINGER.
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DR EMBL; X87329; E246075; -
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.
 FT TRANSMEMBRANE; PEROXISOME; ZINC-FINGER.
 FT TRANSMEM 256 271
 FT TRANSMEM 307 325 POTENTIAL.
 FT ZN_FING 366 435
 FT DOMAIN 466 554 C3HC4-TYPE (ATYPICAL).
 FT DOMAIN 21 25 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 145 150 POLY-ALA.
 FT DOMAIN 501 508 POLY-GLY.
 FT DOMAIN 541 546 POLY-GLU.
 SO SEQUENCE 554 AA; 61533 MW; 7F9A6748 CRC32;

Query Match 8.9%; Score 77; DB 1; Length 554;
 Best Local Similarity 21.4%; Pred. No. 4.8; Matches 33; Conservative 20; Mismatches 45; Indels 56; Gaps 7;

14 GYGSKKAG--IMSESHPTASTPRSEPPG----- 45
 210 GLTGLMTVSGRYMSKKNENLRDGDGYDEPSPYORLSMTDRSLTHAASFAFLVF 269
 45 -----GVCPEPPGEPSSGPYRRE-----LQFLGMLKHAACSNLSTRL-----Y 85
 270 LLOGRYTLLDRVLRRLAPPTIS-QYSREVSFEYLNQVW---HAFTEFLVLPVGI 325
 86 DQPRAMQKSHKTRNOVGKLEACVYGKAEEER 119
 326 NWRWRMLARTWRTKTKI-----NSTGTGGEAEKK 355

RESULT 12
 TEGU_HSV11 STANDARD; PRT; 3164 AA.
 AC P10220;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36).
 GN UL36.
 OS HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
 OC VIRUSES; DSDNA VIRUSES; NO RNA STAGE; HERPESVIRIDAE;
 CC ALPHAHERPESVIRINAE; SIMPLEXVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88274327.
 RA MCGEOCH D.J., DALRYMPLE M.A., DAVIDSON A.J., DOLAN A., FRAME M.C.,
 RA MCNAB D., PERRY L.J., SCOTT J.E., TAYLOR P.;
 RT "The complete DNA sequence of the long unique region in the genome of
 RT herpes simplex virus type 1";
 RT J. GEN. VIROL. 69:1531-1574(1988).
 CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC HSV-1 24, EBV BFLF1, HSV-1 64, VZV 22, AND HCMV UL48.
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DR EMBL; X14112; G59536; -
 DR EMBL; X14112; E312351; -
 DR PIR; I30085; WMBEH6.

KW REPEAT 2911 2980 35 X 2 AA TANDEN REPEATS OF P-Q.
 SQ SEQUENCE 3164 AA; 335857 MW; 6B3C2958 CRC32;

Query Match 8.4%; Score 73; DB 1; Length 3164;
 Best Local Similarity 23.5%; Pred No. 70;
 Matches 27; Conservative 10; Mismatches 42; Indels 36; Gaps 3;

QY 50 PRGGEPSGPVRRRLKQFLGWLKKAHYNCSNLSFRLYDQWRAVWQK-----SHKTR 99
 DB 242 PGGPEPAA-----PADLTAAALHLGASSETYLQDAFSEKRAVAIHPRL 285
 QY 100 NQYKLGKAGVCGKGAKEERDPECPPOHRTLSKRTGSCPRADGVRRVRS 154
 DB 286 GELAGGEPCVGVGPREGVGGPQHP-----TAASPPPTARRDRRAS 330

RESULT 13
 GUNG_CLOCE STANDARD; PRT; 725 AA.

AC P37700;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ENDOGLUCANASE G PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE G)
 DE (CELLULOSE G) (EGCG).
 GN CELCG.
 OS CLOSTRIDIUM CELLULOLYTICUM.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
 CC CLOSTRIDIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35319;
 RX MEDLINE; 93012971.
 RA BAGNARA-TARDIF C., GAUDIN C., BELAICH A., HOEST P., CITARD T.,
 RA BELAICH J.-P.;
 RT "Sequence analysis of a gene cluster encoding cellulases from
 RT Clostridium cellulolyticum.";
 RL GENE 119:17-28(1992).

-1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 (2) EXOCELLULOHYDROLASES THAT CUT THE DISACCHARIDE CELLULOSE
 FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
 SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
 CC LINKAGES IN CELLULOSE.
 CC -1- PATHWAY: CELLULOSE DEGRADATION.
 CC -1- DOMAIN: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZYME AS
 CC WELL AS IN OTHER C.THERMOCELLUM CELLULOSE ENZYMES. THIS DOMAIN
 CC MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY E (FAMILY 9 OF GLYCOSYL
 CC HYDROLASES).

-1- SIMILARITY: CONTAINS 1 CELLULOSE-BINDING DOMAIN (CBD).
 CC -----
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CC EMBL; M87018; G531774;
 CC DR PIR; JCI300; JCI300.
 CC DR PROSITE; PS00018; EF_HAND; UNKNOWN 1
 CC DR PROSITE; PS00448; CLOS_CELLULOSE_RPT; 1
 CC DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1
 CC DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1
 CC DR PFAM; PF00371; GLYCOSYL_HYDROL_1
 CC DR PFAM; PF00404; celcc; 2

PFAM; PF00759; glycosyl_hydrl2; 1.

DR HSSP; P26221; 3TR4.
 KW CELLULOSE DEGRADATION; HYDROLASE; GLYCOSIDASE; REPEAT; SIGNAL.

FT SIGNAL 1 35
 FT CHAIN 36 725
 FT DOMAIN 485 662
 FT ACT_SITE 408 408
 FT ACT_SITE 446 446
 FT ACT_SITE 455 455
 FT ACT_SITE 664 719
 FT DOMAIN 664 719
 FT REPEAT 664 687
 FT REPEAT 719 719
 SQ SEQUENCE 725 AA; 79886 MW; 61CEFC9E CRC32;

Query Match 8.4%; Score 72.5; DB 1; Length 725;
 Best Local Similarity 24.8%; Pred No. 17;
 Matches 39; Conservative 12; Mismatches 55; Indels 51; Gaps 11;

QY 4 YFVQVRCNPF-GIY-----GSKKAGIWEWSHPTASTPSEKPG-----PGGYCE 49
 DB 138 YF--IKNPTPGVYYGYGDGDKHSMWG-----PAEYMGHRSFYKDAKSPSAVCA 189
 QY 50 PRGGE-----PSSGVRR-----IKQFLGWLKKAHYNCSNLSFRLYD 86
 DB 190 STAAIASAAVVFKSDPTVAEKCSHAKNLFDMADKAKSDAGYTAAGYSSSF--YD 247
 QY 87 --QWRA--WQKSHKTRNOYKLGKAGVCGKGAKEERD 120
 DB 248 DISMAAVMLYLTNDSTYLDK-AESYVPMWKEQOTD 283

RESULT 14
 MCAS_MYCBO STANDARD; PRT; 2110 AA.

AC Q02231;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE MYCOCEROSIC ACID SYNTHASE.
 GN MAS.
 OS MYCOBACTERIUM BOVIS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;
 CC ACTINOMYCETACEAE; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE; 92406887.
 RA MATHUR M., KOLATTUKUDY P.E.;
 RT "Molecular cloning and sequencing of the gene for mycroceroic acid
 RT synthase, a novel fatty acid elongating multifunctional enzyme, from
 RT Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guérin.";
 RL J. Biol. Chem. 267:19388-19395(1992).

-1- FUNCTION: CATALYZES THE ELONGATION OF N-FATTY ACYL-COA WITH
 METHYLMALONYL-COA (NOT MALONYL-COA) AS THE ELONGATING AGENT TO
 CC FORM MYCOCEROSYL LIPIDS.
 CC -1- COFACTOR: CONTAINS ONE COVALENTLY BOUND PHOSPHOPANTHETHEINE
 CC -1- SUBUNIT: HOMODIMER WHOSE MONOMERS PROBABLY HAVE A HEAD TO TAIL
 CC ARRANGEMENT

-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
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CC EMBL; M95808; G149980;
 CC DR PIR; B44110; B44110.
 CC DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:05 ; Search time 68.96 Seconds

(Without alignments)
138.330 Million cell updates/sec

Title: US-09-037-657-17

Perfect score: 864

Sequence: 1 GTVYEVQVNCNPFQIGSKRK.....RTGSCPADGVREVRSRG 155

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_PROTOZOA:*
- 12: SP_VIRUS:*
- 13: SP_VIRIDIA:*
- 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	65.9	422	4	075462
2	88	10.2	425	6	002661
3	79.5	9.2	294	4	095873
4	79.5	9.2	433	10	064807
5	78	9.0	593	2	083470
6	78	9.0	957	5	019204
7	78	9.0	1309	10	064428
8	78	9.0	1379	11	062868
9	78	9.0	1388	11	P70336
10	77.5	9.0	292	2	0928F5
11	76.5	8.9	790	10	080394
12	76.5	8.9	297	10	0920C7
13	76	8.8	481	6	097641
14	75.5	8.7	561	13	090711
15	75	8.7	336	2	044128
16	74.5	8.6	990	10	080770
17	74.5	8.6	435	10	081009
18	74	8.6	756	4	075154
19	74	8.6	712	11	070204
20	73.5	8.5	264	3	043981
21	73	8.4	316	12	069088
22	73	8.4	211	2	P96291
23	72.5	8.4	594	4	093239
24	72.5	8.4	346	13	093404
25	72.5	8.4	437	2	052205
26	72	8.3	312	4	097994
27	72	8.3	312	4	P78549
28	72	8.3	312	4	P78549
29	72	8.3	431	4	095615

ALIGNMENTS

30	72	8.3	670	11	088935	088935 mus musculus
31	72	8.3	1537	13	092072	092072 gallus galli
32	71.5	8.3	457	4	013518	013518 homo sapien
33	71.5	8.3	1208	4	094761	094761 homo sapien
34	71.5	8.3	140	5	025212	025212 junonia coe
35	71.5	8.3	207	5	076587	076587 caenorhabdit
36	71.5	8.3	697	5	093645	093645 caenorhabdit
37	71.5	8.3	296	12	069118	069118 human herpe
38	71	8.2	629	2	092C17	092C17 streptomyce
39	71	8.2	736	6	018805	018805 cercopithec
40	71	8.2	1804	11	092101	092101 mesocricetu
41	70.5	8.2	448	4	015468	015468 homo sapien
42	70.5	8.2	1522	4	060242	060242 homo sapien
43	70.5	8.2	984	4	060297	060297 homo sapien
44	70.5	8.2	819	4	013443	013443 homo sapien
45	70.5	8.2	411	12	081813	081813 hepatitis C

RESULT 1						
ID 075462	PRELIMINARY	PRT	422 AA.			
AC 075462						
DT 01-NOV-1998 (TREMBLrel. 08, Created)						
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)						
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)						
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.						
GN CLF-1.						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;						
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.						
RN [1]						
RP SEQUENCE FROM N.A.						
RA ELSON G.C.A., GRABER P., LOSBERGER P., HERRER S., GREUTNER D.,						
RA MENOD L.N., WELLS T.N.C., ROSCO-VILBOIS M.H., GAUCHAT J.F.;						
RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the						
RT Cytokine Type-1 Receptor Family."						
RL J. Immunol. 0:0-0(1998).						
DR EMBL: AF059293; AAC28335.1; ..						
DR PRAM: PF00041; fn3; 2.						
KW Signal.						
FT SIGNAL	1	37	POTENTIAL.			
FT CHAIN	38	422	CYTOKINE-LIKE FACTOR-1.			
SC SEQUENCE	422 AA;	46301 MW;	877F9BC9 CRC32;			

Query Match	65.9%	Score 569;	DB 4;	Length 422;	
Best Local Similarity	99.0%	Pred. No. 1.9e-51;			
Matches 100;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	GTVYEVQVNCNPFQIGSKRKAGIWSWSHPTAASPPRSGGVCCEPRGESSGTV	60		
DB	304	GTVYEVQVNCNPFQIGSKRKAGIWSWSHPTAASPPRSGGVCCEPRGESSGTV	363		
QY	61	REELKQFLGMLKKHAYCSUTLSPRLDQWAAWQSHKTRNQ	101		
DB	364	REELKQFLGMLKKHAYCSUTLSPRLDQWAAWQSHKTRNQ	404		
RESULT 2					
ID 002661	PRELIMINARY	PRT	425 AA.		
AC 002661					
DT 01-JUL-1997 (TREMBLrel. 04, Created)					
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)					
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)					
DE SCO-SPONDIN (FRAGMENT).					
OS Bos taurus (Bovine).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;					

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBCOMMISSURAL ORGAN;
 RA GGBRON 5.1;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y08561; CAA69868.1;
 DR PFAM: PF00050; tsp_1; 3.
 FT NON-TER 1
 FT SEQUENCE 425 AA; 43721 MW; 20D06545 CRC32;
 SQ
 Query Match 10.2%; Score 88; DB 6; Length 425;
 Best Local Similarity 28.6%; Pred. No. 0.17;
 Matches 34; Conservative 4; Mismatches 47; Indels 34; Gaps 6;
 QY 24 MSEMSEH-----PTASTPRSER--PGGGGVC--EPGGESSGPPVRELKQFLGWL 71
 Db 196 WAPMSACSGCLVPGGGPALRSRLCPGPDJSCIGENTEEPCSPV----- 245
 QY 72 KHAAYCSNLSFRLYDQNRAMQSHKTRNOVGLGACVGGKGAEEERDPEQPPQHT 130
 Db 245 -----C-LGLGYWQWMAWMSACSPANGGVQTRGRNC-----SASAPGDGCGGPHSGT 292
 RESULT 3
 AC 095873 PRELIMINARY; PRT; 294 AA.
 ID 095873;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)
 DE NG34.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROMEN L., MADAN A., QIN S., SHAFFER T., JAMES R., RATCIFFEE A.,
 RA ABBASI N., DICHROFF R., LORETT C., MADAN A., DORS M., YOUNG J.,
 RA LASKY S., HOOD L.;
 RT "Sequence of the human major histocompatibility complex III
 RT region".
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A129756; AAD18083.1;
 SQ SEQUENCE 294 AA; 31809 MW; B0E58CB3 CRC32;
 QY 27 WSHPTASTPRSERPG--PGGVCPEPGGPPSGPVRELKQFLGWL 72
 Db 117 WDHVDSGCT---RRPGVSPGGGLSVPGAPLKEPKRRE--KLLGLWK 159
 Query Match 9.2%; Score 79.5; DB 4; Length 294;
 Best Local Similarity 41.7%; Pred. No. 0.85;
 Matches 20; Conservative 4; Mismatches 17; Indels 7; Gaps 3;
 QY 27 WSHPTASTPRSERPG--PGGVCPEPGGPPSGPVRELKQFLGWL 72
 Db 117 WDHVDSGCT---RRPGVSPGGGLSVPGAPLKEPKRRE--KLLGLWK 159
 RESULT 4
 AC 064807 PRELIMINARY; PRT; 433 AA.
 ID 064807;
 DT 01-AUG-1998 (TEMBLrel. 07, Created)
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)
 DE PUTATIVE SERINE CARBOXYPEPTIDASE 1.
 GN F11P24.3 OR T20K9.18
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004401; AAC17814.1;
 DR EMBL: AC004786; AAC32443.1;
 DR PFAM: PF00450; serine_carboxypeptidase.
 KW Carboxypeptidase.
 SQ SEQUENCE 433 AA; 49233 MW; 07D281C3 CRC32;
 QY 70 WTKHAYCSNLSFRLYDQNRAM--QKSHKTRNOVGLGACVGGKGAEEERDPE 123
 Db 363 FLATQAMIKSLNSYIDENRPMIRDIQITGYTRYSNKMTFATVKGSGHTAENKPPQ 419
 RESULT 5
 AC 083470 PRELIMINARY; PRT; 593 AA.
 ID 083470;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN TP0457.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 96332770.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.R., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTERBACK T.,
 RA MCDONALD L., ARTLACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete".
 RL Science 281:375-388(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.R., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTERBACK T.,
 RA MCDONALD L., ARTLACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE001222; AAC65441.1;
 SQ SEQUENCE 593 AA; 65567 MW; 16898991 CRC32;
 QY 2 TYT-----FVQVKNPFGITGSKKAGIWSMSHTPA--STPSPRPPGGGVCPEPR--GG 53
 Query Match 9.0%; Score 78; DB 2; Length 593;
 Best Local Similarity 32.0%; Pred. No. 2.6;
 Matches 33; Conservative 9; Mismatches 39; Indels 22; Gaps 6;

431 TVPAGGVVYVPEPVEGPKRIKQENRHPGIAAPPSTP-----AGAVPPTOG 482
 Y 54 EPSSGPRRELKQFLGMLKKHAYCSNLSFLYDQWRAMQKSH 96
 b 483 ETAGGPR-----YLGVLPHAGGTGTGVALF-YLVANMERGH 519
 RESULT 6
 19204
 D Q19204 PRELIMINARY; PRT: 957 AA.
 Q19204:
 01-NOV-1996 (Tremblrel. 01, Created)
 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 SIMILAR TO THROMBOSPONDIN.
 F08C6.1.
 Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdittia; Rhabdittidae;
 Rhabdittina; Rhabdittidae; Rhabdittidae; Peloderinae; Caenorhabdittis.
 [1]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 MEDLINE: 94150718.
 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 BOFFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSON L.,
 JONES M., KESHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 PARSONS J., PERCY C., RITKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,
 SHALDON N., SMITH A., SONNHAMER E., STADEN R., SILSTON J.,
 THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 Nature 368:32-38(1994).
 [2]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 BENTLEY D.;
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 WATERSTON R.;
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 EMBL: U28378; AAA68721.1;
 PRAM: PF00080; tsp_1; 6;
 SEQUENCE 957 AA; 106808 MW; 03F05B40 CRC32;
 Query Match 9.0%; Score 78; DB 5; Length 957;
 Best Local Similarity 23.98; Pred. No. 4.3;
 Matches 34; Conservative 16; Mismatches 40; Indels 52; Gaps 8;
 22 GINSEHMPAASTPRSEPPGGG-----VCEPRGEPSSGPVRLKFLGMLKHA 75
 608 GTWSLWTSRATC-----GGCYKRKNACISITG-----OCENEDETE 645
 76 YGSNLS-----FLYDQWRAMQKSHKTRNVGKLGECVCGKAEERDPGEPPOHRTL 131
 646 VCSSESCPSVLKVGNEWSTWEMNH-----CSVSC--GRSG-----ARIYKC 686
 132 LSKHRTG-SCPRADGVRREVR 152
 687 LSPRLTAFDCPGENKVTNELR 708
 SULT 7
 4428
 064428 PRELIMINARY; PRT: 1309 AA.
 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE REVERSE TRANSCRIPTASE.
 OS Chlorella vulgaris.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlorellales;
 OC Chlorellaceae; Chlorella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-ZEP.
 RX MEDLINE: 97361851.
 RA HIGASHIYAMA T., NOUTOSHI Y., FUJIE M., YAMADA T.,
 RT "Zep, a LINE-like retrotransposon accumulated in the Chlorella
 telomeric region";
 RL EMBL J. 16:3715-3723(1997).
 DR EMBL: AB008896; BAA25763.1;
 DR PFAM: PF00078; tvt; 1.
 KW RNA-directed DNA polymerase.
 SQ SEQUENCE 1309 AA; 141659 MW; C874E321 CRC32;

Query Match 9.0%; Score 78; DB 10; Length 1309;
 Best Local Similarity 24.28; Pred. No. 6.1;
 Matches 36; Conservative 19; Mismatches 46; Indels 48; Gaps 10;

QY 17 GSKAGINSEHMPAASTPRSEPP-----GFGGVCPRGEPSSGPV---RRELKOF 67
 DB 973 GGSTGSEMED-----SCSPPSQSRMTPRPSAYSTCPTS---SCGPTGSSRRSAFT 1024
 QY 68 LGMKKHAYCSNLSFLYDQWRAMQKSHKTRNVGKLGECVCGKAEERDPGEP 126
 DB 1025 GSTV---SHCS-----TGSSRMQSAAL---CLGLG---QAMPQDQPP 1060
 QY 127 QHRTLSKRTGSCPRADGVRREVRGSG 155
 DB 1061 -----ARCARAPGASGSDGARAPRPSG 1083

RESULT 8
 062868
 ID 062868 PRELIMINARY; PRT: 1379 AA.
 AC 062868:
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE ROK-ALPHA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96094284.
 RA LEUNG T., MANSEER E., TAN L., LIM L.,
 RT "A novel serine/threonine kinase binding the Ras-related RhoA GTPase
 RT which translocates the kinase to peripheral membranes";
 RL J. Biol. Chem. 270:29051-29054(1995).
 DR EMBL: U38481; AAB37540.1;
 DR PFAM: PF00130; DAG-PE-bind; 1.
 DR PFAM: PF00069; Pkinase; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 SQ SEQUENCE 1379 AA; 159434 MW; 9BCBECFC CRC32;

Query Match 9.0%; Score 78; DB 11; Length 1379;
 Best Local Similarity 38.58; Pred. No. 6.4;
 Matches 20; Conservative 4; Mismatches 20; Indels 8; Gaps 2;

QY 42 GPGGVCPRGEPSSG-----PYRELKQFLGMLKKHAYCSNLSFLYD 86
 DB 1127 GSGGDAEPDGDPEPESRLGWLSPVYNNTKF-GWKKYVIYSSKILTYD 1177
 RESULT 9
 P70336

ID P70336 PRELIMINARY; PRT; 1388 AA.
 AC P70336;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE RHO-ASSOCIATED COILED-COIL FORMING KINASE 2
 DE (RHO-ASSOCIATED, COILED-COIL FORMING PROTEIN KINASE P160 ROCK-2).
 GN ROCK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96368048.
 RA NAKAGAWA O., FUJISAWA K., ISHIZAKI T., SAITO Y., NAKAO K.,
 RA NARUMIYA S.;
 RT "ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil
 RT forming protein serine/threonine kinase in mice."
 RL FEBS Lett. 392:189-193(1996).
 DR EMBL; U58513; AAC53133.1; -
 DR MGD; MGI:107926; ROCK2.
 DR PFAM; PF00130; DAG-PE-Bind. 1.
 DR PFAM; PF00069; Pkinase. 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST. 1.
 SQ SEQUENCE 1388 AA; 160584 MW; FCB26B88 CRC32;

Query Match 9.0%; Score 78; DB 11; Length 1388;
 Best Local Similarity 38.5%; Pred. No. 6.5;
 Matches 20; Conservative 4; Mismatches 20; Indels 8; Gaps 2;

QY 42 GPGGVCCEPRGEPSSG-----PVREELKQFLGMLKNAKNCSTLSERLD 86
 Db 1136 GSGPDADPDGPFESRLEGWLSLPRVNTKRF-GWVKYIVYSKRLFLFD 1186

RESULT 10
 Q92BF5 PRELIMINARY; PRT; 292 AA.
 AC Q92BF5;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE HYPOTHETICAL 32.4 KD PROTEIN.
 GN SC9B5.25.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA SEGER K.J., HARRIS D.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA REIDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 MB Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-86(1996).
 DR EMBL; AL035206; CAA22767.1; -
 DR Hypothetical protein.
 SQ SEQUENCE 292 AA; 32399 MW; 61D7FCEE CRC32;

Query Match 9.0%; Score 77.5; DB 2; Length 292;
 Best Local Similarity 23.5%; Pred. No. 1.4;

Matches 40; Conservative 20; Mismatches 57; Indels 53; Gaps 9;
 QY 6 VOVRONCPGIGYSKKAGIMSE-----WSHPT-AASRP---RSRRGP-- 44
 Db 43 VVDAGATYAPSRNSLWERTPPDGRFPYKAFSLTGHPTAESLPADLRTGDPPLR 102
 QY 44 -----GGGVCCEPRGEPSSG---PVARE-----LKQFLGM-----LKKHAY 76
 Db 103 RGRAGEGLDLEWGRFAPGEPLEPKRAGRLGTVLFPFPWFAFGDPATLEACALRTGOW 162
 QY 77 CNSLSFRLYQWRAMMOKSHKTRNQVGLCEACVGGKAGEERDGPQPP 126
 Db 163 PLAVEFRHPGWEP--ERAETRTASLSALGASAVGTDMA--QRLPGSLPP 208

RESULT 11
 ID 080394 PRELIMINARY; PRT; 790 AA.
 AC 080394;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE TRANSCRIPTION FACTOR VPL.
 GN MCVPL.
 OS Mesembryanthemum crystallinum (Common Ice plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Caryophyllidae; Caryophyllales; Alzooceae;
 OC Mesembryanthemum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA FUKUHARA T., BOHNERT H.J.;
 RT "Expression of Vpl and water channel proteins during seed
 RT germination."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015183; BAA28779.1; -
 SQ SEQUENCE 790 AA; 86467 MW; 6FFE0075 CRC32;

Query Match 8.9%; Score 76.5; DB 10; Length 790;
 Best Local Similarity 33.9%; Pred. No. 5;
 Matches 39; Conservative 8; Mismatches 37; Indels 31; Gaps 9;
 QY 21 AGIWSHPTASTPSERP--GPGGVCCEPRGCE--PSSGPVR--ELKQFLGWL 71
 Db 580 AGNMYTSHPPPL-PPQVSHVPGPPPPVGMQGLEAAPSNGKFOQGVYKNO--GWK 636
 QY 72 KHAVCNLSFRLYQWRAMMOKSHKTRNQVGLCEACVGGKAGE-----EERD 120
 Db 637 SE-----KNLRL-----QKYLK-QSDVGNLGRITVLPKKEATHLPELEARD 678

RESULT 12
 ID 0920C7 PRELIMINARY; PRT; 297 AA.
 AC 0920C7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE T2N18.14 PROTEIN.
 GN T2N18.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
 RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENTO M.,
 RA CARREIRA A.J., CREASY T.H., BOELL C.R., TOWN C.D., NIERMAN W.C.,
 RA FRASER C.M., VENTER J.C.;

RT "Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006260; AAD18149.1;
 SQ SEQUENCE 297 AA; 33756 MW; 0921E56E CRC32;

Query Match 8.9%; Score 76.5; DB 10; Length 297;
 Best Local Similarity 20.5%; Pred. No. 1.8;
 Matches 33; Conservative 20; Mismatches 55; Indels 53; Gaps 7;

19 KRAGIWSHSPAAATP-----RSEPRG-----GGVCEPRGSGPVRRELK 65
 46 KNAASAEEOETSPVTCGVIRNKRKPKETARVSGATE-----RRROS 94
 66 QELGWLK---HAYCSNLSFRLYDO-WRAMOKSH-----KTRNOYKLGACVCGKA 115
 95 RRCGWKNKAFPCHSFGILKPCFSPVWRKMSFSHASFKEKSSSRSEPIERST 154
 116 EERBPGE-----QPPQHTLLSKHRT 137
 155 VEPEPEETRKEENOEEASCKSFATPPRNALFLTRCS 195

RESULT 13
 097641 PRELIMINARY; PRT; 481 AA.

01-MAY-1999 (TREMBLrel. 10; Created)
 01-MAY-1999 (TREMBLrel. 10; Last sequence update)
 01-MAY-1999 (TREMBLrel. 10; Last annotation update)
 FIRINGEN A-ALPHA CHAIN (FRAGMENT).
 Equus caballus (Horse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Perissodactyla; Equidae; Equus.
 [1]
 P SEQUENCE FROM N.A.
 MORAKAWA M.;
 Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 EMBL: AF095462; AAC67561.1;
 NON_TER 1
 NON_TER 1
 SEQUENCE 481 AA; 49506 MW; 5B5EFF36 CRC32;

Query Match 8.8%; Score 76; DB 6; Length 481;
 Best Local Similarity 25.6%; Pred. No. 3.3;
 Matches 42; Conservative 10; Mismatches 56; Indels 56; Gaps 9;

17 GSKRAGIWSHSH-PTAAT--PRSERPGPG-----GVCEPRGEP--SSGPV 60
 120 GSGSASTWTSGSYGSGASTWNPSSGSSGSGSGLASASTWNPSSSEPSDGP- 179
 61 RRELKQFLGKKAHAYCSNLSFRLYDOWRAMOKSHKTRNOYKLGACVCGKAEEERD 120
 179 -----RKPGSSGGLTASAI-----WTSGS-----SGLSASTWNPSSSEPSGS 214
 121 PGEOPP-OHTLLSKHRTGSC-----PRADGVR 149
 215 DGPCKPSSGTLSTISWTSSGSGSASTRHPGSSSEPSDGP 258

RESULT 14
 090711 PRELIMINARY; PRT; 561 AA.

01-NOV-1996 (TREMBLrel. 01; Created)
 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 01-NOV-1998 (TREMBLrel. 08; Last annotation update)
 AE2-2 ANION EXCHANGER (FRAGMENT).
 AE2.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PROVENTRICULUS (FORESTOMACH);
 RX MEDLINE; 96224107.
 RA COX R.H., ADAIR-KIRK T.L., COX J.V.;
 RT "Variant AE2 anion exchanger transcripts accumulate in multiple cell
 RL types in the chicken gastric epithelium."
 DR J. Biol. Chem. 271:8895-8902(1996).
 EMBL: U48890; AAC59882.1;
 NON_TER 561
 SEQUENCE 561 AA; 61186 MW; D1452E16 CRC32;

Query Match 8.7%; Score 75.5; DB 13; Length 561;
 Best Local Similarity 23.6%; Pred. No. 4.4;
 Matches 45; Conservative 17; Mismatches 66; Indels 63; Gaps 9;

9 RCNPFYIGSKKIGISENSHP-----ASTPRSEPRGCGVCEPRGSGPV----- 61
 22 RVPQSGGVKTA--WIRGAPAPSPAPSPQPEPPAPG-----PASPPAEE 69
 61 RRELKQFLG-----WLKHAICSNLSFRLYDOWRAMOKSHK 97
 70 EKDNLALGVERREELISDAHPSVDEPRITGEEDFEYHROSSLIHPLAHLPPDR 129
 98 TRNOYKLGACVCGKAEEERDPEOP-----OHTLLSKHRTGSCPRAD 145
 130 RKKGVKKRKKRGRALA-----PGENPIEGEEDDEACCTERSAELRGC--PAE 182
 146 GVR-REVRGSG 155
 183 GVOVGEARAG 193

RESULT 15
 044128 PRELIMINARY; PRT; 336 AA.

01-NOV-1996 (TREMBLrel. 01; Created)
 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 01-NOV-1998 (TREMBLrel. 08; Last annotation update)
 PROTEIN A.
 Acetobacter pasteurianus.
 Plasmid pap12875.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 AC Acetobacter.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95309714.
 RA FOMENKOV A., XIAO J.P., XU S.Y.;
 RT "Nucleotide sequence of a small plasmid isolated from Acetobacter
 RL pasteurianus."
 DR Gene 158:143-144(1995).
 EMBL: U20550; AAA86883.1;
 NON_TER 336
 SEQUENCE 336 AA; 36948 MW; CF24DEA4 CRC32;

Query Match 8.7%; Score 75; DB 2; Length 336;
 Best Local Similarity 25.0%; Pred. No. 2.9;
 Matches 49; Conservative 17; Mismatches 82; Indels 48; Gaps 10;

1 GTVFVQVRCNPF-----IYSGKAGIWSF-----WSHPTA 32
 95 GAYFADEAYEAAGPSPAMEHRLVAVWTHLAASIGSK--WSQTVKHITDALGMSQYA 151
 33 ASTPRSEPRGCGVCEPRGSGP-----PRRELKQFLGKKAHAYCSNLSFR 83
 152 KHARGARHIORSCHCPSGMOGOTGMNDKSGVPAEALKEFGMAAYAPRL-MR 210
 84 LYDQWRAMOKSHKTRNOYKLGACVCGKAEEERDPEOP--POHTLLSKHRT--GSC 141
 211 SYNAQARVEENNAARSALVQAQQA--GGTARPTHTSLTSSPNARKTMVREARQSGSA 269

OY 142 ---PRA-DGVREYNG 153
|:| | | |
Db 270 VGOFRKVSRSVRSAAAG 285

Search completed: September 16, 1999, 20:40:08
Job time: 5559 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:14 ; Search time 64.1 Seconds

(without alignments)
102.726 Million cell updates/sec

Title: US-09-037-657-19
Perfect score: 1505
Sequence: 1 PTLIGSSLIATCSIHGDRP.....VFYQVACNPFQIGSKKAG 278

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	100.0	413	1 M55011	Novel haemopoietin
2	1505	100.0	425	1 M55012	Novel haemopoietin
3	1501	99.7	278	1 M55014	Protein sequence o
4	1501	99.7	425	1 M59804	Nucleotide sequenc
5	1500	99.7	385	1 W70841	Human zcyto5 vari
6	1500	99.7	425	1 W70862	Human zcyto5 vari
7	1464	97.2	389	1 W70850	Human zcyto5 protei
8	1463	97.2	408	1 M59805	Human zcyto5 vari
9	1463	97.2	382	1 W70840	Human zcyto5 vari
10	1463	97.2	389	1 W70844	Human zcyto5 vari
11	1463	97.2	303	1 W70845	Human zcyto5 vari
12	1463	97.2	425	1 W70861	Human zcyto5 vari
13	1462	97.1	389	1 W70851	Allelic variant of
14	1461	97.1	389	1 W70852	Human zcyto5 vari
15	1460	97.0	389	1 W70846	Human zcyto5 vari
16	1460	97.0	389	1 W70847	Human zcyto5 vari
17	1460	97.0	389	1 W70849	Human zcyto5 vari
18	1459	96.9	389	1 W70848	Human zcyto5 vari
19	1459	96.9	303	1 W70843	Human zcyto5 vari
20	1459	96.9	422	1 W70860	Human zcyto5 protei
21	1458	96.9	389	1 W70853	Human zcyto5 vari
22	1452	96.5	388	1 W70839	Human zcyto5 vari
23	1452	96.5	385	1 W70842	Human zcyto5 vari
24	1330	87.7	350	1 M55015	Human zcyto5 vari
25	690	45.8	186	1 M55016	Amino acid sequenc
26	308.5	20.5	622	1 R10795	Human zcyto5 vari
27	304	20.2	211	1 R24273	Human zcyto5 vari
28	302	20.1	211	1 R22228	Truncated human pr
29	290	19.3	918	1 R10545	Recombinant human
30	290	19.3	708	1 R37804	Human gp130 N-term
31	290	19.3	708	1 R46233	Human gp130 N-term
32	290	19.3	658	1 R94576	Human soluble glyco
33	290	19.3	918	1 R75368	Human gp130 splice
34	290	19.3	708	1 R85911	Human gp130 N-term
35	290	19.3	329	1 M17859	Human gp130 N-term
36	290	19.3	951	1 W10798	Rheumatoid arthrit
37	290	19.3	332	1 W70799	Human gp130-C-gam
38	290	19.3	859	1 W70796	Human gp130-Fc-His
39	290	19.3	917	1 R26334	Human gp130-Fc-His
40	250.5	16.6	180	1 W00404	gp130. New mouse G
41	233	15.5	630	1 R93120	Interleukin-6 anta
42	233	15.5	606	1 R93121	Tilapia prolactin
43	222	14.8	783	1 R11741	Granulocyte colony

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	M55011	100.0	100.0	413	1 M55011	Novel haemopoietin
2	M55011	100.0	100.0	425	1 M55012	Novel haemopoietin
3	M55011	100.0	100.0	278	1 M55014	Protein sequence o
4	M55011	100.0	100.0	425	1 M59804	Nucleotide sequenc
5	M55011	100.0	100.0	385	1 W70841	Human zcyto5 vari
6	M55011	100.0	100.0	425	1 W70862	Human zcyto5 vari
7	M55011	100.0	100.0	389	1 W70850	Human zcyto5 protei
8	M55011	100.0	100.0	408	1 M59805	Human zcyto5 vari
9	M55011	100.0	100.0	382	1 W70840	Human zcyto5 vari
10	M55011	100.0	100.0	389	1 W70844	Human zcyto5 vari
11	M55011	100.0	100.0	303	1 W70845	Human zcyto5 vari
12	M55011	100.0	100.0	425	1 W70861	Human zcyto5 vari
13	M55011	100.0	100.0	389	1 W70851	Allelic variant of
14	M55011	100.0	100.0	389	1 W70852	Human zcyto5 vari
15	M55011	100.0	100.0	389	1 W70846	Human zcyto5 vari
16	M55011	100.0	100.0	389	1 W70847	Human zcyto5 vari
17	M55011	100.0	100.0	389	1 W70849	Human zcyto5 vari
18	M55011	100.0	100.0	389	1 W70848	Human zcyto5 vari
19	M55011	100.0	100.0	303	1 W70843	Human zcyto5 vari
20	M55011	100.0	100.0	422	1 W70860	Human zcyto5 protei
21	M55011	100.0	100.0	389	1 W70853	Human zcyto5 vari
22	M55011	100.0	100.0	388	1 W70839	Human zcyto5 vari
23	M55011	100.0	100.0	385	1 W70842	Human zcyto5 vari
24	M55011	100.0	100.0	350	1 M55015	Human zcyto5 vari
25	M55011	100.0	100.0	186	1 M55016	Amino acid sequenc
26	M55011	100.0	100.0	622	1 R10795	Human zcyto5 vari
27	M55011	100.0	100.0	211	1 R24273	Human zcyto5 vari
28	M55011	100.0	100.0	211	1 R22228	Truncated human pr
29	M55011	100.0	100.0	918	1 R10545	Recombinant human
30	M55011	100.0	100.0	708	1 R37804	Human gp130 N-term
31	M55011	100.0	100.0	708	1 R46233	Human gp130 N-term
32	M55011	100.0	100.0	658	1 R94576	Human soluble glyco
33	M55011	100.0	100.0	918	1 R75368	Human gp130 splice
34	M55011	100.0	100.0	708	1 R85911	Human gp130 N-term
35	M55011	100.0	100.0	329	1 M17859	Human gp130 N-term
36	M55011	100.0	100.0	951	1 W10798	Rheumatoid arthrit
37	M55011	100.0	100.0	332	1 W70799	Human gp130-C-gam
38	M55011	100.0	100.0	859	1 W70796	Human gp130-Fc-His
39	M55011	100.0	100.0	917	1 R26334	Human gp130-Fc-His
40	M55011	100.0	100.0	180	1 W00404	gp130. New mouse G
41	M55011	100.0	100.0	630	1 R93120	Interleukin-6 anta
42	M55011	100.0	100.0	606	1 R93121	Tilapia prolactin
43	M55011	100.0	100.0	783	1 R11741	Granulocyte colony

Query Match 100.0%; Score 1505; DB 1; Length 413;

Best Local Similarity 100.0%; Pred. No. 8.8e-139;

Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	PTLIGSSLIATCSIHGDRPAGTAEGLYWTNGRRLPSEISRLNTSTLALANLNGSR	60
DB	51	PTLIGSSLIATCSIHGDRPAGTAEGLYWTNGRRLPSEISRLNTSTLALANLNGSR	110
QY	61	QOSGDNLYVCHARDGSIAGCLYVGLPPEKPFNISCWSRNKDLCTCHPAGAGEFLHT	120
DB	111	QOSGDNLYVCHARDGSIAGCLYVGLPPEKPFNISCWSRNKDLCTCHPAGAGEFLHT	170
QY	121	NTSKYKLYRWYGDNDCEHYHTGPHSCHIPKDLAFTPEIVVENTNRIGSARSDVLT	180
DB	171	NTSKYKLYRWYGDNDCEHYHTGPHSCHIPKDLAFTPEIVVENTNRIGSARSDVLT	230
QY	181	DVLDVYTTDPPPVHVSRYVGLDOLSVKRVSPALKDFFOAKYQIRVENVSDVMKVY	240
DB	231	DVLDVYTTDPPPVHVSRYVGLDOLSVKRVSPALKDFFOAKYQIRVENVSDVMKVY	290
QY	241	DVVSNOTSCLAGLKPGTYFVQVRCNPFQIGSKKAG	278
DB	291	DVVSNOTSCLAGLKPGTYFVQVRCNPFQIGSKKAG	328
RESULT	2		
ID	M55012		
AC	M55012	standard; Protein: 425 AA.	

29-SEP-1998 (first entry)
 DE Novel haemopoietin receptor NR6.2 protein.
 KM Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KM cell survival; therapeutic; neuronal proliferation; drug screening;
 KM Mouse.
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997: G02479.
 PR 11-SEP-1996: AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEMSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J.
 DR WPI: 98-260970/23.
 DR N-PSDB: V27141.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 15: Page 84-87: 182pp: English.
 CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 425 AA:

Query Match 100.0%; Score 1505; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 9.2e-139;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRRLPSELRLNTSTALANLNGSR 60
 DB 51 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRRLPSELRLNTSTALANLNGSR 110
 QY 61 QOSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 120
 DB 111 QOSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 170
 QY 121 NYSLKTKLWYQODNCEHYHVGPSCHIPKDLALFTPEIWEATNRLGSRSDVLT 180
 DB 171 NYSLKTKLWYQODNCEHYHVGPSCHIPKDLALFTPEIWEATNRLGSRSDVLT 230
 QY 181 DVLDDVYTTDPPDVHVSRYVGLLEDQLSVRWVSPALKDLPFOAKYQIRRVEDSDVMKYV 240
 DB 231 DVLDDVYTTDPPDVHVSRYVGLLEDQLSVRWVSPALKDLPFOAKYQIRRVEDSDVMKYV 290
 QY 241 DVSNOTSCRLAGLKPRTYFVQVRCNPGIYSKKAG 278
 DB 291 DVSNOTSCRLAGLKPRTYFVQVRCNPGIYSKKAG 328

RESULT 3
 W55014
 ID W55014 standard; Protein: 278 AA.
 AC W55014;
 DT 02-OCT-1998 (first entry)
 DE Protein sequence of products generated by 5N race of brain CDNA.
 KM Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KM cell survival; therapeutic; neuronal proliferation; drug screening;
 KM Mouse.
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997: G02479.
 PR 11-SEP-1996: AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.

(DZIE/) DZIEGLEMSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J.
 DR WPI: 98-260970/23.
 DR N-PSDB: V27143.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 17: Page 93-95: 182pp: English.
 CC The protein sequence was generated by a 5N RACE of brain CDNA using
 CC NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 278 AA:

Query Match 100.0%; Score 1505; DB 1; Length 278;
 Best Local Similarity 100.0%; Pred. No. 5e-139;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRRLPSELRLNTSTALANLNGSR 60
 DB 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRRLPSELRLNTSTALANLNGSR 60
 QY 61 QOSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 120
 DB 121 NYSLKTKLWYQODNCEHYHVGPSCHIPKDLALFTPEIWEATNRLGSRSDVLT 180
 QY 181 DVLDDVYTTDPPDVHVSRYVGLLEDQLSVRWVSPALKDLPFOAKYQIRRVEDSDVMKYV 240
 DB 181 DVLDDVYTTDPPDVHVSRYVGLLEDQLSVRWVSPALKDLPFOAKYQIRRVEDSDVMKYV 240
 QY 241 DVSNOTSCRLAGLKPRTYFVQVRCNPGIYSKKAG 278
 DB 241 DVSNOTSCRLAGLKPRTYFVQVRCNPGIYSKKAG 278

RESULT 4
 W59804
 ID W59804 standard; Protein: 425 AA.
 AC W59804;
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of the murine U4 protein.
 KM Murine U4 protein; haemopoietin receptor superfamily;
 KM cell proliferation; immune response; antibody; cell differentiation;
 KM autoimmune disease; cancer; allergy.
 OS Mus sp.
 PN MO9831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998: U00334.
 PR 16-JAN-1997: U5-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M,
 DR WPI: 98-414109/35.
 DR N-PSDB: V41688.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and auto-immune disease
 PS Claim 9: Pages 26-27: 38pp: English.
 CC This is the amino acid sequence of the murine U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune

CC response. Transformed mammalian cells are used to produce recombinant
CC u4 protein. The u4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
CC Sequence 425 AA;

Query Match 99.7%; Score 1501; DB 1; Length 425;
Best Local Similarity 99.6%; Pred. No. 2.3e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTISSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
DB 51 PTLTISSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 110
QY 61 QOSGDLVCHARGSILASCLYVGLPPEKPFNISCMSRMKDLTCRMTGAGETFLHT 120
DB 111 QOSGDLVCHARGSILASCLYVGLPPEKPFNISCMSRMKDLTCRMTGAGETFLHT 170
QY 121 NYSLKTKLRMYGQDNTCEEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDYTL 180
DB 171 NYSLKTKLRMYGQDNTCEEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDYTL 230
QY 181 DVLDVYTTDPPPPVHVSRYGGLDQLSVKWSPPALKDFLFOAKYQIRYVEDSDVMKVV 240
DB 231 DVLDVYTTDPPPPVHVSRYGGLDQLSVKWSPPALKDFLFOAKYQIRYVEDSDVMKVV 290
QY 241 DVYSNOTSCLAGLKPQTYEYVQVRCNPFGIYSGKRG 278
DB 291 DVYSNOTSCLAGLKPQTYEYVQVRCNPFGIYSGKRG 328

RESULT 5
W70841 standard; Protein: 385 AA.
W70841:
AC 17-MAR-1999 (first entry)
DE Human Zcyto5 variant.
KM Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
PN WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 83-84; 55pp; English.

CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 385 AA;

Query Match 99.7%; Score 1500; DB 1; Length 385;
Best Local Similarity 99.6%; Pred. No. 2.5e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTISSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
DB 11 PTLTISSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 70
QY 61 QOSGDLVCHARGSILASCLYVGLPPEKPFNISCMSRMKDLTCRMTGAGETFLHT 120
DB 71 QOSGDLVCHARGSILASCLYVGLPPEKPFNISCMSRMKDLTCRMTGAGETFLHT 130
QY 121 NYSLKTKLRMYGQDNTCEEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDYTL 180
DB 131 NYSLKTKLRMYGQDNTCEEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDYTL 190
QY 181 DVLDVYTTDPPPPVHVSRYGGLDQLSVKWSPPALKDFLFOAKYQIRYVEDSDVMKVV 240
DB 191 DVLDVYTTDPPPPVHVSRYGGLDQLSVKWSPPALKDFLFOAKYQIRYVEDSDVMKVV 250
QY 241 DVYSNOTSCLAGLKPQTYEYVQVRCNPFGIYSGKRG 278
DB 251 DVYSNOTSCLAGLKPQTYEYVQVRCNPFGIYSGKRG 288

RESULT 6
W70862 standard; Protein: 425 AA.
W70862:
AC 17-MAR-1999 (first entry)
DE Rat Zcyto5 protein.
KM Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand.
OS Rattus sp.
PN WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 75-76; 55pp; English.

CC The present sequence represents a protein designated Zcyto5, which is
CC a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 425 AA;

Query Match 99.7%; Score 1500; DB 1; Length 425;
Best Local Similarity 99.6%; Pred. No. 2.8e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTISSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
|||||

Db 51 PTLIGSSLATGSIHSDTPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 110
QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 120
Db 111 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 170
QY 121 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 180
Db 171 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 230
QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 240
Db 231 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 290
QY 241 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 278
Db 291 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 328

RESULT 7
W70850 standard; Protein: 389 AA.
AC W70850:
DT 17-MAR-1999 (first entry)
DE Human zcyto5 variant.
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
OS Homo sapiens.
PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; 008865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1: Page 95-96; 55pp; English.
CC The present sequence represents a zcyto5 variant protein. zcyto5
CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 389 AA;

Query Match 97.38; Score 1464; DB 1; Length 389;
Best Local Similarity 96.88; Pred. No. 8.1e-135;
Matches 268; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATGSIHSDTPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 60
Db 11 PTLIGSSLATGSIHSDTPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 70
QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 120
Db 71 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 130
QY 121 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 180
Db 131 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 190

QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 240
Db 191 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 250
QY 241 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 278
Db 251 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 288

RESULT 8
W59805 standard; Protein: 408 AA.
AC W59805:
DT 26-OCT-1998 (first entry)
DE Amino acid sequence of the human U4 protein.
KW Human; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy.
OS Homo sapiens.
PN WO9831811-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;
PI WPI: 98-41409/35.
DR N-PSDB: V41689.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and autoimmune disease
PS Claim 9; Pages 29-30; 38pp; English.
CC This is the amino acid sequence of the human U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 408 AA;

Query Match 97.28; Score 1463; DB 1; Length 408;
Best Local Similarity 96.48; Pred. No. 1.1e-134;
Matches 268; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATGSIHSDTPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 60
Db 34 PTLIGSSLATGSIHSDTPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 93
QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 120
Db 94 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMTPGAGETFLHT 153
QY 121 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 180
Db 154 NYSLKTKLRMYGODNTCEEYHTVGPSPCHIPKDLAFTPEIWEATNRLGARSVDLT 213
QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 240
Db 214 DVLAVYTTDPPDPVHVSRYVGLLEDQLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKVY 273
QY 241 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 278
Db 274 DVVSNQTSCLAGLKPRTYFVQVRCNPFGIYSKRAK 311

RESULT 9
W70840

ID W70840 standard; Protein; 392 AA.
 AC W70840;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 392 AA;

Query Match 97.2%; Score 1463; DB 1; Length 392;
 Best Local Similarity 96.4%; Pred. No. 1e-134; 5; Indels 0; Gaps 0;
 Matches 268; Conservative 5; Mismatches 5;

QY 1 PTLIGSSLATGCSIHGDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 60
 DB 14 PTLIGSSLATGCSVHDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 73
 QY 61 QOSGDNLYCHARGSLIAGSLYGLPEKPFNISCMSRNMKDLTCMTGAGETFLHT 120
 DB 74 QOSGDNLYCHARGSLIAGSLYGLPEKPFNISCMSRNMKDLTCMTGAGETFLHT 133
 QY 121 NYSIKYLRMYGDNCEEHYVGPBSCHPKDLALFTPEIWEATNRLGARSVDLTL 180
 DB 134 NYSIKYLRMYGDNCEEHYVGPBSCHPKDLALFTPEIWEATNRLGARSVDLTL 193
 QY 181 DVIDVYTTDPPDVHVSRRVGLDQLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKVY 240
 DB 194 DVIDVYTTDPPDVHVSRRVGLDQLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKVY 253
 QY 241 DDVSNOTSCLAGLKGRTYVFOVRCNPFGIYSKRAG 278
 DB 254 DDVSNOTSCLAGLKGRTYVFOVRCNPFGIYSKRAG 291

RESULT 10
 ID W70844
 AC W70844 standard; Protein; 389 AA.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.

PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA;

Query Match 97.2%; Score 1463; DB 1; Length 389;
 Best Local Similarity 96.4%; Pred. No. 1e-134; 5; Indels 0; Gaps 0;
 Matches 268; Conservative 5; Mismatches 5;

QY 1 PTLIGSSLATGCSIHGDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATGCSVHDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARGSLIAGSLYGLPEKPFNISCMSRNMKDLTCMTGAGETFLHT 120
 DB 71 QOSGDNLYCHARGSLIAGSLYGLPEKPFNISCMSRNMKDLTCMTGAGETFLHT 130
 QY 121 NYSIKYLRMYGDNCEEHYVGPBSCHPKDLALFTPEIWEATNRLGARSVDLTL 180
 DB 131 NYSIKYLRMYGDNCEEHYVGPBSCHPKDLALFTPEIWEATNRLGARSVDLTL 190
 QY 181 DVIDVYTTDPPDVHVSRRVGLDQLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKVY 240
 DB 191 DVIDVYTTDPPDVHVSRRVGLDQLSVRWVSPALKDFLFOAKYQIRYVEDSVDMKVY 250
 QY 241 DDVSNOTSCLAGLKGRTYVFOVRCNPFGIYSKRAG 278
 DB 251 DDVSNOTSCLAGLKGRTYVFOVRCNPFGIYSKRAG 288

RESULT 11
 ID W70845
 AC W70845 standard; Protein; 303 AA.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;

DR WPI: 99-034662/03.
 PR New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 88-89; 55pp; English.
 CC The present sequence represents a Zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble Zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SO Sequence 303 AA.

Query Match 97.2%; Score 1463; DB 1; Length 303;
 Best Local Similarity 96.4%; Pred. No. 7e-135;
 Matches 268; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 1 PILLIGSSLOATCSHGDTPGATAGLWTLNGRLPSELRLNTSLATLALANLNGSR 60
 11 PILLIGSSLOATCSHGDTPGATAGLWTLNGRLPSELRLNTSLATLALANLNGSR 70
 OY 61 QOSGDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSWRNKKDLTCRMTPGAHGETFLHT 120
 DB 71 QRSQDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSWRNKKDLTCRMTPGAHGETFLHT 130
 OY 121 NYSLKXKLRTWYGQDNTCEHYHTVGPCHIRKDLALFTPEIWEATNRLSARSADVTL 180
 DB 131 NYSLKXKLRTWYGQDNTCEHYHTVGPCHIRKDLALFTPEIWEATNRLSARSADVTL 190
 OY 181 DVLVYTTDPPDVHVSNGLEDDLSVRWSPPALKDFLQAKQIIRVEDSDVMKRV 240
 DB 191 DILVYTTDPPDVHVSNGLEDDLSVRWSPPALKDFLQAKQIIRVEDSDVMKRV 250
 OY 241 DDVSNQTSCLAGLKPCTVYFVQVRCNPFGIYGSKKAG 278
 DB 251 DDVSNQTSCLAGLKPCTVYFVQVRCNPFGIYGSKKAG 288

RESULT 12
 W70861
 ID W70861 standard; Protein; 425 AA.
 AC W70861;
 DT 17-MAR-1999 (first entry)
 DE Allelic variant of human Zcytors.
 KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcytors ligand; allelic variant.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; US-08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 71-72; 55pp; English.
 CC The present sequence represents an allelic variant of protein designated
 CC Zcytors, which is a cytokinin-like receptor. Soluble Zcytors may be
 CC administered to down-regulate the effects of a growth and/or maintenance

CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SO Sequence 425 AA.

Query Match 97.2%; Score 1463; DB 1; Length 425;
 Best Local Similarity 96.4%; Pred. No. 1.1e-134;
 Matches 268; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 1 PILLIGSSLOATCSHGDTPGATAGLWTLNGRLPSELRLNTSLATLALANLNGSR 60
 47 PILLIGSSLOATCSHGDTPGATAGLWTLNGRLPSELRLNTSLATLALANLNGSR 106
 OY 61 QOSGDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSWRNKKDLTCRMTPGAHGETFLHT 120
 DB 107 QRSQDNLYCHARDGSIILAGSCLYGLPEPEKPNISCSWRNKKDLTCRMTPGAHGETFLHT 166
 OY 121 NYSLKXKLRTWYGQDNTCEHYHTVGPCHIRKDLALFTPEIWEATNRLSARSADVTL 180
 DB 167 NYSLKXKLRTWYGQDNTCEHYHTVGPCHIRKDLALFTPEIWEATNRLSARSADVTL 226
 OY 181 DVLVYTTDPPDVHVSNGLEDDLSVRWSPPALKDFLQAKQIIRVEDSDVMKRV 240
 DB 227 DILVYTTDPPDVHVSNGLEDDLSVRWSPPALKDFLQAKQIIRVEDSDVMKRV 286
 OY 241 DDVSNQTSCLAGLKPCTVYFVQVRCNPFGIYGSKKAG 278
 DB 287 DDVSNQTSCLAGLKPCTVYFVQVRCNPFGIYGSKKAG 324

RESULT 13
 W70851
 ID W70851 standard; Protein; 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)
 DE Human Zcytors variant.
 KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcytors ligand; variant.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; US-08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a Zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble Zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SO Sequence 389 AA.

Query Match 97.1%; Score 1462; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 1.3e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 180
 DB 131 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 190
 QY 181 DVLDTVTDDPPDVHVSRYVSGLELDLSYRWVSPPALKDFLFOAKYQIRYVEDSYDMKVV 240
 DB 191 DILDVTTDDPPDVHVSRYVSGLELDLSYRWVSPPALKDFLFOAKYQIRYVEDSYDMKVV 250
 QY 241 DDVSNQTSCLAGLKPQYTYVQVRCNPFGIYGSKKAG 278
 DB 251 DDVSNQTSCLAGLKPQYTYVQVRCNPFGIYGSKKAG 288

RESULT 14

W70852
 ID W70852 standard; Protein; 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 cardiac pathology; heart enlargement; zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998
 PR 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.,
 PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and the
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 97.1%; Score 1461; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 1.6e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 70

QY 61 QOSGDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 180
 DB 131 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 190
 QY 181 DVLDTVTDDPPDVHVSRYVSGLELDLSYRWVSPPALKDFLFOAKYQIRYVEDSYDMKVV 240
 DB 191 DILDVTTDDPPDVHVSRYVSGLELDLSYRWVSPPALKDFLFOAKYQIRYVEDSYDMKVV 250
 QY 241 DDVSNQTSCLAGLKPQYTYVQVRCNPFGIYGSKKAG 278
 DB 251 DDVSNQTSCLAGLKPQYTYVQVRCNPFGIYGSKKAG 288

RESULT 15

W70846
 ID W70846 standard; Protein; 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 cardiac pathology; heart enlargement; zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998
 PR 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.,
 PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 89-90; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and the
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 97.0%; Score 1460; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 2e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLRRLPSELRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDOSIILAGSCLTYGLPPEKPNISCSNKKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 180
 DB 131 NYSLKYLKRWYGODNTECEHYHTVGPCHSHPKDLALFTPEYIWEATNRLGSARSVDYLT 190

OY 181 DVLDTTDPDPDVHVSRLGLEDOLSVRWSPPALNDLFOAKYQIRRVEDSVDMKV 240
DB 191 DILDVTTDPDPDVHVSRLGLEDOLSVRWSPPALNDLFOAKYQIRRVEDSVDMKV 250
OY 241 DDVSNQTSCLAGLPGTVYFVQVRCNPFGLYGSKKAG 278
DB 251 DDVSNQTSCLAGLPGTVYFVQVRCNPFGLYGSKKAG 288

Search completed: September 17, 1999, 03:08:15
Job time: 306 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:08 ; Search time 53.94 seconds

(without alignments)
50.860 Million cell updates/sec

ALIGNMENTS

40	135.5	9.0	888	1	US-08-445-640-35	Sequence 35, Appl
41	134	8.9	229	2	US-08-684-687-2	Sequence 2, Appl
42	133.5	8.9	719	1	US-07-943-843-4	Sequence 4, Appl
43	133.5	8.9	719	2	US-08-347-003-4	Sequence 4, Appl
44	133.5	8.9	1452	2	US-08-652-971-4	Sequence 4, Appl
45	132	8.8	230	3	PCT-US93-09636-6	Sequence 6, Appl

Title: US-09-037-657-19

Sequence: 1505

Sequence: 1 PTLIGSSLOATCSIHGDP.....VYFVQVRCNPFQYKSKKG 278

Scoring table: BLOSUM62

Searched: 106577 seqs, 986381 residues

Database:

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/PCTUS9.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	19.3	708	1	US-07-797-556-2
2	290	19.3	708	1	US-08-308-881-2
3	290	19.3	708	3	PCT-US95-06530-2
4	222	14.8	836	1	US-07-923-976-4
5	222	14.8	771	1	US-07-923-976-6
6	222	14.8	863	1	US-07-923-976-8
7	221.5	14.7	837	1	US-07-923-976-2
8	199	13.2	602	2	US-08-419-653-6
9	184	12.2	572	2	US-08-419-653-5
10	178	11.8	862	2	US-08-685-118-2
11	178	11.8	862	2	US-08-915-495-2
12	172.5	11.5	372	1	US-07-865-878A-4
13	172.5	11.5	372	1	US-07-676-647-2
14	172.5	11.5	372	1	US-08-449-329-2
15	172.5	11.5	372	2	US-08-445-073-2
16	172.5	11.5	372	3	PCT-US91-03896-2
17	166	11.0	635	1	US-08-184-327A-4
18	166	11.0	635	3	PCT-US95-00670-4
19	165.5	11.0	633	1	US-08-250-859-17
20	165.5	11.0	633	1	US-08-490-803-17
21	165.5	11.0	633	3	PCT-US94-08806-17
22	165.5	11.0	633	3	PCT-US95-01775-17
23	165.5	11.0	633	3	PCT-US95-16626-7
24	159.5	10.6	626	1	US-08-184-327A-2
25	159.5	10.6	482	1	PCT-US95-00670-8
26	159.5	10.6	626	3	PCT-US95-00670-8
27	159.5	10.6	482	3	PCT-US95-00670-8
28	147.5	9.8	1001	1	US-07-797-556-6
29	147.5	9.8	1001	1	US-07-943-843-6
30	147.5	9.8	1097	1	US-07-943-843-6
31	147.5	9.8	1097	2	US-08-347-003-2
32	147.5	9.8	1097	2	US-08-347-003-6
33	146	9.7	569	1	US-08-306-231-3
34	146	9.7	569	2	US-08-355-888A-8
35	146	9.7	960	2	US-08-693-697-8
36	146	9.7	908	2	US-08-693-697-33
37	146	9.7	908	2	US-08-693-697-36
38	145	9.6	908	2	US-08-588-526-3
39	141	9.4	960	2	US-08-588-190-3

RESULT 1
US-07-797-556-2
Sequence 2, Application US/07/97556

Patent No. 5262522

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia

NUMBER OF SEQUENCES: 17

INVENTOR: Inhibitory Factor

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/797,556

FILING DATE: 19911122

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2607

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 708 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-797-556-2

Query Match

Best Local Similarity 28.38; Pred. No. 1.2e-21;

Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY	1	PTLIGSSLOATCSIHG---DPTGATAGLWTLNGRRLSELSTLALALANL	57
DB	36	PVVOHSHNFANVCYKEKCMDFHNNANTYWKTNHFTPEQYITINRTASSVFTDIA	95
QY	58	GSROOQGNLVCHADGSIILAGSCLYVGLPEPEKPNISCSWRNMKDLTCRWTPGAGETP	117
DB	96	SLNIGLTNLTLEFGLQENYGITISLPEKPNISCIYNEGKMKCEMDGGR--ETH	153
QY	118	LATNLSLKYLKRWQGDTCGEYHVGPHSCHIRDLALFTPEYIWEATRLRSARSDV	177
DB	134	LETNLTLSKEMATNHFACCKARDT--PTSCYDYSTVYFVNIEVWEAENALGKVS	211
QY	178	LTIDVLDVYTDPPDVSVRGLEQLSVRWSPPLKDFLQAVQIQRVEDSDV	237
DB	212	INFDVYVKNRPNPNLSVITSEISLTKLTWTN-PSIKSVII-LATINIQYRKVDASTW	269
QY	238	KVY---DDVSNQTSRGLGRLGTYFVQVRC	266

DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIC 301

RESULT 2

US-08-308-881-2

Sequence 2, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 708 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-308-881-2

Query Match 19.3%; Score 290; DB 2; Length 708;
Best Local Similarity 28.3%; Pred. No. 1.2e-21;
Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY 1 PTLIGSSLOATCSIHG---DTGATAGLTYTLNGRRLPSELRLNTSLALANLN 57
DB 36 PVOQLHSNFTAVCVLKEKCMDFHVNNAYIWKTNHFTIKRQYTIINRTASSVTFDIA 95
QY 58 GSRQSGDNVCHARGDSILAGSCLVGLPPEKPFNISCWSRNKKDLTCWTGARGETF 117
DB 96 SLNIQLCNLTITGQLEONYGTTISGLPEKPKMLSCIVNKGKRCMDGR--ETH 153
QY 118 LHTNYSKYLKRWYGODNTECEHYTVGPHSCHIPKDLALFTPEIWEATNRIGSARSDV 177
DB 154 LETNFTLKSEWATHKFADCKAKRDT--PTSCVDYSTVYFVNIEVWEAENALGKVTSDH 211
QY 178 LITDLVDVYTTDPPDPVHVSVRVGLLEQDLSVRVSPALKDFLEQAKYQIRYVEDSDV 237
DB 212 INFDPYKVKPNPNNHNSVINSSELSILKLTWTN-PSISVYI-LKYNIQYRTKASTW 269
QY 238 KVV---DVSNOTSCRLAGLKGFTGVYVOVRC 266
DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIC 301

RESULT 3

PCT-US95-06530-2

Sequence 2, Application PC/TUS9506530

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06530

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,881

FILING DATE: 09-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 708 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-06530-2

Query Match 19.3%; Score 290; DB 3; Length 708;
Best Local Similarity 28.3%; Pred. No. 1.2e-21;
Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY 1 PTLIGSSLOATCSIHG---DTGATAGLTYTLNGRRLPSELRLNTSLALANLN 57
DB 36 PVOQLHSNFTAVCVLKEKCMDFHVNNAYIWKTNHFTIKRQYTIINRTASSVTFDIA 95
QY 58 GSRQSGDNVCHARGDSILAGSCLVGLPPEKPFNISCWSRNKKDLTCWTGARGETF 117
DB 96 SLNIQLCNLTITGQLEONYGTTISGLPEKPKMLSCIVNKGKRCMDGR--ETH 153
QY 118 LHTNYSKYLKRWYGODNTECEHYTVGPHSCHIPKDLALFTPEIWEATNRIGSARSDV 177
DB 154 LETNFTLKSEWATHKFADCKAKRDT--PTSCVDYSTVYFVNIEVWEAENALGKVTSDH 211
QY 178 LITDLVDVYTTDPPDPVHVSVRVGLLEQDLSVRVSPALKDFLEQAKYQIRYVEDSDV 237
DB 212 INFDPYKVKPNPNNHNSVINSSELSILKLTWTN-PSISVYI-LKYNIQYRTKASTW 269
QY 238 KVV---DVSNOTSCRLAGLKGFTGVYVOVRC 266
DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIC 301

RESULT 4

US-07-923-976-4
 ; Sequence 4, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullar & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923.976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP91/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 514853
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1508
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 836 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-923-976-4

Query Match 14.88; Score 222; DB 1; Length 836;
 Best Local Similarity 29.28; Pred. No. 1.5e-14;
 Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

QY 1 PTLIGSSLOATCSHGTPGTAEGLYTLNGRRRLPSELRLN--TSTLALANLN 57
 DB 34 PIVHGDITTSKIKKNSHLDPPQILMRGALPGRGQRSDGQESITLPHLN 93
 QY 58 GSROOSGDNLYCHADGS---ILAGSCLYVGLPPKRPENISC-WSRNNKMDLTCRWTPGAH 113
 DB 94 HTQA---FLSCCLMNGMSLQILDVELRAGYPAIPHNLSCLMLTSSLSLCOHEPGR- 149
 QY 114 GETFLHTVYSK-YLTRYGQ---DNCEEHYTVGPHSCHIP-KDLAFTPEYIWEATN 168
 DB 149 -ETHLPSTFTLKSFRKNCQOGSILDCVPRKQSHCCIPRKHLLLYQNMGIWQAE 207
 QY 169 RLGSARSDVLTLDVAVY-----TDPDPDVHVSRRVGGLEDOLSVRWVSPALKNFL 220
 DB 208 ALGISMSPQLCLDPRDVKLEPPLKRTMDPSPEAPRQAGCQ---LCW--EPWQPGH 261
 QY 221 FOAKYQIRYVE-DSVDMKVVDVSNQT-SCRLAGLKPQTVYFVQVRC 266
 DB 262 INOKELHKKPRGSEASWALVGPLLEALQYELCGILPATATTLQIR 309

RESULT 5
 US-07-923-976-6
 ; Sequence 6, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullar & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923.976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP91/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 514853
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1508
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-923-976-6

Query Match 14.88; Score 222; DB 1; Length 771;
 Best Local Similarity 29.28; Pred. No. 1.4e-14;
 Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

QY 1 PTLIGSSLOATCSHGTPGTAEGLYTLNGRRRLPSELRLN--TSTLALANLN 57
 DB 34 PIVHGDITTSKIKKNSHLDPPQILMRGALPGRGQRSDGQESITLPHLN 93
 QY 58 GSROOSGDNLYCHADGS---ILAGSCLYVGLPPKRPENISC-WSRNNKMDLTCRWTPGAH 113
 DB 94 HTQA---FLSCCLMNGMSLQILDVELRAGYPAIPHNLSCLMLTSSLSLCOHEPGR- 149
 QY 114 GETFLHTVYSK-YLTRYGQ---DNCEEHYTVGPHSCHIP-KDLAFTPEYIWEATN 168
 DB 149 -ETHLPSTFTLKSFRKNCQOGSILDCVPRKQSHCCIPRKHLLLYQNMGIWQAE 207
 QY 169 RLGSARSDVLTLDVAVY-----TDPDPDVHVSRRVGGLEDOLSVRWVSPALKNFL 220
 DB 208 ALGISMSPQLCLDPRDVKLEPPLKRTMDPSPEAPRQAGCQ---LCW--EPWQPGH 261
 QY 221 FOAKYQIRYVE-DSVDMKVVDVSNQT-SCRLAGLKPQTVYFVQVRC 266

Db 262 INOKELRHKFORGEASWALVGPLLEALQYELGCLLPATAYTLCIRC 309

RESULT 6

US-07-923-976-8
Sequence 8, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 863 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-8

Query Match 14.8%; Score 222; DB 1; Length 863;

Best Local Similarity 29.2%; Pred. No. 1.6e-14;

Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

Db 1 PTLIGSSLOATCSIHGDPGTATAG-GLWTNGRRLPSELRL--NSTLALANL 57

Db 34 PIVHLDGPITASCITIKONCHLDEPQITRLAELOPGROQLSDGTOESTITLPHN 93

Db 58 GSROSGDNLYCHARDG--ILAGSLVYGLPERPFNIS-WSRNMDDLTCRWTPGAH 113

Db 94 HTQA---FLSCGLNMGNSLQILIDYELRAGYPPALPHNLSCLMNTTSLICQWEPGP 149

Db 114 GEFPLHNTSLK-YKLRTYG--DNTCEYHNVGPHSCHIP-KDLALFTPEYIWEATNL 168

Db 149 -EHLPLSFILKSFKSGKNCOTGDSILDCVPRDGSHCICPRKHLILYONMGIWQAEH 207

Db 169 RLGSARSDELTLVDLVV-----TTDPDPVHVSRYGGLDEQLSVRYVSPALKDLF 220

Db 208 ALGTSMSPOLCLDPMVYKLEPPALRTMDSPEAAPPQACLO---LCW--EPWPGGLH 261

QY 221 FOAKYQIRYVE-DSVDMKVVYDVSNOT-SCRLAGKAGTYFPQVRC 266

RESULT 7

US-07-923-976-2
Sequence 2, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-2

Query Match 14.7%; Score 221.5; DB 1; Length 837;

Best Local Similarity 28.9%; Pred. No. 1.7e-14;

Matches 83; Conservative 46; Mismatches 127; Indels 31; Gaps 14;

QY 1 PTLIGSSLOATCSIHGDPGTATAG-LYWTNGRRL-PSELRL--NSTLALANL 56

Db 34 PIVHLDGPITASCITIPNSCKLDQAKILMRQDEPIQGDQHHLPDQTOESLITLPHL 93

Db 57 NSROSGDNLYCHARDG--ILAGSLVYGLPERPFNISQWR-NMKDLTCRWTPGAH 115

Db 94 HT-QLFELVPMWEDSVOLLDQAEIHAGYPPASFSNLSCLMHLTTNSLYCQWEPGP-E 150

Db 116 TELHNTSLK-YKLRTY--WYGDNTCEYHNVGPHSCHIP-KDLALFTPEYIWEATNL 170

Db 151 TELPISFILKSFKSGKNCOTGDSILDCVPRDGSHCICPRKHLILYONMGIWQAEH 210

QY 171 GSARSDELTLVDLVV-----PDVHVSRYGGLDEQLSVRYVSPALKDLF 221

Db 211 GSSESPKCLDPMDVVKLEPMLQALDGPVVSHPGCL-----WLSMKPMSSEYM 263
 QY 222 OAKTOIRYRVE-DSVDMKVYVDV-SNOTSCLAGLKPGTYFYOVRC 266
 Db 264 EDCCELRYPOLKGNMTLVFHLPSKDFELCGLHQAFTYTLQMR 310

RESULT 8

US-08-419-652-6
 ; Sequence 6, Application US/08419652
 ; Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: Chua, Anne O
 APPLICANT: Gubler, Ulrich A
 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,652
 FILING DATE: 11-APR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,532
 FILING DATE: 31-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/094,713
 FILING DATE: 19-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kass, Alan P
 REGISTRATION NUMBER: 32142
 REFERENCE/DOCKET NUMBER: CD 9174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-4205
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 602 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..602
 OTHER INFORMATION: /note- "Represents residues 98 to
 OTHER INFORMATION: 731 of human granulocyte colony-stimulating
 factor-receptor."
 US-08-419-652-6

Query Match 13.2%; Score 199; DB 2; Length 602;
 Best Local Similarity 32.1%; Pred. No. 2.2e-12;
 Matches 63; Conservative 28; Mismatches 81; Indels 24; Gaps 10;

QY 87 PEKPFNISC-WSRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYQ--DNTCEEYH 141
 Db 3 PPAIPNLSCLMNLITSSILCOWEPGP--ETHLPSTFLKSFSGRCQCGSGSIIDCV 60
 QY 142 TVGPHSCHLP-KDLALFTPEIWEATNRIGSARSVDLTLDVIVV-----TTDPPP 192
 Db 61 KGGOSHCCIPRKHLLTYQNNGIWVQAEMLGTSMSPOLCLDPMDVVKLEPMLRTMDPSP 120
 QY 193 DVHVSNGGLEQLSVRWVSPALKDPLFOAKTOIRYRVE-DSVDMKVYVDVSNQ-SCR 250

Db 121 EAAFPAGGLQ-----LCW--EPWQPLHINQCELRHKQRGASNAALVGPLPLELOYE 174
 QY 251 LAGLPGTYFYOVRC 266
 Db 175 LCGLLPATATVTLQIRC 190

RESULT 9

US-08-419-652-5
 ; Sequence 5, Application US/08419652
 ; Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: Chua, Anne O
 APPLICANT: Gubler, Ulrich A
 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,652
 FILING DATE: 11-APR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,532
 FILING DATE: 31-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/094,713
 FILING DATE: 19-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kass, Alan P
 REGISTRATION NUMBER: 32142
 REFERENCE/DOCKET NUMBER: CD 9174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-4205
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 572 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..572
 OTHER INFORMATION: /note- "Represents residues 124 to
 OTHER INFORMATION: 742 of human gp130."
 US-08-419-652-5

Query Match 12.2%; Score 184; DB 2; Length 572;
 Best Local Similarity 27.2%; Pred. No. 7.3e-11;
 Matches 50; Conservative 21; Mismatches 59; Indels 54; Gaps 5;

QY 86 LPEKPFNISCWSRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYQ--DNTCEEYH 145
 Db 1 LPEKPFNISCWSRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYQ--DNTCEEYH 145
 QY 146 HSCHEPKDLALFTPEIWEATNRIGSARSVDLTLDVIVV-----TTDPPP 192
 Db 57 TSCOTVSYVYEVNIEWVQAEMLGTSMSPOLCLDPMDVVKLEPMLRTMDPSP 120
 QY 206 LSVRWVSPALKDPLFOAKTOIRYRVE-DSVDMKVYVDVSNQ-SCR 250

Db 91 -----FOYRTRKASTWQIPEDASTSSFTYVDLKPFTYEVF 129
QY 263 QVRC 266
Db 130 RIRC 133

RESULT 10
US-08-685-118-2
Sequence 2, Application US/08685118
Patent No. 5840530
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2863
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 11.8%; Score 178; DB 2; Length 862;
Best Local Similarity 24.8%; Pred. No. 5.5e-10;
Matches 73; Conservative 43; Mismatches 106; Indels 72; Gaps 12;

QY 3 LIGSSLAATCSIHGDTGATAEGLYWTL-----NGRRLPSELRL-L 44
Db 41 ILGSTVNIITCSL-----KPRGCFHYSRRNKLILYKFDRIHFHGHSLNSQVGTGLP 94
QY 45 NTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYGLPPEKPFNISCMSRNK-D 103
Db 95 GTTFVCKLACTINSDEIO-----ICGAELFVGVAPEQPONLSICIQGEGGT 140
QY 104 LTCRWTPGAGETFLHTNYSKY-----KLRYWQ--DNTCEHYTVG-----PHSCHI 150
Db 141 VACTWERGR--DTHLYETYLQLSGPNLWQKCKDIYC-DYLDGFINLTPESPESNFT 197
QY 151 PKDLALFPYEIWEATNRLGSASDVLTLDVLYTTDPPPDVHVSRYGLEDQLSVRW 210
Db 198 AK-----VTAVNSLSSSSLSSTFTFLDIYRPLPPMDIRIKOKASVSRCITLYW 246
QY 211 VSPPALKDFLFOAKYQIRYVEDSDMKVYVDVNSQTSCLAGLKPCTVYFVQY 264
Db 247 -----RDGGLVNLNRLRIRPSNRLMNMVNTAKGRHDLIDLKPFTEYEFQI 294

RESULT 11
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2863
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 11.8%; Score 178; DB 2; Length 862;
Best Local Similarity 24.8%; Pred. No. 5.5e-10;
Matches 73; Conservative 43; Mismatches 106; Indels 72; Gaps 12;

QY 3 LIGSSLAATCSIHGDTGATAEGLYWTL-----NGRRLPSELRL-L 44
Db 41 ILGSTVNIITCSL-----KPRGCFHYSRRNKLILYKFDRIHFHGHSLNSQVGTGLP 94
QY 45 NTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYGLPPEKPFNISCMSRNK-D 103
Db 95 GTTFVCKLACTINSDEIO-----ICGAELFVGVAPEQPONLSICIQGEGGT 140
QY 104 LTCRWTPGAGETFLHTNYSKY-----KLRYWQ--DNTCEHYTVG-----PHSCHI 150
Db 141 VACTWERGR--DTHLYETYLQLSGPNLWQKCKDIYC-DYLDGFINLTPESPESNFT 197
QY 151 PKDLALFPYEIWEATNRLGSASDVLTLDVLYTTDPPPDVHVSRYGLEDQLSVRW 210
Db 198 AK-----VTAVNSLSSSSLSSTFTFLDIYRPLPPMDIRIKOKASVSRCITLYW 246
QY 211 VSPPALKDFLFOAKYQIRYVEDSDMKVYVDVNSQTSCLAGLKPCTVYFVQY 264
Db 247 -----RDGGLVNLNRLRIRPSNRLMNMVNTAKGRHDLIDLKPFTEYEFQI 294

RESULT 12
US-07-865-878A-4
Sequence 4, Application US/07865878A

Patent No. 5332672
GENERAL INFORMATION:
APPLICANT: Yancopoulos, George D. et al.
TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
Factor/Receptor Complex
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,878A
FILING DATE: 19911202
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/801/562
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-082
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-865-878A-4

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;
QY 5 IGSSLAQCSIHGDIPGATAGELVTLNGRRLPSELSRLNTSTLALANNGSRQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSQLV-----LHGELGHS 84
QY 65 DNLYVCHARDGSLIAGS-CLYVGLPPEKPFNISCWSRNM-KDLTCRW-----TGAGGE 115
DB 85 GLYACFHHDSWHLRQVLLHVLGFLPPREP-VLSCRSNTYKGYCSNHLPTPIYINTFN 143
QY 116 TELHTNYSIKYKLRMYGDNQCEEYHTVGPCHSHPKDLALFT--PYELWEATNRLGSA 173
DB 144 TVLHRSKIM-----VCEKDPAL-KNRCHT-RYWHLPSTIKYKVISVSNALGH- 190
QY 174 RSDVLTLDLVDTTDPDPDVHVSRYGLEDLSVRWVSPPALKD-FLQAYQYQIRYRE 232
DB 190 NATATTFDEFTIVKDDPPENVAVRPVSNPRLEVTWQTPSPWPESEPLKFLFATRRL 249
QY 233 DSDVWKVVDVSNQTSCLRAGLPGTYFVQY 264
DB 250 ILDDQWQH-V-ELSDGTAHTITDAVAGREYIIQY 280

RESULT 13
US-07-676-647-2
Sequence 2, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 19910328
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-676-647-2

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;
QY 5 IGSSLAQCSIHGDIPGATAGELVTLNGRRLPSELSRLNTSTLALANNGSRQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSQLV-----LHGELGHS 84
QY 65 DNLYVCHARDGSLIAGS-CLYVGLPPEKPFNISCWSRNM-KDLTCRW-----TGAGGE 115
DB 85 GLYACFHHDSWHLRQVLLHVLGFLPPREP-VLSCRSNTYKGYCSNHLPTPIYINTFN 143
QY 116 TELHTNYSIKYKLRMYGDNQCEEYHTVGPCHSHPKDLALFT--PYELWEATNRLGSA 173
DB 144 TVLHRSKIM-----VCEKDPAL-KNRCHT-RYWHLPSTIKYKVISVSNALGH- 190
QY 174 RSDVLTLDLVDTTDPDPDVHVSRYGLEDLSVRWVSPPALKD-FLQAYQYQIRYRE 232
DB 190 NATATTFDEFTIVKDDPPENVAVRPVSNPRLEVTWQTPSPWPESEPLKFLFATRRL 249
QY 233 DSDVWKVVDVSNQTSCLRAGLPGTYFVQY 264
DB 250 ILDDQWQH-V-ELSDGTAHTITDAVAGREYIIQY 280

RESULT 14
US-08-449-329-2
Sequence 2, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-329-2

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;

QY 5 IGSSIQATCSIHGDTPGATAGELWYTLNGRRPSELSRLNTSLALANLNGSRQSG 64
DB 38 LGSVDYTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSOLV-----LHGLELGS 84
QY 65 DNLVCHARDGSLIAGS-CLYVGLPPEKPFNISCWSRNM-KDITCRW-----TEGARGE 115
DB 85 GLYACFHRDSWHLRHQVLLHVLGFLPREPV-LSCRSNTYPKGYCSMHLPTPTIINTENV 143
QY 116 TELHNTYSLKYLKRMVGDNTCEEHYTVGPHSCHIPKDLAFT--PYEIWEATNRLGSA 173
DB 144 TYLHGSKIM-----VCEKDPAL-KNRCHI-RYHMLPSTIKYKVISVSNALGH- 190
QY 174 RSDVTLTDLVDVYTTDPPDVHVSRYVGLLEQLSVRWVSPPALKD-FLFQAKYQIRYRE 232
DB 190 NATATITPEFTIVKRPDENYVARVPSPNPRLEVTWQIPSTWPDSPESPLKFLIRYRL 249
QY 233 DSVDMKVVDDVSNQTSCLAGLKPGTYVYVOY 264
DB 250 ILDMQOHV-ELSDGTATHTTDAVAGKEYITIQY 280

RESULT 15
US-08-445-073-2
Sequence 2, Application US/08445073
Patent No. 3849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furt, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 11.5%; Score 172.5; DB 2; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;

QY 5 IGSSIQATCSIHGDTPGATAGELWYTLNGRRPSELSRLNTSLALANLNGSRQSG 64
DB 38 LGSVDYTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSOLV-----LHGLELGS 84
QY 65 DNLVCHARDGSLIAGS-CLYVGLPPEKPFNISCWSRNM-KDITCRW-----TEGARGE 115
DB 85 GLYACFHRDSWHLRHQVLLHVLGFLPREPV-LSCRSNTYPKGYCSMHLPTPTIINTENV 143
QY 116 TELHNTYSLKYLKRMVGDNTCEEHYTVGPHSCHIPKDLAFT--PYEIWEATNRLGSA 173
DB 144 TYLHGSKIM-----VCEKDPAL-KNRCHI-RYHMLPSTIKYKVISVSNALGH- 190
QY 174 RSDVTLTDLVDVYTTDPPDVHVSRYVGLLEQLSVRWVSPPALKD-FLFQAKYQIRYRE 232
DB 190 NATATITPEFTIVKRPDENYVARVPSPNPRLEVTWQIPSTWPDSPESPLKFLIRYRL 249
QY 233 DSVDMKVVDDVSNQTSCLAGLKPGTYVYVOY 264
DB 250 ILDMQOHV-ELSDGTATHTTDAVAGKEYITIQY 280

Search completed: September 16, 1999, 20:41:09
Job time: 5438 sec

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:09 ; Search time 49.27 Seconds

(Without alignments)
226.065 Million cell updates/sec

Title: US-09-037-657-19

Perfect score: 1505
Sequence: 1 PTLIGSSLQATCSIHGDFP.....VFVOVRCNPGIYGSKKAG 278

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR_60: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308.5	20.5	622	2	A40144	prolactin receptor
2	302	20.1	206	2	A57018	prolactin receptor
3	292	19.4	830	2	I50455	prolactin receptor
4	291	19.3	303	2	I77524	prolactin receptor
5	291	19.3	292	2	I77525	prolactin receptor
6	291	19.3	608	2	I53269	prolactin receptor
7	290	19.3	918	2	A36337	membrane glycoprot
8	288.5	19.2	610	2	A36331	lactogen receptor
9	288.5	19.2	610	2	A36116	prolactin receptor
10	288.5	19.2	412	2	A41070	prolactin receptor
11	288.5	19.2	310	2	A29384	prolactin receptor
12	286	19.0	616	2	A30304	prolactin receptor
13	281.5	18.7	918	2	A44257	interleukin-6 sign
14	281	18.7	831	2	U01655	prolactin receptor
15	279	18.5	917	2	I49699	glycoprotein 130 -
16	276	18.3	581	2	I45971	prolactin receptor
17	233	15.5	630	2	I51086	prolactin receptor
18	222	14.8	783	2	JH0329	granulocyte colony
19	222	14.8	771	2	B38252	granulocyte colony
20	222	14.8	863	2	C38252	granulocyte colony
21	221.5	14.7	837	2	A42898	granulocyte colony
22	197.5	13.1	156	2	A32868	prolactin receptor
23	190	12.6	150	2	B34631	prolactin receptor
24	178.5	11.9	372	2	I58141	lactogen receptor
25	176.5	11.7	362	2	S60614	ciliary neurotroph
26	175	11.6	422	2	I57891	growth promoting a
27	172.5	11.5	372	1	UHHUCN	interleukin-11 rec
28	166	11.0	579	2	A45266	ciliary neurotroph
29	166	11.0	635	2	A45266	MP-1 protein prec
30	164	10.9	432	2	I48343	interleukin-11 rec
31	163.5	10.9	625	2	S35317	hematopoietic grow
32	161	10.7	894	2	UC4797	leptin receptor pr
33	161	10.7	1162	2	PC4184	leptin receptor, O
34	161	10.7	805	3	JC4897	leptin receptor, O
35	159.5	10.6	626	2	S37622	proto-oncogene - m
36	159	10.6	638	2	B28176	somatotropin recep
37	159	10.6	894	2	S68437	leptin receptor (V
38	159	10.6	900	2	S68440	leptin receptor (V
39	159	10.6	805	2	S68441	leptin receptor (V

40 158.5 10.5 468 1 A41242 interleukin-6 rece
41 156 10.4 895 2 S74225 leptin receptor, 1
42 154.5 10.3 460 2 J10145 interleukin-6 rece
43 154.5 10.3 440 2 J10144 interleukin-6 rece
44 151 10.0 638 2 S12136 somatotropin recep
45 147.5 9.8 1097 2 S17308 leukemia inhibitor

ALIGNMENTS

RESULT 1

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C:Accession: A40144

R:Boutin, J.M.; Ederly, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, M.L. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in hum

A:Reference number: A40144; MUID:90114212

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MUT>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.5%; Score 308.5; DB 2; Length 622;

Best Local Similarity 38.5%; Pred. No. 2.4e-20;

Matches 77; Conservative 27; Mismatches 85; Indels 11; Gaps 7;

DB 76 ILASGLIVYG-LPEKPNISCSNMKDLTRMTPGAHEFTLNTSLKRLMYGOD 134

DB 15 LFLNCLLNGOLPGKPEIFKCRSPNKETFLWMRPGTDG--LPTNYSLYHREGETLM 72

DB 135 NTCEHYHVGVPSCHIPRD-LALFPPEIHWATNRIGARSBDVLTDVLDVVTDDPPD 193

DB 73 HECPTITGGPNSCHFGQYTSMTFTYIMVNATQKSSFSFDELYVDYTYVQDPDPLE 132

DB 134 VVSNVGGLEDOLSVRWV--SPPALKDF---LEQAKYQIRYVEDSDVKVVDVSNOTS 248

DB 133 LAV-EVKPPEDRKPYLMIKMSPTLIDLTGTGFTLLYEIRLKPENKAWE-IHFGQOTE 190

DB 249 CRMLAGKPGTYVFVGRCP 268

DB 191 FKILSLHFGKRYLVGRCKP 210

RESULT 2

A57018

prolactin receptor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996

C:Accession: A57018

R:Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cel

A:Reference number: A57018; MUID:95286597

A:Accession: A57018

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-206 <RES>

A:Cross-references: GB:S78505; NID:9999114; PID:9999115

Query Match 20.1%; Score 302; DB 2; Length 206;
 Best Local Similarity 39.2%; Pred. No. 2,2e-20;
 Matches 74; Conservative 25; Mismatches 80; Indels 10; Gaps 6;

QY 86 LPEKPFNISCWNRNMDLTCRMTPGAHGETFLHTNYSLKTKLMTYGQDNTCEHYTAVP 145
 DB 2 LPPGKEEIFRCRSPNRETFCWMPGPGIDG--LPTNYSLYHREGETLMECPDIYIGSP 59
 QY 146 HSHPIKPD-LALTPYEIWEATNRIGSARSVDLTLDVYVTTDPPDVHVSRYGLED 204
 DB 60 NSCHFGRQYTSMTKRTIIMVYVATNOMGSSFSDELYDVYIYVOPDPLELAY-EVKQPED 118
 QY 205 QLSVRYV--SPPALKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTV 259
 DB 119 RKRYLWIKNSPPLILDLTQTMFTLLVEIRLKPKAEMWE-IHFRAGQOTEEKIISLHGOK 177
 QY 260 YFVQVRCNP 268
 DB 178 YLVQVRCRP 186

RESULT 3
 prolactin receptor - pigeon
 C:Species: Columba livia (domestic pigeon)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
 C:Accession: 150455
 R:Chen, X.; Horseman, N.D.
 Endocrinology 135, 269-276, 1994
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
 A:Reference number: 150455; MUID:94283267
 A:Accession: 150455
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:9466381; PID:9466382

Query Match 19.4%; Score 292; DB 2; Length 830;
 Best Local Similarity 37.0%; Pred. No. 1,1e-18;
 Matches 70; Conservative 29; Mismatches 78; Indels 12; Gaps 7;

QY 87 PEKPFNISCWNRNMDLTCRMTPGAHGETFLH-TNYSLKTKLMTYGQDNTCEHYTAVP 145
 DB 231 PEKPTIILICRSPREKFTFCWMPGSDG--HPTNYTLLSKSGEGERVEECDFYTAGP 287
 QY 146 HSGH-LPRLAFTPEIWEATNRIGSARSVDLTLDVYVTTDPPDV--HVSRYGGL 202
 DB 288 NSCYDDKHTSMITNINIVKATNEIGSNVSDPLVYDVYIYVQIDPPVNTLELKTNR 347
 QY 203 EDQLSVRYVSPALD--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTV 259
 DB 348 KRYLVLTW-SPPLLDVNRSGWLTLDYELRLKPEAEEMETI-FVGQOTHYKMSLNPGRK 405
 QY 260 YFVQVRCNP 268
 DB 406 YLVQVRCRP 414

RESULT 4
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: 177524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261824
 A:Accession: 177524
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-303 <RES>

A:Cross-references: GB:M22958; NID:9200479; PID:9200480

Query Match 19.3%; Score 291; DB 2; Length 303;
 Best Local Similarity 33.6%; Pred. No. 3,7e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

QY 40 LSRLLNTSTLALANLNGSRQSGDNLYCHARDGSIAGSCLYGLPPEKPFNISCWNR 99
 DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKREIHKCRSP 34
 QY 100 NMKDLTCRMTPGAHGETFLHTNYSLKTKLMTYGQDNT--CEHYHVGPSCHLPKD-LAL 156
 DB 35 DKETFCWMPGSDG--LPTNYSLYSKE--GKNYTCBPDKTSGPNSCFESKQYTSI 90
 QY 157 FPEIWEATNRIGSARSVDLTLDVYVTTDPPDVHVSRYGLEDOLSVRWVS--PP 214
 DB 91 WKIYITVATNEMGSSSTDPLVYDVYIYVEPPRNLT-LYKQLKDKKTYLWYKMLPP 149
 QY 215 ALKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTVYFVQVRCNPFGI 271
 DB 150 TITDVKTGWFTEYERLKSSEADWE-IHFGHOTQFVFLYPOKYLVOYTRCKPDHG 208
 QY 272 YGSK 275
 DB 209 YMSR 212

RESULT 5
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: 177525
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261824
 A:Accession: 177525
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:9200481; PID:9200482

Query Match 19.3%; Score 291; DB 2; Length 292;
 Best Local Similarity 33.6%; Pred. No. 3,5e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

QY 40 LSRLLNTSTLALANLNGSRQSGDNLYCHARDGSIAGSCLYGLPPEKPFNISCWNR 99
 DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKREIHKCRSP 34
 QY 100 NMKDLTCRMTPGAHGETFLHTNYSLKTKLMTYGQDNT--CEHYHVGPSCHLPKD-LAL 156
 DB 35 DKETFCWMPGSDG--LPTNYSLYSKE--GKNYTCBPDKTSGPNSCFESKQYTSI 90
 QY 157 FPEIWEATNRIGSARSVDLTLDVYVTTDPPDVHVSRYGLEDOLSVRWVS--PP 214
 DB 91 WKIYITVATNEMGSSSTDPLVYDVYIYVEPPRNLT-LYKQLKDKKTYLWYKMLPP 149
 QY 215 ALKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTVYFVQVRCNPFGI 271
 DB 150 TITDVKTGWFTEYERLKSSEADWE-IHFGHOTQFVFLYPOKYLVOYTRCKPDHG 208
 QY 272 YGSK 275
 DB 209 YMSR 212

RESULT 6
 prolactin receptor, long form - mouse
 153269

C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Jan-1999
 C:Accession: I53269; J10671; S34356
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A:Reference number: I53269; MUID:93307149
 A:Accession: I53269
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:g293769; PID:g293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J10671; MUID:94085788
 A:Accession: J10671
 A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:g347398; PID:g347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: S34356
 A:Accession: S34356
 A:Molecule type: mRNA
 A:Residues: 1-557, F, 559-608 <EDE>
 A:Cross-references: EMBL:X73372; NID:g312696; PID:g312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domain: transmembrane #status predicted <TMO>

Query Match 19.3%; Score 291; DB 2; Length 608;
 Best Local Similarity 33.6%; Pred. No. 9.3e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

40 ISRLNTSLALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISCMR 99
 1 MSSALAYMLVLSILNG--QS-----PPEKPIHCRSP 34
 100 NKKDLTCRTPGAHGTEFLHTNYSLKTKRWGQDNT--CEEYHTVGPSPHCPKD-LAL 156
 35 DEETFCWNNPSSDGS--LPTNYSLSYKSE--GEKNTYCPDPKTSGPSNCFPSKQYTSI 90
 157 FFPYELWEATNRIGSARSDVLLDVLDTVDPPDVHVSRYGLEDLSVTRWS--PP 214
 91 WRTYITVATNEMGSISSDPLVDVTYVEPEPRNLT--EVKQKDKKTYLVMKMLPP 149
 215 ALKDF---LFOAKYQIRYVEDSVDMKVVDDVSNOTSCHLAGKPGTYFVQRCNPPGI 271
 150 TITDVKTGTFMEYELRLKSEFADENE-IHFTGHOTQFVFDLYPQOKYLVQTRCKPDHG 208
 272 YGSK 275
 209 YWSR 212

RESULT 7
 A36337
 membrane glycoprotein gp130 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
 C:Accession: A36337
 R:Hihi, M.; Murakami, M.; Satto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
 Cell 63, 1149-1157, 1990
 A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
 A:Reference number: A36337; MUID:91084844
 A:Accession: A36337
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:g186353; PID:g186354
 C:Genetics:
 A:Gene: GDB:11657; GP130
 A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 19.3%; Score 290; DB 2; Length 918;
 Best Local Similarity 28.3%; Pred. No. 2e-18;
 Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

1 PTLIGSSIQATCSING---DTPGATAGGYTLNGRRLPSELRLNTSLALANLN 57
 36 PVALGNSNFAVCLVLEKCDYFHVANNTYKTNFTLPKEQYTIINNTASSVTDTDA 95
 58 GSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISCMRMDLTCRWTPGAHGETF 117
 96 SLNIQTLNLTFRGLEQNVYGTITISGLPPEKPNLSCLVNGSKMKRCENOGGR--ETH 153
 118 LHTNYSLKTKRWGQDNTCEEYHTVGPSPHCPKD-LALFTPEIWEATNRLGARSQV 177
 154 LETNFTLKEEMATKRPADKAKRDT--PTSCYDYSTVYFVNIEVWEAENALGKVTSDH 211
 178 LITDVLDTVDPPDVHVSRYGLEDLSVTRWSPPALKDFQAKKQIRYVEDSVDM 237
 212 INDDPYKTKRPNPPLNLSINSELSILKLTNTN--PSIKSVIT--LKNIQYRTKDASTM 269
 238 KVV---DDVSNOTSCHLAGLKPGTYFVQVRC 266
 270 SQIPEDTASTRSSFTVODLKPEYVFRIRC 301

RESULT 8
 A36331
 lactogen receptor 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
 C:Accession: A36331
 R:Zhang, R.; Buczek, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
 Biochem. Biophys. Res. Commun. 168, 415-422, 1990
 A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA.
 A:Reference number: A36331; MUID:902441201
 A:Accession: A36331
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <ZHA>
 A:Cross-references: GB:M34083; NID:g205122; PID:g205123
 A:Note: the authors translated the codon GAG for residue 533 as Gly

Query Match 19.2%; Score 288.5; DB 2; Length 610;
 Best Local Similarity 36.4%; Pred. No. 1.6e-18;
 Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

75 SILAGSCLVGLPPEKPNISCMRMDLTCRWTPGAHGETFLHTNYSLKTKRWGQD 134
 15 SLKQGS---PPEKPIHCRSPDKETFCWNPNGTGG--LPTNYSLSYKSE--GEK 65
 135 NT--CEEYHTVGPSPHCPKD-LALFTPEIWEATNRLGARSQVLLDVLDTVDPP 191
 66 TTYECPDYKTSGPSNCFPSKQYTSIMKTIITVNTNOMGSSSDPLVDVTYIYEPBP 125
 192 PDVHVSRYGLEDLSVTRWS--SPALNDF---LFOAKYQIRYVEDSVDMKVVDDV 246
 126 RNLTL--EVKQKDKKTYLVMKSPPLIIDVKTGWTMEYELRLKSEFADENE-IHFTGHQ 183
 247 TSCRAGLKPGTYFVQVRCNPPGIYGSK 275
 184 TQKVFEDLYPQOKYLVQTRCKPDHGYNSR 212

RESULT 9

A36116
 prolactin receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
 C:Accession: A36116
 R:Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Ederly, M.; Djiane, J.
 M.Ol. Endocrinol. 4, 1136-1143, 1990
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A:Reference number: A36116; MUID:91155946
 A:Accession: A36116
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <SH1>
 A:Cross-references: GB:M57668; NID:g206366; PID:g206367; GB:M60728

Query Match 19.2%; Score 288.5; DB 2; Length 610;
 Best Local Similarity 36.4%; Pred. No. 1.6e-18;
 Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

QY 75 SLAGSCLYGLPPEKPNISCSRNKMDLTCRMTPGAGHETFLHTNYSLKRLRWYGOD 134
 DB 15 SLKGS-----PPGKPEIHKCRSPDKETFCWNNPGDGG--LPTNYSLYSKE--GEK 65
 QY 135 NT--CEEYHTVGPCHIPND-LALFTPEIWEATNRRLGSASDVLTLDVLYVTDDP 191
 DB 66 TTECPDYKISGPNSCFFSKQYTSIMKIITVNATNOMGSSSDPLYVDVTVIPEEP 125
 QY 192 PDVHVSRYGLEDQLSVRWV--SPALKDF--LFOAKYQIRVVEDSVMKVYDVDSNQ 246
 DB 126 RNLT-L-EVKOLKDKKTYLWKMSPPTITDVKTGTFMEYERLRKPEAEEME-IHFTGHQ 183
 QY 247 TSCRLAGLRPGTYFVQVRCNPGIYGSK 275
 DB 184 TQFKVFDLYPGQKYLVTGRCKPDHGYSR 212

RESULT 10

A41070
 prolactin receptor Nb2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; MUID:92041834
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <AL1>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 R:O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
 A:Reference number: 155417; MUID:95014442
 A:Accession: 155417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RBS>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: Nb2-11C cell line
 C:Keywords: transmembrane protein

Query Match 19.2%; Score 288.5; DB 2; Length 412;
 Best Local Similarity 36.4%; Pred. No. 9.4e-19;
 Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

QY 75 SLAGSCLYGLPPEKPNISCSRNKMDLTCRMTPGAGHETFLHTNYSLKRLRWYGOD 134
 DB 15 SLKGS-----PPGKPEIHKCRSPDKETFCWNNPGDGG--LPTNYSLYSKE--GEK 65
 QY 135 NT--CEEYHTVGPCHIPND-LALFTPEIWEATNRRLGSASDVLTLDVLYVTDDP 191

DB 66 TTECPDYKISGPNSCFFSKQYTSIMKIITVNATNOMGSSSDPLYVDVTVIPEEP 125
 QY 192 PDVHVSRYGLEDQLSVRWV--SPALKDF--LFOAKYQIRVVEDSVMKVYDVDSNQ 246
 DB 126 RNLT-L-EVKOLKDKKTYLWKMSPPTITDVKTGTFMEYERLRKPEAEEME-IHFTGHQ 183
 QY 247 TSCRLAGLRPGTYFVQVRCNPGIYGSK 275
 DB 184 TQFKVFDLYPGQKYLVTGRCKPDHGYSR 212

RESULT 11

A23984
 prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A23984
 R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ederly, M.; Shirota, M.; Br
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the GPC
 A:Reference number: A23984; MUID:86165059
 A:Accession: A23984
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 19.2%; Score 288.5; DB 2; Length 310;
 Best Local Similarity 36.4%; Pred. No. 6.5e-19;
 Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

QY 75 SLAGSCLYGLPPEKPNISCSRNKMDLTCRMTPGAGHETFLHTNYSLKRLRWYGOD 134
 DB 15 SLKGS-----PPGKPEIHKCRSPDKETFCWNNPGDGG--LPTNYSLYSKE--GEK 65
 QY 135 NT--CEEYHTVGPCHIPND-LALFTPEIWEATNRRLGSASDVLTLDVLYVTDDP 191
 DB 66 TTECPDYKISGPNSCFFSKQYTSIMKIITVNATNOMGSSSDPLYVDVTVIPEEP 125
 QY 192 PDVHVSRYGLEDQLSVRWV--SPALKDF--LFOAKYQIRVVEDSVMKVYDVDSNQ 246
 DB 126 RNLT-L-EVKOLKDKKTYLWKMSPPTITDVKTGTFMEYERLRKPEAEEME-IHFTGHQ 183
 QY 247 TSCRLAGLRPGTYFVQVRCNPGIYGSK 275
 DB 184 TQFKVFDLYPGQKYLVTGRCKPDHGYSR 212

RESULT 12

A30304
 prolactin receptor 2 precursor - rabbit
 M:Alternate names: prolactin receptor, mammary gland
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
 C:Accession: A30304; MUID:89184578
 R:Ederly, M.; Jolicoeur, C.; Levi-Meynuel, C.; Dusanter-Fourt, I.; Petridou, B.; B
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A:Title: Identification and sequence analysis of a second form of prolactin recept
 A:Reference number: A30304; MUID:89184578
 A:Accession: A30304
 A:Molecule type: mRNA
 A:Residues: 1-616 <EDF>
 A:Cross-references: GB:J04510; NID:g165669; PID:g165670
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin r
 A:Reference number: A60380; MUID:91146782
 A:Accession: A60380
 A:Molecule type: protein

A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167
 A>Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domain: transmembrane #status predicted <TM>
 F:59,104,132,347,369,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.0%; Score 286; DB 2; Length 616;
 Best Local Similarity 37.8%; Pred. No. 2, 7e-18;
 Matches 71; Conservative 26; Mismatches 81; Indels 10; Gaps 6;

QY 87 PPEKPNISCSRNKMDLTCRWTPGAGHETFLHNTSLKYKLRMYGDNCEHYHTVGP 146
 |||||
 DB 27 PPKKPIFKCRSPKERTFTCMWRPGADG--LPNTLYLHKEGETITHECDYKNGGN 84
 QY 147 SCHI-PKDALFTPEIWEATNRLGASASDVLTDVYVTTDPPDVHVSRGLEDP 205
 |||||
 DB 85 SCYFSKHTSWTITITVYVATNMQSSVSDRYVDVITVDPDVNLT-EVKHPEDR 143
 QY 206 LSVRWVS--PPALKDF---LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLPGTV 260
 |||||
 DB 144 KYLWVKKMPLPLVDVRSGLTLQYELRLKPEKALEWE-THRAGQOTQKILSLYPGKY 202
 QY 261 FYQVRCNP 268
 |||||
 DB 203 LYQVRCNP 210

RESULT 13
 A44257
 Interleukin-6 signal transducing molecule gp130 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C:Accession: A44257
 R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
 A:Reference number: A44257; MUID:99052397
 A:Accession: A44257
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-918 <MAN>
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
 C:Keywords: transmembrane protein

Query Match 18.7%; Score 281.5; DB 2; Length 918;
 Best Local Similarity 29.0%; Pred. No. 1, 2e-17;
 Matches 79; Conservative 46; Mismatches 132; Indels 15; Gaps 7;

QY 1 PTLIGSLQATGSIHG--DTPGATAGLYTLNGRLPELSRLTLSTALATLNLN 57
 |||||
 DB 36 PVOVGRSMTATCYLKEKCLQVSVNATYIWKTNHVAPEQVTVIRKTSVTFIDV 95
 QY 58 GSROSGDNVCHARDGSIILGSLYGLPEKPFNISCWERNMDLTCRWTPGAGHET 117
 |||||
 DB 96 FQNVQLCNILSGQIEQVNYGIIISGYPDIPNLNCIYNBKNMQLQDPER--EY 153
 QY 118 LHTNYSLKLRMYGOD--NTCEEYHTVPSCHIPKDALFTPEIWEATNRLGASASD 176
 |||||
 DB 154 LETVYTLKSE--WATEKFPDCRTH--GTSCAMGYPIYVNTVEWAEALGNVSE 209
 QY 177 VLLIDVLDVTTDPPDVHVSARGLEDPQLSVRWVSPPALDFTFOAKYQIRYVEDSV 236
 |||||
 DB 210 PINFDPVDKVSPPHNLVSNSELSILKLVANSL--DSLRLKSDIQYTKDAST 267
 QY 237 MKVY--DDVSNQTSCLAGLPGTVFYQVR 265
 |||||
 DB 268 WQVPLEDVTSPRTSFTVQDLKPFTEYFRI 299

RESULT 14
 J01655
 prolactin receptor precursor - chicken

C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997
 C:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 450-456, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
 A:Reference number: J01655; MUID:93075121
 A:Accession: J01655
 A:Molecule type: mRNA
 A:Residues: 1-831 <MAN>
 A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
 A:Experimental source: kidney
 C:Keywords: glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-831/Product: prolactin receptor #status predicted <MAT>
 F:439-463/Domain: transmembrane #status predicted <TM>
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (C

Query Match 18.7%; Score 281; DB 2; Length 831;
 Best Local Similarity 36.0%; Pred. No. 1, 1e-17;
 Matches 68; Conservative 27; Mismatches 82; Indels 12; Gaps 7;

QY 87 PPEKPNISCSRNKMDLTCRWTPGAGHETFLH-TNYSKYKLRMYGDNCEHYHTVGP 145
 |||||
 DB 230 PPKKPIFKCRSPKERTFTCMWRPGADG---HPNTLLSKSEEDQVYCPDRTAGP 286
 QY 146 HSCHT-PKDALFTPEIWEATNRLGASASDVLTDVYVTTDPPDV--HVSARGVL 202
 |||||
 DB 287 NSCYFKNHTSFTITVYVATNMQSSSDPHVDVITVQPPVNTLTKKPINR 346
 QY 203 EDOLSVRWVSPPALKDF---LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLPGTV 259
 |||||
 DB 347 KYLWVLTN-SPPPLADVRSGLTLQYELRLKPEGEWEETI-FVGOQYKMFSLNPKK 404
 QY 260 FYQVRCNP 268
 |||||
 DB 405 YIQVRCNP 413

RESULT 15
 I49699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
 C:Accession: I49699; I48370
 R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, g
 A:Reference number: I48370; MUID:92291532
 A:Accession: I49699
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: GB:M83336; NID:g193591; PID:g193592
 A:Accession: I48370
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: EMBL:X62646; NID:g840816; PID:g840817
 C:Genetics:
 A:Gene: gp130
 C:Keywords: glycoprotein

Query Match 18.5%; Score 279; DB 2; Length 917;
 Best Local Similarity 28.7%; Pred. No. 2e-17;
 Matches 78; Conservative 46; Mismatches 132; Indels 16; Gaps 7;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:13 ; Search time 35.09 Seconds

(without alignments)
223.955 Million cell updates/sec

Title: US-09-037-657-19

Sequence: 1 PTLIGSSLIQATCSIHGDP.....VFVQRCNPFYGSKKAG 278

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308.5	20.5	622	1	PRLR_HUMAN	P16471 homo sapien
2	292	19.4	830	1	PRLR_COLLI	O90374 columba liv
3	291	19.3	608	1	PRLR_MOUSE	O08501 mus musculu
4	290	19.3	918	1	IL6B_HUMAN	P40189 homo sapien
5	288.5	19.2	610	1	PRLR_RAT	P05710 ratu
6	286	19.0	616	1	PRLR_RABIT	P14787 oryctolagus
7	281	18.7	918	1	IL6B_RAT	P40190 ratu
8	281	18.7	831	1	PRLR_CHICK	O04594 gallu
9	280	18.6	917	1	PRLR_MELGA	O91094 melagris g
10	279	18.5	917	1	IL6B_MOUSE	O00560 mus musculu
11	276.5	18.4	581	1	PRLR_CEREL	O28335 cervus elap
12	276	18.3	581	1	PRLR_BOVIN	O28172 bos tauru
13	233	15.5	630	1	PRLR_ORENT	O91513 oreochromis
14	222	14.8	836	1	GCSR_HUMAN	O90622 homo sapien
15	221.5	14.7	837	1	GCSR_MOUSE	P40223 mus musculu
16	178.5	11.9	372	1	CNTR_RAT	O08406 ratu
17	176.5	11.7	362	1	CNTR_HUMAN	P51641 gallu
18	172.5	11.5	372	1	CNTR_CHICK	P26992 homo sapien
19	166	11.0	635	1	TPOR_HUMAN	P40238 homo sapien
20	163.5	10.9	625	1	TPOR_MOUSE	O08351 mus musculu
21	159	10.6	638	1	GHR_RABIT	P19941 oryctolagus
22	159	10.6	1165	1	LEPR_MOUSE	P48356 mus musculu
23	158.5	10.5	468	1	IL6A_HUMAN	P08887 homo sapien
24	154.5	10.3	460	1	IL6A_MOUSE	P22272 mus musculu
25	154.5	10.3	462	1	IL6A_RAT	P22272 mus musculu
26	151	10.0	638	1	GHR_PIG	P19756 sus scrofa
27	147.5	9.8	1097	1	LEPR_HUMAN	P47302 homo sapien
28	146	9.7	1165	1	LEPR_MOUSE	P48357 mus musculu
29	145	9.6	638	1	GHR_HUMAN	P10912 homo sapien
30	143.5	9.5	634	1	AXOI_RAT	P22063 ratu
31	142.5	9.5	634	1	GHR_SHEEP	O28575 ovis aries
32	142	9.4	638	1	GHR_MOUSE	P16310 ratu
33	140.5	9.3	650	1	GHR_MOUSE	P16882 mus musculu
34	140.5	9.3	297	1	GHR_MOUSE	P16590 mus musculu
35	136	9.0	608	1	GHR_CHICK	O02092 gallu
36	136	9.0	638	1	GHR_MOUSE	P79194 macaca mula
37	135.5	9.0	888	1	UFO_MOUSE	O00993 mus musculu
38	134	8.9	634	1	GHR_BOVIN	P73108 bos tauru
39	133.5	8.9	1092	1	LEPR_MOUSE	P42703 mus musculu
40	133.5	8.9	1452	1	PRPM_MOUSE	P28828 mus musculu
41	131.5	8.7	611	1	GHR_COLLI	O90375 columba liv
42	130.5	8.7	1452	1	PRPM_HUMAN	P28827 homo sapien
43	129.5	8.6	507	1	EPOR_HUMAN	O07303 ratu

ALIGNMENTS

RESULT	1	PRLR_HUMAN	STANDARD	PRT	622 AA.
AC	P16471				
DT	01-AUG-1990 (REL. 15, CREATED)				
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	PROLACTIN RECEPTOR PRECURSOR (PRL-R).				
GN	PRLR.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95075462				
RA	SOMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;				
RT	"The X-ray structure of a growth hormone-prolactin receptor complex."				
RL	NATURE 372:478-481(1994).				
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: M3161; G190362; -				
DR	PIR: A40144; A40144.				
DR	PDB: 1BP3; 23-SEP-98.				
DR	MM: 1BP3; 23-SEP-98.				
DR	PROSITE: PS00241; RECEPTOR CYTOKINES 1; 1.				
DR	PROSITE: PS00340; RECEPTOR CYTOKINES 2; 1.				
DR	PFAM: PF00041; fn3; 2.				
DR	RECEPTOR; TRANSMEMBRAN; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.				
FT	SIGNAL	1	24		
FT	CHAIN	25	622		
FT	DOMAIN	25	234		
FT	DOMAIN	25	258		
FT	TRANSMEM	259	622		
FT	DOMAIN	25	122		
FT	DOMAIN	123	227		
FT	DISULFD	36	46		
FT	DISULFD	75	86		
FT	CARBOHYD	59	59		
FT	CARBOHYD	104	104		
FT	CARBOHYD	233	233		
FT	SEQUENCE	622 AA;	69505 MW;	6924E155 CAC32;	

Query Match 20.58; Score 308.5; DB 1; Length 622;
Best Local Similarity 38.58; Pred. No. 3.5e-20;
Matches 77; Conservative 27; Mismatches 85; Indels 11; Gaps 7;

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QY 76 ILASCLYVG-LPPEKFNISCSNRNMKDLCTWTPGAHGETFLHTNYSIKYLRMGOD 134
DB 15 LFLNTCLLNGQLPPGKKEIFKCRSPNKEFTTCWMPGTIDG--LPTNYSILYHREGETLM 72
QY 135 NTCSEYHTVGHSCHEPRD-LALFTPYEIVWEATNTRGASADVLTLDVDTDPDP 133
DB 73 HECDDPYITGGNSCHFRKQTSMTRTYIMAVNATNGSSSDLYDYVYIYQDPDPLE 132
QY 194 VHSRVGGLLEDQLSRVV--SPPLAKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTS 248
DB 133 LAV-EVQPEDRKRYLTKNSPPLTLDKGTWFLTYELRLKPKAEWE- IHPAGQOTE 190
QY 249 CRLAGLKPGTYFYQVQCNP 268
DB 191 FKILSLHPGKRYLVQVCKP 210

RESULT 2
PRLR_COLL1 STANDARD; PRT; 830 AA.
ID PRLR_COLL1 STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS COLUMBA LIVIA (DOMESTIC PIGEON).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COPIASAC;
RX MEDLINE; 94283267.
RA CHEN X., HORSEMAN N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
RT ENDOCRINOLOGY 135:269-276(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; U07694; G466382;
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PRAM; PF00041; fn3; 4.
DR HSSP; P16471; 1BP3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 125 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112

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FT CARBOHYD 132 132
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
SQ SEQUENCE 830 AA; 94507 MW; 5EFAED51 CRC32;

Query Match 19.4%; Score 292; DB 1; Length 830;
Best Local Similarity 37.0%; Pred. No. 1,5e-18;
Matches 70; Conservative 29; Mismatches 78; Indels 12; Gaps 7;

QY 87 PPEKFNISCSNRNMKDLCTWTPGAHGETFLH-TNYSIKYLRMGODNTECEYHTVGP 145
DB 231 PPEKFTILCRSEPEKETFTCWMPGSDG--HPTNYSILYHREGERYECPDYTAGP 287
QY 146 HSCHEI-PKDLALFTPYEIVWEATNTRGASADVLTLDVDTDPDPDPV--VHSRVGGL 202
DB 288 NSCYFDPKHTSEFTIINITYKATNEIGSNVSDLYDYVYIYQDTPPVNTLELKKTYNR 347
QY 203 EDQLSRVWSPPLAKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTY 259
DB 348 KPYLVLTW--SPPLADVRSGWLTLDYELRLKPEAEWEETI-FVGOQTHYKMFSLNPGKK 405
QY 260 YFYQVQCNP 268
DB 406 YIVQIHCKP 414

RESULT 3
PRLR_MOUSE STANDARD; PRT; 608 AA.
ID PRLR_MOUSE STANDARD; PRT; 608 AA.
AC Q08501; Q62099; P15213; P15212;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=C3H; TISSUE=MAMMARY GLAND;
RX MEDLINE; 94085788.
RA MOORE R.C., OKA T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland long-form prolactin receptor.";
RT GENE 134:263-265(1993).
RN [2]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 93307149.
RA CLARKE D.L., LINZER D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the mouse ovary.";
RT ENDOCRINOLOGY 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA SASAKI M.;
RN [4]
RP SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
RA EDERER M., PEZER A., NANDI S., KELLY P.A.;
RN SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RP [5]
RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 89261824.
RA DAVIS J.A., LINZER D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse liver."

```


FT DOMAIN 223 324 FIBRONECTIN TYPE-III.
 FT DOMAIN 423 423 FIBRONECTIN TYPE-III.
 FT DOMAIN 424 517 FIBRONECTIN TYPE-III.
 FT DOMAIN 518 613 FIBRONECTIN TYPE-III.
 FT DOMAIN 725 755 SER-RICH.
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 83 83 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 227 227 POTENTIAL.
 FT CARBOHYD 379 379 POTENTIAL.
 FT CARBOHYD 383 383 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 553 553 POTENTIAL.
 FT CARBOHYD 564 564 POTENTIAL.
 SO SEQUENCE 918 AA, 103522 MW, 7C00605 CRC32;

Query Match 19.3%; Score 290; DB 1; Length 918;
 Best Local Similarity 28.3%; Pred. No. 2.6e-18;
 Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY 1 PILLISSIAQATCSHG---DPGATAEELVTLNRRRLPSELRLNTSTALANLN 57
 DB 36 PVVQLSHNFATVAVLKEKCMDFHVNANIYMTNHTIPKEQYTIINTASSYPTDIA 95
 QY 58 GSRQSGDNLVNCARGCSLGLAVGAPPEPFHISCSRMADLTCTWTPGAGET 117
 DB 96 SLNTQITCNILTFGLEQNVYGTITISGPEPKNLSCIVNEGKKRCEWGGGR--ETH 153
 QY 118 LHTNLSLKYKLMVYGODNTCEHYHVPSCHIPKDLFTPEIWEATNRLGSARSDV 177
 DB 154 LENEFLKEMVTHKRAADOKAKRDT--PSCIVDYSTVYFVNIWEVLEMLKGYTSDH 211
 QY 178 LILDVLDVYTTDPDPVHVSRVGLDQSVRWSPALKDLEFOAKYQIRRVSDVDM 237
 DB 212 INEDPYKVPNPNNLSYINSEELSSILKLTWNTN-PSIKSYII-LKYNIGYRTDASW 269
 QY 238 KVV---DVSNOTSCLAGKPGTYFVQVC 266
 DB 270 SQIPEDNASTRSSFTVQDLKPEYEVFRIC 301

RESULT 5
 PRIR_RAT STANDARD: PRT: 610 AA.
 ID P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
 AC 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
 GN RATTUS NORVEGICUS (RAT).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91155946.
 RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
 EDERY M., DJIANE J., KELLY P.A.;
 RT "Expression of two forms of prolactin receptor in rat ovary and
 liver".
 RL MOL. ENDOCRINOL. 4:1136-1143(1990).
 RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 RX MEDLINE: 90241201.
 RA ZHANG R., BUCKHO E., TSAI-MORRIS C.H., HU Z.Z., DUBAU M.L.;
 RT "Isolation and characterization of two novel rat ovarian lactogen
 receptor cDNA species".
 RL BIOCHEM. BIOPHYS. RES. COMMON. 168:415-422(1990).

RN [3]
 RP SEQUENCE OF 281-610 FROM N.A.
 RA BANVILLE D., STOCO R., MURPHY K.K., BOYE Y., KELLY P.A.;
 RN SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
 RL [4]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
 RC TISSUE-LIVER;
 RX MEDLINE: 88165059.
 RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
 SHIROTA M., BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.;
 RT "Cloning and expression of the rat prolactin receptor, a member of
 the growth hormone/prolactin receptor gene family".
 RL CELL 53:69-77(1988).
 RP [5]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RC TISSUE-LYMPHOMA;
 RX MEDLINE: 92041834.
 RA ALI S., PELLIGRINI I., KELLY P.A.;
 RT "A prolactin-dependent immune cell line (NB2) expresses a mutant form
 of prolactin receptor".
 RL J. BIOL. CHEM. 266:20110-20117(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RX MEDLINE: 95014432.
 RA O'NEAL K.D., YU-LEE L.Y.;
 RT "Differential signal transduction of the short, NB2, and long
 prolactin receptors. Activation of interferon regulatory factor-1 and
 cell proliferation".
 RL J. BIOL. CHEM. 269:26076-26082(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING OF THE PRLR GENE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M57668; G206367; -
 DR EMBL: M34083; G205123; -
 DR EMBL: L48060; G1019651; -
 DR EMBL: U34730; G1223859; -
 DR EMBL: M19304; G206365; -
 DR EMBL: M74152; G206380; -
 DR EMBL: U07567; G641964; -
 DR PIR: A29884; A29884.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1;
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM: PF00041; fn3; 2.
 DR HSSP: P16471; 1BP3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 KW ALTERNATIVE SPLICING.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 610 PROLACTIN RECEPTOR.
 FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
 FT TRANSMEM 230 253 BY SIMILARITY.
 FT DOMAIN 254 610 CYTOPLASMIC (BY SIMILARITY).
 FT DOMAIN 119 117 FIBRONECTIN TYPE-III.
 FT DISULFID 31 41 FIBRONECTIN TYPE-III.
 FT DISULFID 70 81 BY SIMILARITY.
 FT CARBOHYD 54 54 BY SIMILARITY.
 FT CARBOHYD 99 99 POTENTIAL.
 FT CARBOHYD 127 127 EVKOLKRYIYLNWKNSSPT -> DYKWEVSCHEALPKSA
 FT VARSPLIC 131 150 KLN (IN SHORT FORM).

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FT  VARSLIC 151 610 MISSING (IN SHORT FORM).
FT  VARSLIC 281 310 KGRSEELSLAGCODEPTDCEDLIVEFL ->
FT  VARSLIC 311 610 TGSPPKRYVLYALPGGFOKLDNAGLDY (IN
FT  VARSLIC 342 539 MEDIUM FORM).
FT  CONFLICT 236 236 MISSING (IN MEDIUM FORM).
FT  CONFLICT 236 236 V -> A (IN REF. 2).
FT  CONFLICT 345 345 G -> V (IN REF. 2).
FT  CONFLICT 465 465 E -> K (IN REF. 1).
FT  CONFLICT 466 466 Q -> E (IN REF. 2).
FT  CONFLICT 469 469 A -> G (IN REF. 2).
FT  CONFLICT 541 541 T -> M (IN REF. 1).
FT  CONFLICT 555 555 Q -> K (IN REF. 2).
SQ  SEQUENCE 610 AA: 68599 MW: C579BC43 CRC32;

Query Match 19.2%; Score 288.5; DB 1; Length 610;
Best Local Similarity 36.4%; Pred. No. 2.1e-18;
Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

OY 75 SLIAGSCLYVGLPPEKPFNISCWSRNKDLTCRTPGANGETFLHNYSLKYLRTYGOD 134
DB 15 SLKSGS-----PPGRPELHKCSPPKERTFCWMPGTGG--LPNYSLTYSKE--GEK 65
OY 135 NT--CEEHYTVGPHSCHIPKD-LALFTPEIWEATNRLGSARSVDLTLDVYTTDPP 191
DB 66 TTYECPDYTSGSPNSCFESKOYTSIKKIYIITVNAINOMGSSSDLYDYVYIVPEPP 125
OY 192 PDVHVSRYGLEDOLSVRV--SPPLAKDF--LFOAKQIIRYVEDSDVMKRVVDVSNQ 246
DB 126 RNULT-EVKQLDKTKTYLWVKWSPPTITVKTGMFMEYERILKPEAEAEWE-IHTGHO 183
OY 247 TSCRLAGLKPGTYEVQVRCNPFYIGSK 275
DB 184 TQFKYEDLYPGOKYLVOTRCRDPHGWMSR 212

RESULT 6
PRLR_RABIT STANDARD: PRT: 616 AA.
AC P14787;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS ORCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORCTOLAGUS.
RN [1]
RN RP RP
RN RC TISSUE-MAMMARY GLAND;
RN RX MEDLINE: 89184578;
RN RX EDEBT W., JOLICOEUR C., LEVI-MEYRUEIS C., DUSANTER-FOUR I.,
RN RX PETRIDOU B., BOUIN J.M., LESUEUR L., KELLY P.A., DJANE J.;
RN RX Identification and sequence analysis of a second form of prolactin
RN RX receptor by molecular cloning of complementary DNA from rabbit
RN RX mammary gland".
RN RX PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
RN [2]
RN RP 3D-STRUCTURE MODELLING OF 30-228.
RN RX MEDLINE: 97248733.
RN RX HALABY D., THOREAU E., DJANE J., MORNON J.P.;
RN RX "Homology modeling of rabbit prolactin hormone complexed with its
RN RX receptor".
RN RX PROTEINS 27:459-468(1997).
RN [3]
RN RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
RN RP PROLACTIN.
RN [4]
RN RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
RN [5]
RN RP SIMILARITY: BELONGS TO THE CYTORINE FAMILY OF RECEPTORS.
RN [6]
RN RP SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
RN [7]
RN RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----
DR EMBL: J04510; G165670; -
DR PIR: A30304; A30304.
DR PDB: 1AN3; 03-DEC-97.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PRAM: PF00041; fn3; 2.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 616 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 235 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 132 132 POTENTIAL.
SQ SEQUENCE 616 AA: 68840 MW: FB6170B1 CRC32;

Query Match 19.0%; Score 286; DB 1; Length 616;
Best Local Similarity 37.8%; Pred. No. 3.6e-18;
Matches 71; Conservative 26; Mismatches 81; Indels 10; Gaps 6;

OY 87 PREKPNISCWSRNKDLTCRTPGANGETFLHNYSLKYLRTYGODTCEEHYTVGPH 146
DB 27 PGKAPFIFCRSPKERTFCWMPGTGG--LPNYSLTYSKE--GEK 65
OY 147 SCHI-KDIALFTPEIWEATNRLGSARSVDLTLDVYTTDPPVHVSRYGLEDQ 205
DB 85 SCYFSKHTSIWITIIITVNAINOMGSSSDRYVYIVPEPPVLT-L-EVNHPEBR 143
OY 206 LSVHVS--PPALKDF--LFOAKQIIRYVEDSDVMKRVVDVSNQSCRLAGLKPGTY 260
DB 144 KYELWVKMLPPTLVDSRGWLTQYERILKPEAEAEWE-THPAGQOTFKILSLPGKY 202
OY 261 FYOVRCPN 268
DB 203 LVQVCRP 210

RESULT 7
IL6B_RAT STANDARD: PRT: 918 AA.
ID IL6B_RAT
AC P40190;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIRURGNAHTH; MORIDAE; MORINAE; RATTUS.
RN [1]
RN RP RP
RN RC TISSUE-LIVER;
RN RX MEDLINE: 93052397.
RN RX WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
RN RX "Molecular cloning and characterization of the rat liver IL-6 signal
RN RX transducing molecule gp130.".
RN RX GENOMICS 14:666-672(1992).
RN [2]
RN RP FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
RN RP IL-6, ILF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING

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CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: M92340; -; NOT ANNOTATED_CDS.
 DR PIR: A44257; A44257.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 DR HSP: P40189; 1B0U.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KM REPEAT.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT TRANSMEM 619 640 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 641 918 POTENTIAL.
 FT DOMAIN 26 120 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 124 221 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 221 221 FIBRONECTIN TYPE-III.
 FT DOMAIN 222 333 FIBRONECTIN TYPE-III.
 FT DOMAIN 334 422 FIBRONECTIN TYPE-III.
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III.
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III.
 FT DOMAIN 724 754 SER-RICH.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 172 181 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 61 61 POTENTIAL.
 FT CARBOHYD 83 83 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 205 205 POTENTIAL.
 FT CARBOHYD 226 226 POTENTIAL.
 FT CARBOHYD 382 382 POTENTIAL.
 FT CARBOHYD 389 389 POTENTIAL.
 FT CARBOHYD 477 477 POTENTIAL.
 FT CARBOHYD 552 552 POTENTIAL.
 SQ SEQUENCE 918 AA; 102450 MW; E6EFCDD0 CRC32;

Query Match 18.7%; Score 281.5; DB 1; Length 918;
 Best Local Similarity 29.0%; Pred. No. 1.5e-17;
 Matches 79; Conservative 46; Mismatches 132; Indels 15; Gaps 7;

QY 1 PTLIGSSLOATCSIHG--DFPGATAGLYWTLNGRRLPSELRLNTSTLALANLN 57
 DB 36 PVGQRSGNFATLVKCKLOYVSVNATYIVKTNHVAIVKEQVYINIRASSVFTDV 95
 QY 58 GSRQSGSDNLYCARQDSILAGSCLYGLPEPEFNISCSRNKADLCMTGANGETP 117
 DB 96 FQNVOLCNLTISGQLEQNYGTLISGYPPDIPFNISCIYVNSGKNMLCOLDPGR--EY 153
 QY 118 LHNYSKLYKLWYAGD--NTCEVHTVGRSHCHPDLAFTYEIVTEATNRLSGARSD 176
 DB 154 LENTYILKSE--WATEFPPCKRTKH--GTSSCMAGTPIYFVNIWEVLENLGNVSS 209
 QY 177 VLLIDVLDVVTDPDPDVHVSRYVGGLEDQLSVRWSPALKDLFLQAKYQIRRVEDSDV 236

DB 210 PINEDPVAKRSPPHNLSYNSSELSILKLAWNSGL--DSLRLKSDIQYRFDKAST 267
 QY 237 MKVY--DDYSNOTSCRLAGLKPQIVYFQVR 265
 DB 268 MIVPLEDVTSPRSFTVODLKPFEYFVR 299

RESULT 8
 PRLR_CHICK 831 AA.
 AC 004594;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 15-JUN-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CRLP).
 GN PRLR.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; GALLIFORMES; PHASIINIDAE; PHASIININAE; GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE, DEGHORN; TISSUE-KIDNEY;
 RX MEDLINE; 93075121.
 RA TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from
 the cDNA sequence".
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: D13154; G222849; -
 DR PIR: J01655; J01655.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFAM: PF00041; fn3; 4.
 DR HSP: P16471; 1BP3.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438 PROLACTIN RECEPTOR.
 FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 123 225 FIBRONECTIN TYPE-III.
 FT DOMAIN 228 325 FIBRONECTIN TYPE-III.
 FT DOMAIN 326 428 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 91 91 POTENTIAL.
 FT CARBOHYD 100 100 POTENTIAL.
 FT CARBOHYD 112 112 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 FT CARBOHYD 303 303 POTENTIAL.
 FT CARBOHYD 315 315 POTENTIAL.
 FT CARBOHYD 335 335 POTENTIAL.
 SQ SEQUENCE 831 AA; 94102 MW; B977BE07 CRC32;

Query Match 18.7%; Score 281; DB 1; Length 831;

FT	DISULEID	35	46	BY SIMILARITY.
FT	CARBOHYD	75	86	BY SIMILARITY.
FT	CARBOHYD	59	59	POTENTIAL.
FT	CARBOHYD	91	91	POTENTIAL.
FT	CARBOHYD	100	100	POTENTIAL.
FT	CARBOHYD	112	112	POTENTIAL.
FT	CARBOHYD	132	132	POTENTIAL.
FT	CARBOHYD	262	262	POTENTIAL.
FT	CARBOHYD	303	303	POTENTIAL.
FT	CARBOHYD	315	315	POTENTIAL.
FT	CARBOHYD	335	335	POTENTIAL.
SO	SEQUENCE	831 AA.	94394 MW.	FB15C98 CRC32;

Query Match 18.6%; Score 280; DB 1; Length 831;
Best Local Similarity 36.5%; Pred. No. 1.8e-17;
Matches: 69; Conservative 25; Mismatches 83; Indels 12; Gaps 7;

QY	PEPKPENICSRNKKDLCTKRTPGAGETFLH-TNYSLKTKLRMYGODNTCEEYHTVGP	145
DB	230 PEKPTITTCRPERKETFCWKPGLDGG---HPTNYTLKXKEGEGVEYCPDRTAGP	286
QY	146 HSCHI-PRDLATFTPEIWEATNLSGARSQVLLDVLDTVYTDPPDV--HYSRNGGL	202
DB	287 NCCEYPRKRTTSWTYNTYNTVTKATNEMSSSDPHYVDYTYIVQDPDPANVLELKKPINR	346
QY	203 EDOLSVRWVSPALADF--LEQATQIYRYREDSVDKRVVDVDSNOTSCRGLAKGQTV	259
DB	347 KYLLMLTW-SPEPLADVSGWLLTLDYELRLRPEEGEEMETV-FVGGQTOYKMFSLNPGKK	404
QY	260 YVVOVRCPN 268	
DB	405 YVVOHCKR 413	

RESULT 10
IL6_MOUSE
ID IL6_MOUSE STANDARD; PRT; 917 AA.
AC 000560;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS MUS MUSCULUS (MOUSE).
OC EIDAROTIA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
NC ROSENTIA; SCUROGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ICR; TISSUE-MACROPHAGE.
RX MEDLINE; 92281532.
RA SATO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo."
RL J. IMMUNOL. 148:4066-4071(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.
CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES DURING THE REST OF EMBRYOGENESIS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONSTAINS ONE IG-LIKE DOMAIN.


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CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: X62646; G840817; -
DR EMBL: M83336; G193592; -
DR MGD: MGI:96560; IL6ST.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 3.
DR HSSP: P40189; IL6U.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW REPEAT.
FT SIGNAL 1 22
FT CHAIN 23 917
FT TRANSMEM 23 617
FT DOMAIN 618 639
FT DOMAIN 640 917
FT DOMAIN 26 120
FT DOMAIN 124 220
FT DOMAIN 221 322
FT DOMAIN 323 420
FT DOMAIN 422 515
FT DOMAIN 516 611
FT DOMAIN 723 741
FT DISULFID 134 144
FT DISULFID 172 180
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157
FT CARBOHYD 225 225
FT CARBOHYD 388 388
FT CARBOHYD 476 476
FT CARBOHYD 551 551
SQ SEQUENCE 917 AA; 102452 MW; A5DCD259 CRC32;

Query Match 18.5%; Score 279; DB 1; Length 917;
Best Local Similarity 28.7%; Pred. No. 2.5e-11;
Matches 78; Conservative 46; Mismatches 132; Indels 16; Gaps 7;

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AC Q28235;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS CERUUS ELAPHUS (RED DEER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
OC CERUUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 96030711.
RA CLARE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
RA KELLY P.A., JABBOUR H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis.";
RL J. ENDOCRINOL. 146:313-321(1995).
-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
-1- PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: X94953; E218406; -
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 2.
DR HSSP: P14787; IAN3.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
KW REPEAT.
FT SIGNAL 1 24
FT CHAIN 25 581
FT TRANSMEM 25 234
FT DOMAIN 235 258
FT DOMAIN 259 581
FT DOMAIN 122 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 581 AA; 65159 MW; 721F0366 CRC32;

Query Match 18.4%; Score 276.5; DB 1; Length 581;
Best Local Similarity 34.0%; Pred. No. 2.4e-17;
Matches 71; Conservative 35; Mismatches 88; Indels 15; Gaps 7;

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Db 189 TOLKIFSLYPGOKLYVQVRCCKPDHGYMSE 217

RESULT 12

PRLR_BOVIN

STANDARD; PRT: 581 AA.

AC 028172;

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS BOS TAURUS (BOVINE).

OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDEA; BOVINA; BOVINAE; BOS.

RP SEQUENCE FROM N.A.

RC TISSUE-ENDOMETRIUM;

MELINE; 93246019.

RA SCOTT P., KESSLER M.A., SCHULER L.A.;

RT "Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues."

RL MOL. CELL. ENDOCRINOL. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: L02549; G163618;

DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.

DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.

DR PFAM; PF00041; fn3; 2.

DR HSSP; P14787; 1AN3.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 581 PROLACTIN RECEPTOR.

FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 235 258 POTENTIAL.

FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III.

FT DISULFID 123 227 FIBRONECTIN TYPE-III.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 POTENTIAL.

FT CARBOHYD 132 132 POTENTIAL.

SO SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 18.3%; Score 276; DB 1; Length 581;

Best Local Similarity 32.1%; Pred. No. 2.6e-17;

Matches 78; Conservative 37; Mismatches 88; Indels 40; Gaps 9;

Db 41 SRLMTSTLALANINGSHQSGDNLVCHARBGSILAGSCLVGLPPEPFINISCSRN 100

7 SRVFLFLFLSLVSLNG---QS-----PPEPKLVKCRNSPG 40

101 MDLJCRMTPGAHEFTLNTSLKYLKRWYGDNTCEHYHVPSCRI--PDLALFTP 159

41 KEFTCWMPGADGG--LPTNVLTLTKHKESELIHCPDKTKGPNKSCYKSKHTSIWKA 98

160 YELWVATNRLGARSADVLTLDVLDVYTTDPPDVHVSRYVGLDLSYRV--SPALK 217

99 YATTAIVAINOMGSSDPLVHTVYIVPEPPANLTL-ELKHEDRKRPYIMIKMSPPTM 157

QY 218 D-----FLFAKQVIRVEDSYDAKTVDDVSNQTSCLAGLKPGTVYFVQVRCNPFGLY 272

Db 158 DVKSGWFIIO--YEIRLKEKATDWE--THFTLKQOLKIFNFYPGOKLYVQVRCNPDHGY 214

QY 273 GSK 275

Db 215 MSE 217

RESULT 13

PRLR_ORENI

STANDARD; PRT: 630 AA.

AC 091513;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS OROCHOMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).

OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;

OC LABROIDEI; CICHLIDAE; TILAPIA.

RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;

MELINE; 95320210.

RA SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;

RT "Expression cloning of a cDNA encoding a fish prolactin receptor."

RL PROC. NATL. ACAD. SCI U S A. 92:6037-6041(1995).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: L34783; G903847;

DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.

DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.

DR PFAM; PF00041; fn3; 2.

DR HSSP; P16471; 1BP3.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 630 PROLACTIN RECEPTOR.

FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 235 258 POTENTIAL.

FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 24 123 FIBRONECTIN TYPE-III.

FT DISULFID 124 228 FIBRONECTIN TYPE-III.

FT DISULFID 37 47 BY SIMILARITY.

FT DISULFID 76 87 BY SIMILARITY.

FT CARBOHYD 92 92 POTENTIAL.

FT CARBOHYD 101 101 POTENTIAL.

SO SEQUENCE 630 AA; 70810 MW; E9A4E553 CRC32;

Query Match 15.5%; Score 233; DB 1; Length 630;

Best Local Similarity 33.7%; Pred. No. 2.1e-13;

Matches 64; Conservative 25; Mismatches 85; Indels 16; Gaps 8;

QY 88 PEKPFINISCSNRMDLJCRMTPGAHEFTLNTSLKYLKRWYGDNTCEHYHVPSCRI 147

Db 29 PKPFPIKRSRSEKFTFCWMPGSDGG--LPTTALYLRKSGSDVHVECPDYHTAGRNS 86

QY 148 CHIPDIAL-FTPYEIVWATNRLGARSADVLTLDVLDVYTTDPPDVHVSRYVGLDGO 206

DB 87 CFFNNKNTLWVSINTVATNALGKTGTPDIDVYVYVPHRPEKLEVT---YAKDOG 143
 OY 206 ---LSRWVSPALKDF---LEQAKQIRNVED-SVDMKVYDDVSNQTSCLAGKPGT 258
 DB 144 WPELRVSW-EPPKADRTSGWITLIVELRVKLEDESEWE-NMAQOQKMFNFISRSRG 201
 OY 259 VYFVQVRCNP 268
 DB 202 TYLIQVRCNP 211

RESULT 14
 GCSR.HUMAN
 ID GCSR.HUMAN STANDARD: PRT: 836 AA.
 AC 099062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 DE (CD114 ANTIGEN).
 GN CSF3R OR GCSR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RC MEDLINE: 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMPEL S., SIMS J.E., COSMAN D.,
 RA PARK L., SORENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein.";
 RL J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RC MEDLINE: 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor.";
 RL PROC. NATL. ACADE. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor.";
 RL J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RC MEDLINE: 92007729.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor.";
 RL EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RC MEDLINE: 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the W54S
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELLING OF 125-331.
 RC MEDLINE: 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis.";
 RL J. BIOL. CHEM. 273:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION

CC -1- EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSR-1 (SHOWN UNDER),
 CC GCSR-2, GCSR-3 AND GCSR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;
 CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV, NOTE-CD guide CD114 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
 CC -----
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 CC -----
 CC EMBL: X55721; G31697; -;
 CC EMBL: X55720; G31699; -;
 CC EMBL: S71484; G240884; -;
 CC EMBL: M59818; G183047; -;
 CC EMBL: M59819; G485364; -;
 CC EMBL: M59820; G183049; -;
 CC PIR: JH0329; JH0329;
 CC PIR: JH0330; JH0330;
 CC PIR: A38252; A38252;
 CC PDB: 1A27; 28-JAN-98.
 CC MIM: 138971; -;
 CC MIM: 202700; -;
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAV: PF00041; I13; 3.
 CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC REPEAT; ALTERNATIVE SPLICING; 3D-STRUCTURE.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 836
 CC FT
 CC FT DOMAIN 25 627
 CC FT TRANSMEM 628 650
 CC FT DOMAIN 651 836
 CC FT DOMAIN 25 117
 CC FT DOMAIN 121 227
 CC FT DOMAIN 228 332
 CC FT DOMAIN 333 428
 CC FT DOMAIN 429 525
 CC FT DOMAIN 526 621
 CC FT DISULFID 131 142
 CC FT DISULFID 248 295
 CC FT DISULFID 266 309
 CC FT CARBOHYD 51 51
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 128 134
 CC FT CARBOHYD 134 134
 CC FT CARBOHYD 389 389
 CC FT CARBOHYD 474 474
 CC FT CARBOHYD 579 579
 CC FT CARBOHYD 610 610
 CC FT VARSPLIC 750 783
 CC FT
 CC GRANULOCYTE COLONY STIMULATING FACTOR
 CC RECEPTOR.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC IG-LIKE C2-TYPE DOMAIN.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC BY SIMILARITY.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC VLYGGLSPSPGSHYLRCDSTOPLAGLTPS ->
 CC AGPPRSAYFKQMLHAPRGLGCLPPIYSVL

FT VARSPLIC 784 836 (IN GCSF-4/D7).
 FT VARSPLIC 680 680 MISSING (IN GCSF-4/D7).
 FT VARSPLIC 622 836 E -> ELPGPROGOWIGOTSEMSRALTFRPCVO
 (IN GCSF-3).
 FT VARSPLIC 622 836 EGSELIITGLGILLITLCLOCTAMICCSPPRRNPMPV
 PDPAHSHSNSETGMDLQPLVQTVYLOQDPRAVVSQPOS
 GTSQVILGOLIGLSTSPGPHYLACDSTOPLALGIR
 SYENLMFQASPLGLVTPAPSOEDDCVGPILNPLGIR
 VHGMALGSF -> APTGRIPSGVSGSCORCRAAAGCPOS
 WRRMSSCPALARPSPSSQCRMRKRRCGSPITACRPV
 ASPIMRPMGCRGROEPPSPNSBLALAIEMGSCWAAP
 OAGQGTISAVTPLSPSPWRASPPAPSPMTSGSRAPMGPN
 (IN GCSF-2).
 FT SEQUENCE 836 AA; 92156 MM; 9CC075DD CRC32;

Query Match 14.8%; Score 222; DB 1; Length 836;
 Best Local Similarity 28.2%; Pred. No. 2.9e-12;
 Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

QY 1 PTLIGSSLOATCSIHGDPGATAE-GLYTLNGRRRLPSELSRLN--TSTIALALANL 57
 114 GEPFLHNTYSK-KLAWYGO---DNICEEHTYVPHSCHIP-KDLALFTYEIWEVENTN 168
 149 -ETHLPSTFLKSKSGNCGTQSGDILDCVPKDGSHCCIPRHLILLYQNMGIWQAEN 207
 QY 169 RLGSARSDVLTLDVLYV-----TTDPPDVHVSNGLEQQLSVRWSPALNDEL 220
 208 ALGTSMSPOLCLDPMDVVKLEPMLRTMDSPPEAPPAQAGLO---LCW--EPWQGLH 261
 QY 221 FQAKYQIRYVE-DSVWKVYVDVSNQ-TSCRLAGLPGYVYQVNC 266
 262 INKCELRHPRGEMASWALYGLPLALQVLELGLLPATVITQING 309

RESULT 15
 ID GCSR_MOUSE STANDARD; PRT; 837 AA.

AC 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 CSF3R OR CSFGR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDA; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90235283.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., SENO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor."
 RL CELL 61:341-350(1990).
 RN [2]
 RP STRUCTURE BY NMR OF 225-333.
 RX MEDLINE; 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WSKMS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand."
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE Ig-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 or send an email to license@isb-sib.ch).

DR EMBL; M58288; G193455;
 DR PIR; A34898; A34898;
 DR PDB; 1GCF; 22-OCT-97.
 DR PDB; 1CTO; 22-OCT-97.
 DR MGI; 86533; CSFGR.
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM; PFO0041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 FT SIGNAL 1 25
 FT CHAIN 26 837
 FT DOMAIN 26 626
 FT TRANSMEM 627 650
 FT DOMAIN 651 837
 FT DOMAIN 26 118
 FT DOMAIN 122 228
 FT DOMAIN 229 333
 FT DOMAIN 334 431
 FT DOMAIN 432 528
 FT DOMAIN 529 624
 FT DISULFID 132 143
 FT DISULFID 249 296
 FT DISULFID 267 310
 FT CARBOHYD 51 51
 FT CARBOHYD 94 94
 FT CARBOHYD 129 129
 FT CARBOHYD 186 186
 FT CARBOHYD 279 279
 FT CARBOHYD 392 392
 FT CARBOHYD 408 408
 FT CARBOHYD 474 474
 FT CARBOHYD 487 487
 FT CARBOHYD 582 582
 FT CARBOHYD 613 613
 SO SEQUENCE 837 AA; 93406 MM; D55F84D4 CRC32;

Query Match 14.7%; Score 221.5; DB 1; Length 837;
 Best Local Similarity 28.9%; Pred. No. 3.2e-12;
 Matches 83; Conservative 46; Mismatches 127; Indels 31; Gaps 14;

QY 1 PTLIGSSLOATCSIHGDPGATAE-GLYTLNGRRRLPSELSRLN--TSTIALALANL 56
 34 PVRLDPPVLAASCTISPNCKLDOQAKILRLADEPIQGDROHNLDPDQESLITLPHL 93
 QY 57 NGSROOSDNLVCHARDGSIAGSCLYVGLPPEKPNISQMSR-NKKDLTCRWTPAHGE 115
 94 NTA-QAFLCYVPMWESYVLLQDAELHAGYPRASPNELCLHNTINSLYCOWEPGP--E 150
 QY 116 TPLATYSK-KLAWYGO---DNICEEHTYVPHSCHIP-KDLALFTYEIWEVENTNL 170
 151 TPLPSTFLKSKSGNCGTQSGDILDCVPKDGSHCCIPRHLILLYQNMGIWQAENL 210
 QY 171 GSARSDVLTLDVLYV-----TTDPPDVHVSNGLEQQLSVRWSPALNDEL 221
 211 GSSEPKCLDPMDVVKLEPMLRTMDSPPEAPPAQAGLO---LCW--EPWQGLH 263

OY 222 OAKYORRYVE-DSDVMKYVDDV-SNOTSCRLAGLPGYVYVQYRC 266
Db 264 EOCELRIOPOUKGANWILVHLPSSKDOFEICGLHOAPVYTLQWRC 310

Search completed: September 17, 1999, 03:10:14
Job time: 294 sec

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:08 ; Search time 68.96 Seconds
(without alignments)
248.102 Million cell updates/sec

Title: US-09-037-657-19

Sequence: 1505
1 PILLIGSSSQATCSHGDP.....VFYVQVCNPFYIGSKKAG 278

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

SPTREMBL_10:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertibrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1463	97.2	422	4	075462	075462 homo sapien
2	326	21.7	881	13	057519	057519 xenopus lae
3	302	20.1	206	4	016354	016354 homo sapien
4	282.5	18.8	581	6	046561	046561 ovis aries
5	276	18.3	296	6	018880	018880 bos taurus
6	240	15.9	346	13	093404	093404 oreochromis
7	230.5	15.3	198	6	018985	018985 cervus elap
8	208	13.8	217	6	046386	046386 mustela vis
9	203	13.5	335	6	P79203	P79203 ovis aries
10	178	11.8	862	4	099665	099665 homo sapien
11	175	11.6	422	4	016542	016542 homo sapien
12	172.5	11.5	372	11	088507	088507 mus musculu
13	171	11.4	874	11	P97378	P97378 mus musculu
14	165	11.0	432	11	P70225	P70225 mus musculu
15	164	10.9	432	11	064385	064385 mus musculu
16	161.5	10.7	710	13	057520	057520 xenopus lae
17	160	10.6	1165	6	002671	002671 sus scrofa
18	156	10.4	895	11	062960	062960 rattus norv
19	154.5	10.3	440	11	000343	000343 mus musculu
20	148	9.8	1896	4	060468	060468 homo sapien
21	148	9.8	1571	4	060469	060469 homo sapien
22	146	9.7	958	4	092920	092920 homo sapien
23	146	9.7	1165	4	092921	092921 homo sapien
24	146	9.7	958	4	013592	013592 homo sapien
25	146	9.7	906	4	013593	013593 homo sapien
26	146	9.7	896	4	013594	013594 homo sapien
27	146	9.7	896	4	092919	092919 homo sapien
28	142.5	9.5	86	6	018853	018853 mustela put
29	142	9.4	228	11	035228	035228 mus musculu

30	142	9.4	279	11	064236	064236 rattus norv
31	136	9.0	269	6	P79195	P79195 macaca mula
32	134	8.9	229	4	075269	075269 homo sapien
33	134	8.9	634	6	046600	046600 bos taurus
34	132.5	8.8	971	11	070458	070458 mus musculu
35	132.5	8.8	970	11	088821	088821 mus musculu
36	129.5	8.6	316	11	035545	035545 rattus norv
37	128.5	8.5	383	11	086786	086786 mus musculu
38	126	8.4	229	4	014213	014213 homo sapien
39	123	8.2	1299	4	092823	092823 homo sapien
40	123	8.2	2051	5	044328	044328 hirtudo medl
41	123	8.2	229	6	027950	027950 bos indicus
42	123	8.2	229	6	028206	028206 bos taurus
43	120.5	8.0	1093	11	070535	070535 rattus norv
44	120.5	8.0	1277	13	098902	098902 fuigu rubrip
45	117	7.8	1299	4	015179	015179 homo sapien

ALIGNMENTS

RESULT 1

ID 075462 PRELIMINARY; PRT; 422 AA.

AC 075462;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE CYTOKINE-TYPE-1 RECEPTOR

GN CLF-1.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREUTNER D.,

RA MEMOND L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.;

RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the

RT Cytokine Type-1 Receptor Family.";

RL J. Immunol. 0:0-0(1998).

DR EMBL; AF059293; AAC28335.1; -

KW PEFAM; PF00041; fn3; 2.

FT SIGNAL.

FT SIGNAL 1 37 POTENTIAL.

FT CHAIN 38 422 CYTOKINE-TYPE-1.

FT SEQUENCE 422 AA; 46301 MW; 877F9BC9 CRC32;

Query Match 97.2%; Score 1463; DB 4; Length 422;

Best Local Similarity 96.4%; Pred. No. 2.6e-135;

Matches 268; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY	1	PILLIGSSSQATCSHGDPFGATAGCTTTLNGRRLPSELSTLALANLNGSR	60
DB	48	PILLIGSSSLATCSVHGDPFGATAGCTTTLNGRRLPSELSTLALANLNGSR	107
QY	61	QOSGDNVLCVHARDGSIILAGSCLYVGLPPEKPNISCSNMMDLTCRTPPAHGTFEHT	120
DB	108	QSGDNVLCVHARDGSIILAGSCLYVGLPPEKPNISCSNMMDLTCRTPPAHGTFEHT	167
QY	121	NTSLYKRLKMTGQDNTCEHYTVGPHSCHIPEDLALFTPELWVATNRLSARSDVLT	180
DB	168	NTSLYKRLKMTGQDNTCEHYTVGPHSCHIPEDLALFTPELWVATNRLSARSDVLT	227
QY	181	DVLADVYTTDPPDVHVSVGLLEQDLSVRAWSPRLKPFLLQAKQIIRVSDVDMRV	240
DB	228	DILADVYTTDPPDVHVSVGLLEQDLSVRAWSPRLKPFLLQAKQIIRVSDVDMRV	287
QY	241	DDVSNQTSCLAGLKPFTVYFVQVCNPFYIGSKKAG 278	
DB	288	DDVSNQTSCLAGLKPFTVYFVQVCNPFYIGSKKAG 325	

RESULT 2
ID 057519 PRELIMINARY: PRT: 881 AA.
AC 057519;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE GP130P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA CHEN J., GRACE A., CHIEN K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041845; AAC03531.1;
DR PFAM: PF00041; fn3; 4.
SQ SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

Query Match 21.7%; Score 326; DB 13; Length 881;
Best Local Similarity 30.5%; Pred. No. 1.5e-23;
Matches 84; Conservative 41; Mismatches 110; Indels 40; Gaps 8;
QY 15 INGDTEGAT-----ABGLYWTNGRRLPSELRLSTLALALANGSRQ 62
DB 37 VHGEPETACVINGTCLREDASRIYLVGVKVPETQYELNQTSSVTEFLTLNSP 96
QY 63 SGDNVCHARDGSLAGSCIVLPPPEKPNICSRNKKDLTCRTPGAHGTEFLHTY 122
DB 97 LTCNVASGHVANTLGIFFTLGLPPDKPTNLICIVNDNLCTWDPCR--PTNLPY 154
QY 123 SLTKLRM-----YGDNTCEEYHTVPSHCHIPKDLAFTPEIWEATNRLGSAR 174
DB 155 TLSH--RMHFGANYGRANNSC-----TIHSP-GEQFIIDTTFQVEATNELGIOR 202
QY 175 SDVLTDLDVDTTDPDPVHVRVGLGDLQSVRVSPALKDPLFOAKYQIRYVEDS 234
DB 203 SETLITDPVNIKPNPOLSELISLELPALKEKNPFT--NAFNLYNIRYRPVKT 259
QY 235 VDMKRV--DVSNOTSCRLAGLKPGTYFVQVRC 266
DB 260 QDMEMPEEDTASHRDSFTLDLPLTYEVYSIRC 294

RESULT 3
ID 016354 PRELIMINARY: PRT: 206 AA.
AC 016354;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast cancer cell lines."
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL: S78505; AAB34470.1;
DR PFAM: PF00041; fn3; 2.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match 20.1%; Score 302; DB 4; Length 206;
Best Local Similarity 39.2%; Pred. No. 4.9e-22;

Matches 74; Conservative 25; Mismatches 80; Indels 10; Gaps 6;
QY 86 LPEKPFNISCNRNKKDLTCRTPGAHGTEFLHTNYSKYLRYGQNTCEEYTVGP 145
DB 2 LPPGKEIRKCSNPKNETTCMRPCTDGG--LPTNYSLETHHEGTLNHECDYITGGP 59
QY 146 HSCHPKD-LALFTPEIWEATNRLGSARSDVLTLDVDTTDPDPVHVRVGLPD 204
DB 60 NSCHFQKQYTSNWRVYIMAVNATNMGSSFDLYVDVTVIYQDDPLELAV-EVKQPD 118
QY 205 QLSVRNV--SPRLADF--LQAKQIRYVEDSDMKAVDDVSNQTSGLAGLPQVY 259
DB 119 RRPYIMIKWSPPLTLDLKTGWFTLAYEIRLKEKAEME-IRFAGQTEFKLSLHPGOK 177
QY 260 YFVOVRCNP 268
DB 178 YLVQVRCNP 186

RESULT 4
ID 046561 PRELIMINARY: PRT: 581 AA.
AC 046561;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 98001468.
RA BIGNON C., BINAUT N., ORMANDY C., SCHULER L.A., KELLY P.A.,
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA BIGNON C., DIJANE J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041257; AAB96795.1;
DR PFAM: PF00041; fn3; 2.
KV Signal.
FT SIGNAL 1 24
FT CHAIN 25 581 PROLACTIN RECEPTOR LONG FORM.
SQ SEQUENCE 581 AA; 65235 MW; 6792A7C7 CRC32;

Query Match 18.8%; Score 282.5; DB 6; Length 581;
Best Local Similarity 35.3%; Pred. No. 1.6e-19;
Matches 73; Conservative 32; Mismatches 87; Indels 15; Gaps 7;

QY 75 SLIASCILYVGPPEKPFNISCNRNKKDLTCRTPGAHGTEFLHTNYSKYLRYGQD 134
DB 20 SLINQOS-----PPEKPKIKRCSPEKETFTCMWEPGADG--LPTNITLYTRKEGETI 72
QY 135 NTCEEYHTVGPCHIPRD-LALFTPEIWEATNRLGSARSDVLTLDVDTTDPDPD 193
DB 73 HECPPYKTKGPNRCYFSKYSITMAYITVASINOMGSSDPLYVDVTVIYEPDPVN 132
QY 194 VHSVVGLEQDLSVRWV--SPRLADF--LFOAKYQIRYVEDSDMKAVDDVSNQTS 248
DB 133 LTL-ELKHPEDEKRPYLWIKWSPPLTLDVKSQWFSIOYERLPERKATDME-THFAPIKIQ 190
QY 249 CRLAGLKPGTYFVOVRCNPFQYSGK 275
DB 191 LKIFNLVPGQKIVQIRCKPDHGYSW 217

RESULT 5
ID 018880 PRELIMINARY: PRT: 296 AA.
AC 018880:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
SEQUENCE FROM N.A.
MEDLINE: 97375450.
RA SCHUER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
tissues.";
RL Endocrinology 138:3187-3194(1997).
OR EMBL: AF027403; AAB8399.1; -.
OR PFM: PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match
Best Local Similarity 18.3%; Score 276; DB 6; Length 296;
Matches 78; Conservative 37; Mismatches 88; Indels 40; Gaps 9;
41 SLTLTSTLALANLNGSRQSGDNLVCHARGSLASCLYVGLPPEKPNISGWSRN 100
7 SHVVEILLFLFSLNG--QS-----PPEKPLVRCRSPG 40
101 MKDLICRTPGHAGTFTHTNSLKYKLMWYGDNTCEHYHTVPHSCHI-PKDLALFIP 159
41 KETFCWEPGADG--LPTNYTLHYHKEGELIHECPYKKGPNCSFKSKHSHW 98
160 YEIWEATNRGASRSDVLTLDVYVTTDPDVHVSFVGLDQLSYRVY--SPALK 217
99 YVIVNAINONGISSDPLVHYVYVEPEPANTL-ELKHEDRKRYLWKNSPPTMT 157
218 D-----ELFOAKYQIRYVEDSVPMKYVDVSNQTSCLAGLKPCTVTFVQVRCNPFQIY 272
158 DVKSGMPLIO--YEIRLKPEKATDWE-THTLKQTQIKIFMLPGQKYLQVIRCPDHG 214
273 GSK 275
215 WSE 217

SULT 6
ID 093404 PRELIMINARY: PRT: 346 AA.
AC 093404:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DE 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
RN [1]
SEQUENCE FROM N.A.
TISSUE-GILL;
SHIRAIISHI K., MATSUDA M., MORI T., TENSYA H.;
RT "Expression of prolactin and cortisol receptor gene in early-life
stages of tilapia (Oreochromis mossambicus).";
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
OR EMBL: AF080247; AAC31825.1; -.
OR PFM: PF00041; fn3; 2.
NON_TER 346 346
SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match
Best Local Similarity 15.9%; Score 240; DB 13; Length 346;
Matches 64; Conservative 27; Mismatches 83; Indels 16; Gaps 8;
QY 88 PEKPNISGWSRNMDLTCRWTPGAGHGTFTHTNSLKYKLMWYGDNTCEHYTVGHS 147
DB 29 PGKPEITCRSPKEKETFQWKPSPDGG--LPTNYTLHYHKEGELIHECPYKKGPNCSFKSKHSHW 98
QY 148 CHIRK-DLALTPPEIWEATNRGASRSDVLTLDVYVTTDPDVHVSFVGLDQLSYRVY--SPALK 217
DB 87 CFENKNDTLIWSYINITYVATNALGKTSYDVIDVYIYKPHPEKLEVT--VMKDOG 143
QY 206 ---LSVRVSPALKDF---LFOAKYQIRYVED-SYDMKYVDVSNQTSCLAGLKPCT 258
DB 144 WPELRVSW-EPPHADRSGMWTITLYELRVKLEDESEWE-NHAAGQKKNFISLSRSG 201
QY 259 YVIVQVRCNP 268
DB 202 TYLIQVRCNP 211

RESULT 7
ID 018985 PRELIMINARY: PRT: 198 AA.
AC 018985:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE SOLUBLE PROLACTIN RECEPTOR.
OS Cervus elaphus nelsoni (American elk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervidae;
RN [1]
SEQUENCE FROM N.A.
RA JABBOUR H.N.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y14753; CAJ75048.1; -.
OR PFM: PF00041; fn3; 1.
SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match
Best Local Similarity 15.3%; Score 230.5; DB 6; Length 198;
Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;
QY 73 DGSILASCLYVGLPPEKPNISGWSRNMDLTCRWTPGAGHGTFTHTNSLKYKLMWY 132
DB 18 NASLNGS-----PPEKPLVRCRSPGKETFQWEPGSDG--LPTNYTLHYHKEGEL 70
QY 133 QDNTCEHYHTVPHSCHI-PKDLALFPEIWEATNRGASRSDVLTLDVYVTTDP 191
DB 71 LIHECPDYKSGNPTCYFSKHSYKTYITVYNALNONGVSSSDPLVYIYVPEPP 130
QY 192 PDVHVSFVGLDQLSYRVY--PPALKDF---LFOAKYQIRYVEDSVDMKYVDVSNQ 246
DB 131 ANTL-ELKHEDRKRYLWKNSPPTMTLTVKSGMPLIOYEIRLKPEKATDWE-HDDLHP 188
QY 247 TSCR 250
DB 189 TSSR 192

RESULT 8
ID 046386 PRELIMINARY: PRT: 217 AA.
AC 046386:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
RN [1]
SEQUENCE 217 AA; 22652 MW; COABAB0 CRC32;

05 Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA DOUGLAS D.A., SONG J.-H., HOUDE A., MURPHY B.D.;
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF029294; AAB88899.1;
 RF PFM; PF00041; fn3; 1.
 FT NON-TER 1
 FT NON-TER 1
 SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 13.8%; Score 208; DB 6; Length 217;
 Best Local Similarity 32.7%; Pred. No. 8.4e-13;
 Matches 54; Conservative 29; Mismatches 72; Indels 10; Gaps 6;

QY 110 PGHGETFHTNYSLKXKRWGDNCEHYHVGPHSCHI-PKDLALFPEIWEATN 168
 DB 2 PEDGG--PPTTYLTHHEGETTTECPDYITSGPNSCTFKNKTSITMTITINATN 59
 QY 169 RIGSARSDVLTLDVYTTDPPDVHVRVGGLEDQLSVRWVS--PPALKEF--LFOA 223
 DB 60 EMGSSSDRYVTLTYIVEDPPVNST-ELKQPEDKTYLTKWPPTLVDVRSGLML 118
 QY 224 KQIIRVEDSDVKYVDVSNQTSCLAGLKGTYFYOVRCNP 268
 DB 119 QYIIRLKEKATDME-THFAGLQTOFKILSLYPGKYLVOIRCKP 162

RESULT 9
 ID P79203 PRELIMINARY; PRT; 335 AA.
 AC P79203;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY;
 RA FORTONESE D.T., BROOKS J., INGLETON P., MCNEILLY A.S.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; Y10578; CAA71597.1;
 RF PFM; PF00041; fn3; 1.
 FT NON-TER 1
 FT NON-TER 1
 SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 13.5%; Score 203; DB 6; Length 335;
 Best Local Similarity 31.5%; Pred. No. 4.6e-12;
 Matches 53; Conservative 28; Mismatches 63; Indels 24; Gaps 6;

QY 114 GETFHTNYSLKXKRWGDNCEHYHVGPHSCHI-PKDLALFPEIWEATNRLGS 172
 DB 8 GETLH-----ECPDYITGSPNSCTFKNKTSITMTITINATN 51
 QY 173 ARSDVLTLDVYTTDPPDVHVRVGGLEDQLSVRWVS--PPALKEF--LFOA 227
 DB 52 SSSDPLVDYTYIVEDPPVNST-ELKQPEDKTYLTKWPPTLVDVRSGLML 110
 QY 228 RRVEDSDVKYVDVSNQTSCLAGLKGTYFYOVRCNPFGITGSK 275
 DB 111 RLKPEKATDME-THFAPKLTOLKIFNLXPGKYLVOIRCKP 157

RESULT 10
 ID 099665 PRELIMINARY; PRT; 862 AA.
 AC 099665;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE IL-12 RECEPTOR BETA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., MABAYI N., WOU C.Y.,
 RA GATELY M.K., GUBLER U.;
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U64198; AAB36675.1;
 RF PFM; PF00041; fn3; 37134 MW; 5FE4FBD5 CRC32;
 SQ SEQUENCE 862 AA; 97134 MW; 5FE4FBD5 CRC32;

Query Match 11.8%; Score 178; DB 4; Length 862;
 Best Local Similarity 24.8%; Pred. No. 4.6e-09;
 Matches 73; Conservative 43; Mismatches 106; Indels 72; Gaps 12;

QY 3 LIGSSLOATCSIHGDPGATAGLWTL-----NGRRPSELRL-L 44
 DB 41 ILGSTVNTCSL-----KPRGCFHYSRNKLILYKEDRRINRHHGSLNSQVGLPL 94
 QY 45 NSTALANLNGSGNDNLVCHARGSTILAGSCLVGH-PPEKPFNISCVRNMK-D 103
 DB 95 GTTLFVCKLACINSEIDQ-----ICGAEITGVAFEDOPOLSCIQKEOQT 140
 QY 104 LCRWTPGAHGETFHTNYSLKX---KLWYGO--DNTCEHYHVG-----PHSCHI 150
 DB 141 VACTWGRG--DTHLYTETTLQSLGPKNLTKQCKDIDC-DYLDGINKLPSPSNT 197
 QY 151 PKDLALFPEIWEATNRLGSARSDVLTLDVYTTDPPDVHVRVGGLEDQLSVRW 210
 DB 198 AK-----VTAVNSIGSSSSLPSTFTEFDIVRPLPMDIRIKFORASVRCGLY 246
 QY 211 VSPALKEFPAKQIRRVEDSDVKYVDVSNQTSCLAGLKGTYFYOV 264
 DB 247 -----RDEGLVLLNRLRYRPSNLSRLMNVYTKAKGRHDLDPTEYEFQI 294

RESULT 11
 ID 016542 PRELIMINARY; PRT; 422 AA.
 AC 016542; Q14626;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RC MEDLINE; 95399754.
 RA CHEREL M., SOREL M., LEBEAU B., DUBOIS S., MOREAU J.F., BATAILLIE R.,
 RA MINVILLE S., JACOBS Y.;
 RL "Molecular cloning of two isoforms of a receptor for the human
 RT hematopoietic cytokine interleukin-11.";
 RL Blood 86:2534-2540(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA VAN LEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSLER A.;
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 3-390 FROM N.A.
 RC TISSUE-PLACENTA;

45 PCGTASDAVAIVRVNGTDLAPD---LLNGSQLIRSLSELGSHGLYA-----CFHRDSWH 96.

01-FEB-1997 (TEMBLrel. 02, last sequence update)
01-NOV-1998 (TEMBLrel. 08, last annotation update)

DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11RBETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11RBETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1; TISSUE-TESTIS;
 RX MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RX MEDLINE: 96278810.
 RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
 RT Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-TESTIS;
 RX MEDLINE: 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT Identification of a second murine interleukin-11 receptor
 RT alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997).
 CC [1]- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC [1]- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1]- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC [1]- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC [1]- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC [1]- CONTAINS ONE IG-LIKE DOMAIN.
 CC [1]- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X94157; CA63872.1; JOINED.
 DR EMBL: X94158; CA63872.1; JOINED.
 DR EMBL: X94159; CA63872.1; JOINED.
 DR EMBL: X94160; CA63872.1; JOINED.
 DR EMBL: X94161; CA63872.1; JOINED.
 DR EMBL: X98519; CA67144.1; JOINED.
 DR EMBL: U69491; AAC53114.1; JOINED.
 DR MGD: MGI:109123; IL11RA2.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; 1g; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
 FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
 FT TRAMSEK 368 393 POTENTIAL.
 FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
 FT CAROHND 127 127 POTENTIAL.
 FT CAROHND 127 127 POTENTIAL.
 FT CAROHND 194 194 S -> P (IN CA63872).
 FT CONFLICT 200 200 S -> L (IN CA63872).
 FT CONFLICT 384 384 V -> L (IN CA63872).
 SO SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

Query Match 11.0%; Score 165; DB 11; Length 432;
 Best Local Similarity 25.9%; Pred. No. 3.4e-08;
 Matches 63; Conservative 39; Mismatches 105; Indels 36; Gaps 12;

DB 100 VSGWVTLKLGFPNAP-EVSCANDYENFSCWSPGO--VGLPTRTITSTKRTLPDA 156

OY 135 NCEEHVTPSHCHPKD-----LALFPEIWEATNRLGARSVDVLTLDV 183
 DB 157 EGRSPSTGPPMC--PQPLESRGVHGAERWERYINVEVNLG-ASTCLDVRQ 213
 OY 184 DVVTPDPDVHVRVGLLEDQLSVKWSPPALK---DLFOAKYOIRRVEDSVDMKV 240
 DB 214 SILRPPDGLRVESVPGYPRRLHSMWTVPASWRQPHLL--KPRLOYRPAQHPAMSTV 271
 OY 241 DDV 243
 DB 272 EPI 274

RESULT 15
 ID 064385 PRELIMINARY; PRT: 432 AA.
 AC 064385;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
 DE (IL-11RA1RA) (IL11RA1).
 GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE: 95045367.
 RA HILTON D.J., HILTON A.A., RAJCEVIC A., RAKAR S., HARRISON-SMITH M.,
 RA GOUCH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.,
 RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for
 RT gp130 for high affinity binding and signal transduction.";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C. AND C57BL/6; TISSUE-EMBRYO;
 RA NEUHAUS H., BETENHAUSEN B., BILINSKI P., SIMON-CHARZOTTES D.,
 RA GOSLER J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C. AND C57BL/6;
 RA GOSLER A., AND C57BL/6;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 CC [1]- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC [1]- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC [1]- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1]- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC [1]- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC [1]- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC [1]- CONTAINS ONE IG-LIKE DOMAIN.
 CC [1]- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CA532908.1; JOINED.
 DR EMBL: U14412; AA53248.1; JOINED.
 DR EMBL: X94162; CA63873.1; JOINED.
 DR EMBL: X94163; CA63873.1; JOINED.
 DR MGD: MGI:107426; IL11RA1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; 1g; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23

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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:08:15 ; Search time 64.1 Seconds

(without alignments)
129.331 Million cell updates/sec

Title: US-09-037-657-25

Perfect score: 1919

Sequence: 1 TLNGRRLPPELSRVLNASTL.....TRGSCPRADGAREVLPDKL 350

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1919	100.0	350	1 W55015	Amino acid sequence
2	1919	100.0	392	1 W70840	Human zcyto5 vari
3	1919	100.0	389	1 W70844	Human zcyto5 vari
4	1919	100.0	425	1 W70861	Allelic variant of
5	1918	99.9	389	1 W70850	Human zcyto5 vari
6	1918	99.9	389	1 W70851	Human zcyto5 vari
7	1917	99.9	389	1 W70852	Human zcyto5 vari
8	1916	99.8	389	1 W70846	Human zcyto5 vari
9	1916	99.8	389	1 W70847	Human zcyto5 vari
10	1915	99.8	389	1 W70849	Human zcyto5 vari
11	1915	99.8	389	1 W70848	Human zcyto5 vari
12	1914	99.7	389	1 W70853	Human zcyto5 vari
13	1800	93.6	408	1 W59805	Amino acid sequence
14	1796	93.6	422	1 W70860	Human zcyto5 vari
15	1789	93.2	385	1 W70839	Human zcyto5 vari
16	1789	93.2	385	1 W70842	Human zcyto5 vari
17	1772	92.3	413	1 W55012	Novel haemopoietin
18	1768	92.1	425	1 W55011	Novel haemopoietin
19	1768	92.1	425	1 W59804	Nucleotide sequence
20	1768	92.1	385	1 W70841	Human zcyto5 vari
21	1768	92.1	425	1 W70862	Rat zcyto5 vari
22	1436	74.8	303	1 W70845	Human zcyto5 vari
23	1432	74.6	303	1 W70843	Human zcyto5 vari
24	1330	68.8	278	1 W55014	Protein sequence
25	631.5	32.9	155	1 W55013	Novel haemopoietin
26	506	26.4	186	1 W55016	Amino acid sequence
27	332	17.3	622	1 R10795	Human prolactin re
28	331.5	17.3	211	1 R4273	Human prolactin re
29	323.5	17.0	211	1 R2228	Truncated human pr
30	299	15.6	917	1 R26334	Human gp130. New m
31	292.5	15.2	332	1 R70799	Human gp130-delta
32	290.5	15.1	918	1 R10545	Recombinant human
33	290.5	15.1	918	1 R46233	Human soluble glic
34	290.5	15.1	658	1 R94576	Human gp130 splic
35	290.5	15.1	918	1 R75368	Human gp130 protel
36	290.5	15.1	708	1 R85911	Human gp130-termi
37	290.5	15.1	951	1 W70798	Human gp130-C-gam
38	290.5	15.1	859	1 W70796	Human gp130-Fc-His
39	289	15.1	329	1 W17859	Rheumatoid arthrit
40	277.5	14.5	708	1 R37804	Human gp130 N-term
41	263.5	13.7	630	1 R93120	Human prolactin
42	263.5	13.7	606	1 R93121	Human prolactin
43	250.5	13.1	180	1 W00404	Interleukin-6 anta

ALIGNMENTS

RESULT 1

44 236 12.3 837 1 R14254
45 233.5 12.2 334 1 R99140

W55015 standard; Protein; 350 AA.

AC W55015;
DT 29-SEP-1998 (first entry)
DE Amino acid sequence of clone Hfx-66 encoding human NR6.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW human.
OS Homo sapiens.
PN MO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (DZIE/) DIEGLEWSKA H E.
PI Alexander W, Fabrl L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J,
DR WPI; 98-260970/23.
DR N-PSDB; V27144.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PS e.g. neuronal cells
PS Claim 18; Page 102-104; 182pp; English.
CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
CC between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC and survival. The products used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SO Sequence 350 AA;

Query Match. 100.0%; Score 1919; DB 1; Length 350;

Best local Similarity 100.0%; Pred. No. 2.6e-173;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLPPELSRVLNASTLALANLNGSRSGDNLVCHARDGSIILAGSCLYGLPPE 60
DB 1 TLNGRRLPPELSRVLNASTLALANLNGSRSGDNLVCHARDGSIILAGSCLYGLPPE 60
QY 61 KPNVIGGSKNMDLCRTWPGAHGTFILTNLSKYKLRMYGQDNTCEHYTVGPHSCH 120
DB 61 KPNVIGGSKNMDLCRTWPGAHGTFILTNLSKYKLRMYGQDNTCEHYTVGPHSCH 120
QY 121 IPDNLAFPEYEIVENATNRLGARSVDLTLDIVVTDPDPDVHVRGGLDLSVR 180
DB 121 IPDNLAFPEYEIVENATNRLGARSVDLTLDIVVTDPDPDVHVRGGLDLSVR 180
QY 181 WSPPLAKDFLEQAKYQIRVEDSDVMKVDVDSNQTSCRLAGLPGVYFVQVRCNPF 240
DB 181 WSPPLAKDFLEQAKYQIRVEDSDVMKVDVDSNQTSCRLAGLPGVYFVQVRCNPF 240
QY 241 GIGSKKAGTMSWSPHTAASPRSRPPGGGACPRGCEPSSGCVREKLQFLGLMK 300
DB 241 GIGSKKAGTMSWSPHTAASPRSRPPGGGACPRGCEPSSGCVREKLQFLGLMK 300
QY 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNQRTRGSCPRADGAREVLPDKL 350
DB 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNQRTRGSCPRADGAREVLPDKL 350

RESULT 2
 ID W70840 standard; Protein: 392 AA.
 AC W70840:
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 81-82; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 392 AA;

Query Match 100.0%; Score 1919; DB 1; Length 392;
 Best Local Similarity 100.0%; Pred. No. 3e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSEVNLASTLALANLNGSRQSGDNVCHARDGSIAGSLTYGLPE 60
 DB 43 TLNGRRRLPELSEVNLASTLALANLNGSRQSGDNVCHARDGSIAGSLTYGLPE 102
 QY 61 KPVNISCSKNNKDLTCMTGAGETFLHNTSLKYLRYGQDNCEHYHTVGPSSCH 120
 DB 103 KPVNISCSKNNKDLTCMTGAGETFLHNTSLKYLRYGQDNCEHYHTVGPSSCH 162
 QY 121 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 180
 DB 163 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 222
 QY 181 WSPSPALKDFLFOAKYQIRYVEDSVDMKVYDVSNQTSCLAGLKPCTYFVQRCNPF 240
 DB 223 WSPSPALKDFLFOAKYQIRYVEDSVDMKVYDVSNQTSCLAGLKPCTYFVQRCNPF 282
 QY 241 GYISGKAGIWSHSHPTAASPRESRPGGACGEPGSGPVARELKOFLGWLK 300
 DB 283 GYISGKAGIWSHSHPTAASPRESRPGGACGEPGSGPVARELKOFLGWLK 342
 QY 301 HAYCSNLSFRILYDQWRAMQSKHTRNOHRTGSCPRADGARREVLTPKLT 350
 DB 343 HAYCSNLSFRILYDQWRAMQSKHTRNOHRTGSCPRADGARREVLTPKLT 392

DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 87-88; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 100.0%; Score 1919; DB 1; Length 389;
 Best Local Similarity 100.0%; Pred. No. 3e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSEVNLASTLALANLNGSRQSGDNVCHARDGSIAGSLTYGLPE 60
 DB 40 TLNGRRRLPELSEVNLASTLALANLNGSRQSGDNVCHARDGSIAGSLTYGLPE 99
 QY 61 KPVNISCSKNNKDLTCMTGAGETFLHNTSLKYLRYGQDNCEHYHTVGPSSCH 120
 DB 100 KPVNISCSKNNKDLTCMTGAGETFLHNTSLKYLRYGQDNCEHYHTVGPSSCH 159
 QY 121 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 219
 QY 181 WSPSPALKDFLFOAKYQIRYVEDSVDMKVYDVSNQTSCLAGLKPCTYFVQRCNPF 240
 DB 220 WSPSPALKDFLFOAKYQIRYVEDSVDMKVYDVSNQTSCLAGLKPCTYFVQRCNPF 279
 QY 241 GYISGKAGIWSHSHPTAASPRESRPGGACGEPGSGPVARELKOFLGWLK 300
 DB 280 GYISGKAGIWSHSHPTAASPRESRPGGACGEPGSGPVARELKOFLGWLK 339
 QY 301 HAYCSNLSFRILYDQWRAMQSKHTRNOHRTGSCPRADGARREVLTPKLT 350
 DB 340 HAYCSNLSFRILYDQWRAMQSKHTRNOHRTGSCPRADGARREVLTPKLT 389

RESULT 4
 ID W70861 standard; Protein: 425 AA.
 AC W70861:
 DT 17-MAR-1999 (first entry)
 DE Allelic variant of human zcyto5.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; allelic variant.
 OS Homo sapiens.

PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 71-72; 55pp; English.
 CC The present sequence represents an allelic variant of protein designated
 CC Zcyto5, which is a cytokinin-like receptor. Soluble Zcyto5 may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 425 AA:

Query Match 100.0%; Score 1919; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 60
 DB 76 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 135
 QY 61 KPVNISCSKMKMDLTCRTPGAHGETFLHTNYSKYKLRMYGQDNTCEHYHVGHSCH 120
 DB 136 KPVNISCSKMKMDLTCRTPGAHGETFLHTNYSKYKLRMYGQDNTCEHYHVGHSCH 195
 QY 121 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 180
 DB 196 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 255
 QY 181 WSPPLAKDFLFQAKYQIRYVEDSVDMKRVYDVDSNQTSCLAGLPGTYFYVQVRCNPF 240
 DB 256 WSPPLAKDFLFQAKYQIRYVEDSVDMKRVYDVDSNQTSCLAGLPGTYFYVQVRCNPF 315
 QY 241 GIYSGKAGIWEHSPHTAASPRSPRPGGACPRGGEPSGVRRELKQFLGMLKK 300
 DB 316 GIYSGKAGIWEHSPHTAASPRSPRPGGACPRGGEPSGVRRELKQFLGMLKK 375
 QY 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNQHRTGSCPRADGARREVL.PDKL 350
 DB 376 HAYCSNLSFRLYDQWRAMWQKSHKTRNQHRTGSCPRADGARREVL.PDKL 425
 RESULT 5
 W70850
 ID W70850 standard; Protein; 389 AA.
 AC W70850:
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 01-MAY-1997; US-045287.
 PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA:

Query Match 99.9%; Score 1918; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 3.7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 60
 DB 40 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 99
 QY 61 KPVNISCSKMKMDLTCRTPGAHGETFLHTNYSKYKLRMYGQDNTCEHYHVGHSCH 120
 DB 100 KPVNISCSKMKMDLTCRTPGAHGETFLHTNYSKYKLRMYGQDNTCEHYHVGHSCH 159
 QY 121 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 180
 DB 160 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 219
 QY 181 WSPPLAKDFLFQAKYQIRYVEDSVDMKRVYDVDSNQTSCLAGLPGTYFYVQVRCNPF 240
 DB 220 WSPPLAKDFLFQAKYQIRYVEDSVDMKRVYDVDSNQTSCLAGLPGTYFYVQVRCNPF 279
 QY 241 GIYSGKAGIWEHSPHTAASPRSPRPGGACPRGGEPSGVRRELKQFLGMLKK 300
 DB 280 GIYSGKAGIWEHSPHTAASPRSPRPGGACPRGGEPSGVRRELKQFLGMLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNQHRTGSCPRADGARREVL.PDKL 350
 DB 340 HAYCSNLSFRLYDQWRAMWQKSHKTRNQHRTGSCPRADGARREVL.PDKL 389

RESULT 6
 W70851
 ID W70851 standard; Protein; 389 AA.
 AC W70851:
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 96-97; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.9%; Score 1918; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 3.7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 99
 QY 61 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSLSKYLRYGQDNCEEHYHTVGPSSCH 120
 DB 100 KPVNISCSKMKKDLTCRWTPGAGETFLHTNYSLSKYLRYGQDNCEEHYHTVGPSSCH 159
 QY 121 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 180
 DB 160 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 219
 QY 181 WSPPALKDFLFOAKYQIRYVEDSDVMKYVDVSNQTSCLAGIKPGTYVYVOYRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSDVMKYVDVSNQTSCLAGIKPGTYVYVOYRCNPF 279
 QY 241 GIYSKKAIGSEMSHPAASTPRSERPGGACPEPGSSGPVARELKOFLGWLKK 300
 DB 280 GIYSKKAIGSEMSHPAASTPRSERPGGACPEPGSSGPVARELKOFLGWLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMQKSHKTRNQHRTGSCPRADGARREVLDPKTL 350
 DB 340 HAYCSNLSFRLYDQWRAMQKSHKTRNQHRTGSCPRADGARREVLDPKTL 389

RESULT 7
 W70852
 ID W70852 standard; Protein: 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; US-008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood

PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.9%; Score 1917; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 4.6e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 99
 QY 61 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSLSKYLRYGQDNCEEHYHTVGPSSCH 120
 DB 100 KPVNISCSKMKKDLTCRWTPGAGETFLHTNYSLSKYLRYGQDNCEEHYHTVGPSSCH 159
 QY 121 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 180
 DB 160 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 219
 QY 181 WSPPALKDFLFOAKYQIRYVEDSDVMKYVDVSNQTSCLAGIKPGTYVYVOYRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSDVMKYVDVSNQTSCLAGIKPGTYVYVOYRCNPF 279
 QY 241 GIYSKKAIGSEMSHPAASTPRSERPGGACPEPGSSGPVARELKOFLGWLKK 300
 DB 280 GIYSKKAIGSEMSHPAASTPRSERPGGACPEPGSSGPVARELKOFLGWLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMQKSHKTRNQHRTGSCPRADGARREVLDPKTL 350
 DB 340 HAYCSNLSFRLYDQWRAMQKSHKTRNQHRTGSCPRADGARREVLDPKTL 389

RESULT 8
 W70846
 ID W70846 standard; Protein: 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; US-008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 89-90; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and the
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.88; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.78; Pred. No. 5,7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TLNRRRLPELSESLVNLSTALALANLNGSRGSDNLVCHARGSLIAGSCLVGLPPE 60
 40 TLNRRRLPELSESLVNLSTALALANLNGSRGSDNLVCHARGSLIAGSCLVGLPPE 99
 61 KPVNISCSNMKMDLTCRMTPGAAGETFLHTNYSLKRYLRYGODNCEHYHVPSCSCH 120
 100 KPVNISCSNMKMDLTCRMTPGAAGETFLHTNYSLKRYLRYGODNCEHYHVPSCSCH 159
 121 IPPDLALFTPEIWEATNRLGARSVDLTLIDVYTTDPDPVHVSRYVGLDQLSVR 180
 160 IPPDLALFTPEIWEATNRLGARSVDLTLIDVYTTDPDPVHVSRYVGLDQLSVR 219
 181 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGKGTYYFOVRCNPF 240
 220 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGKGTYYFOVRCNPF 279
 241 GYGSKKAGIMSESHPTASTPSESRPGGACPEPSSGPPRRRLKQFLGLTK 300
 280 GYGSKKAGIMSESHPTASTPSESRPGGACPEPSSGPPRRRLKQFLGLTK 339
 301 HAYCSNLSFLYDQWRAMQKSHKTRNQHRTGSCPRADGAREVLPDKL 350
 340 HAYCSNLSFLYDQWRAMQKSHKTRNQHRTGSCPRADGAREVLPDKL 389

RESULT 9

ID W70847 standard; Protein; 389 AA.
 AC W70847;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM.
 PT Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotoxin-1
 in blood
 PS Claim 1: Page 91-92; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.88; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.78; Pred. No. 5,7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TLNRRRLPELSESLVNLSTALALANLNGSRGSDNLVCHARGSLIAGSCLVGLPPE 60
 40 TLNRRRLPELSESLVNLSTALALANLNGSRGSDNLVCHARGSLIAGSCLVGLPPE 99
 61 KPVNISCSNMKMDLTCRMTPGAAGETFLHTNYSLKRYLRYGODNCEHYHVPSCSCH 120
 100 KPVNISCSNMKMDLTCRMTPGAAGETFLHTNYSLKRYLRYGODNCEHYHVPSCSCH 159
 121 IPPDLALFTPEIWEATNRLGARSVDLTLIDVYTTDPDPVHVSRYVGLDQLSVR 180
 160 IPPDLALFTPEIWEATNRLGARSVDLTLIDVYTTDPDPVHVSRYVGLDQLSVR 219
 181 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGKGTYYFOVRCNPF 240
 220 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGKGTYYFOVRCNPF 279
 241 GYGSKKAGIMSESHPTASTPSESRPGGACPEPSSGPPRRRLKQFLGLTK 300
 280 GYGSKKAGIMSESHPTASTPSESRPGGACPEPSSGPPRRRLKQFLGLTK 339
 301 HAYCSNLSFLYDQWRAMQKSHKTRNQHRTGSCPRADGAREVLPDKL 350
 340 HAYCSNLSFLYDQWRAMQKSHKTRNQHRTGSCPRADGAREVLPDKL 389

RESULT 10

ID W70849 standard; Protein; 389 AA.
 AC W70849;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM.
 PT Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotoxin-1
 in blood
 PS Claim 1: Page 94-95; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and the
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.8%; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 5.7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 99

QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKYLKRWYGQDNTCEEYHTVGHSHCH 120
 DB 100 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKYLKRWYGQDNTCEEYHTVGHSHCH 159

QY 121 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 219

QY 181 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 279

QY 241 GYGSKKAGIWSHSPHTASTPRSEPRPGGACPRGEGSSGPRRELKQFLGWLK 300
 DB 280 GYGSKKAGIWSHSPHTASTPRSEPRPGGACPRGEGSSGPRRELKQFLGWLK 339

QY 301 HAYCSNLSFRLYDQWRAMQSKHKTNRNHRGSCPRADGARREVLDPKL 350
 DB 340 HAYCSNLSFRLYDQWRAMQSKHKTNRNHRGSCPRADGARREVLDPKL 389

RESULT 11
 W70848
 ID W70848 standard; Protein: 389 AA.
 AC W70848;
 DT 17-MAR-1999 (first entry)
 DE Human Zcytor5 variant.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 92-93; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.8%; Score 1915; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 7.1e-173;
 Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 60

DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 99
 QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKYLKRWYGQDNTCEEYHTVGHSHCH 120
 DB 100 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKYLKRWYGQDNTCEEYHTVGHSHCH 159

QY 121 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 219

QY 181 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 279

QY 241 GYGSKKAGIWSHSPHTASTPRSEPRPGGACPRGEGSSGPRRELKQFLGWLK 300
 DB 280 GYGSKKAGIWSHSPHTASTPRSEPRPGGACPRGEGSSGPRRELKQFLGWLK 339

QY 301 HAYCSNLSFRLYDQWRAMQSKHKTNRNHRGSCPRADGARREVLDPKL 350
 DB 340 HAYCSNLSFRLYDQWRAMQSKHKTNRNHRGSCPRADGARREVLDPKL 389

RESULT 12
 W70853
 ID W70853 standard; Protein: 389 AA.
 AC W70853;
 DT 17-MAR-1999 (first entry)
 DE Human Zcytor5 variant.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 99-100; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.7%; Score 1914; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 8.8e-173;
 Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLTYGLPPE 99

QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKYLKRWYGQDNTCEEYHTVGHSHCH 120

Db 100 KPVNISCSKNNKMDLTGCRWTPGAGETFLHTNYSLKYYKRWYGODNTCEHYTVGPHSCH 159
QY 121 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 180
Db 160 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 219
QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 240
Db 220 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 279
QY 241 GIGSKKAGIWMSESHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300
Db 280 GIGSKKAGIWMSESHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 339
QY 301 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQHTRSSCPADARREYLPDKL 350
Db 340 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQHTRSSCPADARREYLPDKL 389

RESULT 13

W59805 standard; Protein: 408 AA.
ID W59805
AC W59805;
DE 26-OCT-1998 (first entry)
KW Human; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy.
OS Homo sapiens.
PN WO9831811-N1.
PD 23-JUL-1998.
PE 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
RA (GENE) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Walters M;
DR N-PSDB; V41689.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
chain - potentially useful, e.g. for modulating cell proliferation
or immune response, for treating cancer and auto-immune disease
PS Claim 9; Pages 29-30; 38pp; English.
CC This is the amino acid sequence of the human U4 protein from the
haematopoietin receptor superfamily, used in the method of the
invention for the modulation of cell proliferation, or the immune
response. Transformed mammalian cells are used to produce recombinant
U4 protein. The U4 protein is used to screen for specific binding
agents, raise antibodies. It is also used as reagents for assays and
as tissue markers for isolation of cognate ligands and receptors, and
in pharmaceutical compositions which may modulate cell proliferation,
cell differentiation, and the immune system (e.g. for treating immune
deficiency, inherited or the result of infection, autoimmune diseases,
cancer, and allergy).
SQ Sequence 408 AA;

Query Match 93.8%; Score 1800; DB 1; Length 408;
Best Local Similarity 100.0%; Pred. No. 5.5e-162;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNYCHARGDSIIAGSCLYGLPE 60
Db 63 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNYCHARGDSIIAGSCLYGLPE 122
QY 61 KPVNISCSKNNKMDLTGCRWTPGAGETFLHTNYSLKYYKRWYGODNTCEHYTVGPHSCH 120
Db 123 KPVNISCSKNNKMDLTGCRWTPGAGETFLHTNYSLKYYKRWYGODNTCEHYTVGPHSCH 182
QY 121 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 180
Db 183 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 242
QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 240

Db 243 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 302
QY 241 GIGSKKAGIWMSESHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300
Db 303 GIGSKKAGIWMSESHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 362
QY 301 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQ 328
Db 363 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQ 390

RESULT 14

W70860 standard; Protein: 422 AA.
ID W70860
AC W70860;
DE 17-MAR-1999 (first entry)
KW Human zcyto5 protein sequence.
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand.
OS Homo sapiens.
PN WO9849307-N1.
PD 01-MAY-1998; U08865.
PE 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
RA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lox S, Plesneil SR, Whitmore TE;
DR N-PSDB; V70894.
PT New mammalian cytokinin-like receptor. Zcyto5 - useful for, e.g.
down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
in blood
PS Claim 1; Page 66-67; 55pp; English.
CC The present sequence represents a protein designated zcyto5, which is
a cytokinin-like receptor. Soluble zcyto5 may be administered to
down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
of cardiostrophin-1 on cardiac pathologies, so preventing heart
enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and
CC anti-idiotypic antibody could be used to purify zcyto5 and
therapeutically to modify zcyto5 ligand effects.
SQ Sequence 422 AA;

Query Match 93.6%; Score 1796; DB 1; Length 422;
Best Local Similarity 99.7%; Pred. No. 1.4e-161;

Matches 327; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNYCHARGDSIIAGSCLYGLPE 60
Db 77 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNYCHARGDSIIAGSCLYGLPE 136
QY 61 KPVNISCSKNNKMDLTGCRWTPGAGETFLHTNYSLKYYKRWYGODNTCEHYTVGPHSCH 120
Db 137 KPVNISCSKNNKMDLTGCRWTPGAGETFLHTNYSLKYYKRWYGODNTCEHYTVGPHSCH 196
QY 121 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 180
Db 197 IPKDLAFTPEIWEATNRLGARSVDLTLDIVYTTTTPPPVHVSRRVGGLEDQLSVR 256
QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 240
Db 257 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKGTYYFYVGRNPF 316
QY 241 GIGSKKAGIWMSESHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300

Db 317 GYGSKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLKK 376
 QY 301 HAYCSNLSFRLYDQWRAMOKSHKTRNQ 328
 Db 377 HAYCSNLSFRLYDQWRAMOKSHKTRNQ 404

RESULT 15

W70839
 ID W70839 standard; Protein: 388 AA.
 AC W70839.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc.difference 45
 FT W09849307-A1.
 PN 05-NOV-1998
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Jelmberg AC, Lehner JM,
 PI Lox S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 80-81; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and the
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 388 AA;

Query Match 93.2%; Score 1789; DB 1; Length 388;
 Best Local Similarity 99.4%; Pred. No. 5.6e-161;

Matches 326; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TINGRRRLPELSRVNASTLALANLNGSRGSDNLVCHARDGSIAGSCLYGLPPE 60
 Db 43 TLXGRRLPELSRVNASTLALANLNGSRGSDNLVCHARDGSIAGSCLYGLPPE 102
 QY 61 KPVNISCWSKKNKDLTCMTPEAGETFLHTNYSLSKTKLRYGQDNTCEETHVGPSSCH 120
 Db 103 KPVNISCWSKKNKDLTCMTPEAGETFLHTNYSLSKTKLRYGQDNTCEETHVGPSSCH 162
 QY 121 IPKDLALFTPEIWEATNRLGSARSVDLTLDVYTTDPPDHYVRVGLDQLSVR 180
 Db 163 IPKDLALFTPEIWEATNRLGSARSVDLTLDVYTTDPPDHYVRVGLDQLSVR 222
 QY 181 WSPPALDLEFOAKYQIRYVEDSVDMKVYDVVSNQTSCLAGLKPCTVYFVQRCNPF 240
 Db 223 WSPPALDLEFOAKYQIRYVEDSVDMKVYDVVSNQTSCLAGLKPCTVYFVQRCNPF 282
 QY 241 GYGSKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLKK 300
 Db 283 GYGSKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLKK 342

QY 301 HAYCSNLSFRLYDQWRAMOKSHKTRNQ 328
 Db 343 HAYCSNLSFRLYDQWRAMOKSHKTRNQ 370

Search completed: September 17, 1999, 03:08:16
 Job time: 307 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:09 ; Search time 53.94 Seconds

(Without Alignments)
64,033 Million cell updates/sec

Title: US-09-037-657-25

Sequence: 1 TLNGRRRLPELSRYLNASTL.....TRGSCPRADGARREVLDPDKL 350

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/PTUS9.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290.5	15.1	708	1	US-07-797-556-2
2	290.5	15.1	708	2	US-08-308-881-2
3	290.5	15.1	708	3	PCT-US95-06530-2
4	241	12.6	837	1	US-07-923-976-2
5	220.5	11.5	836	1	US-07-923-976-4
6	220.5	11.5	771	1	US-07-923-976-6
7	220.5	11.5	863	1	US-07-923-976-8
8	219.5	11.4	372	1	US-07-865-878A-4
9	219.5	11.4	372	1	US-07-676-647-2
10	219.5	11.4	372	1	US-08-443-329-2
11	219.5	11.4	372	2	US-08-443-329-2
12	219.5	11.4	372	3	US-08-443-329-2
13	219.5	11.1	602	2	US-08-419-652-6
14	207.5	10.8	862	2	US-08-685-118-2
15	207.5	10.8	862	2	US-08-915-485-2
16	207	10.8	572	2	US-08-418-652-5
17	196	10.2	633	1	US-08-250-859-17
18	196	10.2	633	1	US-08-490-803-17
19	196	10.2	633	1	PCT-US94-08806-17
20	196	10.2	633	3	PCT-US95-01775-17
21	196	10.2	633	3	PCT-US95-16626-7
22	190	9.9	626	3	US-08-184-327A-2
23	190	9.9	482	1	US-08-184-327A-8
24	190	9.9	482	1	PCT-US95-00670-2
25	190	9.9	482	1	PCT-US95-00670-2
26	188.5	9.8	635	3	US-08-184-327A-4
27	188.5	9.8	635	3	PCT-US95-00670-4
28	176	9.2	1001	1	US-07-797-556-6
29	176	9.2	1001	1	US-07-943-843-2
30	176	9.2	1097	2	US-07-943-843-6
31	176	9.2	1001	2	US-08-347-003-2
32	176	9.2	1097	2	US-08-347-003-6
33	166	8.7	719	1	US-07-943-843-4
34	166	8.7	719	2	US-08-306-231-3
35	161	8.4	569	2	US-08-355-888A-8
36	161	8.4	960	2	US-08-693-697-8
37	161	8.4	960	2	US-08-693-697-33
38	161	8.4	908	2	US-08-693-697-33
39	161	8.4	898	2	US-08-693-697-36

40	160	8.3	908	2	US-08-588-526-3	Sequence 3, Appl1
41	159.5	8.3	383	1	US-08-609-572-2	Sequence 2, Appl1
42	156	8.1	960	1	US-08-588-190-3	Sequence 3, Appl1
43	154.5	8.1	508	2	US-08-850-293-5	Sequence 5, Appl1
44	148	7.7	229	2	US-08-684-687-2	Sequence 2, Appl1
45	145.5	7.6	897	1	US-07-960-389-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1	US-07-797-556-2	Sequence 2, Application US/07797556	Patent No. 5262522	GENERAL INFORMATION:
APPLICANT:	Geating, David P.	RECEPTOR FOR ONCOSTATIN M AND LEUKEMIA	INHIBITORY FACTOR	NUMBER OF SEQUENCES: 17
TITLE OF INVENTION:	Receptor for Oncostatin M and Leukemia	INHIBITORY FACTOR	NUMBER OF SEQUENCES: 17	CORRESPONDENCE ADDRESS:
ADDRESS:	Immunex Corporation	STREET:	51 University Street	CITY:
STATE:	Seattle	COUNTRY:	USA	ZIP:
ZIP:	98101	COMPUTER READABLE FORM:	COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS	SOFTWARE:	PatentIn Release #1.0, Version #1.25	CURRENT APPLICATION DATA:
APPLICATION NUMBER:	US/07/797,556	FILING DATE:	1991.11.22	CLASSIFICATION:
CLASSIFICATION:	435	ATTORNEY/AGENT INFORMATION:	NAME:	Seese, Kathryn A.
REGISTRATION NUMBER:	32,172	REFERENCE/DOCKET NUMBER:	2607	TELECOMMUNICATION INFORMATION:
TELEPHONE:	206-587-0430	TELEFAX:	206-587-0606	INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:	LENGTH: 708 amino acids	TYPE:	AMINO ACID	TOPOLOGY:
TOPOLOGY:	linear	MOLECULE TYPE:	protein	US-07-797-556-2
Query Match	15.18;	Score	290.5;	DB 1;
Length	708;	Best Local Similarity	28.76;	Pred. No. 4.6e-21;
Matches	76;	Conservative	46;	Mismatches 128;
Indels	15;	Gaps	7;	
OY	7	LPPELSRYLNASTLALANLNGSRQSGDNLVNCARQSGILAGCLVGPPEKPVNIS	66	
Db	74	IPKEQYTLINFTASSVFTDTSANLQITCNILTFGGLEQVNYGIIISGLPEKPKMLS	133	
OY	67	CMSKMKMDLQRTWPGAGETFLHTNYSLKYLKRWYGODNCEEHYHVGPSCHIPKDLA	126	
Db	134	CIYVNGKMKREMGGR--EHLLENFTLKSEMAHTRADCKAROT--PTSCYVDISTV	189	
OY	127	LFTPEIWEATNRLGARSQVLTLDLDVTTDPPDPVHSRVGGLDQSVRWVSPA	186	
Db	190	YFVNIEVVEAENMLGKVTSDHINFDPPYKVPNPHNLVYINSEELSLIKLMTN-PS	248	
OY	187	LKDLFOAKYQIRIRVEDSVDMKVY---DDVSNQTSCLAGLAKGYTVFVQRCNPGIY	243	
Db	249	IKSVIT-LKNIQIYRTDASQIIPEDPASTRSSFTYVDLKEFTVEYFIRIC-----M	302	
OY	244	GSKRAGIWEVSHPTASTPSESRP	268	

Db 303 KEDGKGWSDMSEASG1T-YEDRP 326

RESULT 2

US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 15.1%; Score 290.5; DB 2; Length 708;
Best Local Similarity 28.7%; Pred. No. 4.6e-21;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;
Db 7 LPELSRVNLASTLALANLNGSRORSRSDNLYCHARDGSLAGSCLVGLPPEKPVNIS 66
Db 74 IPRQYIIINFTASSVFTDIASLNIQITCNILTFQLEQNVYGITIISGLPPEKPNLS 133
QY 67 CWSNNMDELTCRWTGAGHETFLHTNYSLKYLKWYGODNTCEEYHTVGPCHIKDLA 126
Db 134 CIYNEGKMKCEMDGGR--ETHLETFILKSEWATKRFADCKAKRDT--PTSCVYDSTV 189
QY 127 LFTPELWEATNRLSARSVDLTLDLDVYTTDPPDVHVSFVGLDOLSVRWSPPA 186
Db 190 YFVNIEWVAEENALGVTSDFINFDVYKVPNPVNLVINSSELSILKLTWTN-PS 248
QY 187 LKDFLFOAKQOIRRVDSYDMKV---DDVSNQTSCLAGLKPGTVYFVOVRCNPGIY 243
Db 249 IKSYYIT-LKINIQYRTDASTWQIIPEDDASTRSSFTVODLKPFLEYVFRRC-----M 302
QY 244 GSKKAGIWMSESHPTASTPRSERP 268
Db 303 KEDGKGWSDMSEASG1T-YEDRP 326

RESULT 3

PCT-US95-06530-2
Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 15.1%; Score 290.5; DB 3; Length 708;
Best Local Similarity 28.7%; Pred. No. 4.6e-21;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;
Db 7 LPELSRVNLASTLALANLNGSRORSRSDNLYCHARDGSLAGSCLVGLPPEKPVNIS 66
Db 74 IPRQYIIINFTASSVFTDIASLNIQITCNILTFQLEQNVYGITIISGLPPEKPNLS 133
QY 67 CWSNNMDELTCRWTGAGHETFLHTNYSLKYLKWYGODNTCEEYHTVGPCHIKDLA 126
Db 134 CIYNEGKMKCEMDGGR--ETHLETFILKSEWATKRFADCKAKRDT--PTSCVYDSTV 189
QY 127 LFTPELWEATNRLSARSVDLTLDLDVYTTDPPDVHVSFVGLDOLSVRWSPPA 186
Db 190 YFVNIEWVAEENALGVTSDFINFDVYKVPNPVNLVINSSELSILKLTWTN-PS 248
QY 187 LKDFLFOAKQOIRRVDSYDMKV---DDVSNQTSCLAGLKPGTVYFVOVRCNPGIY 243
Db 249 IKSYYIT-LKINIQYRTDASTWQIIPEDDASTRSSFTVODLKPFLEYVFRRC-----M 302
QY 244 GSKKAGIWMSESHPTASTPRSERP 268
Db 303 KEDGKGWSDMSEASG1T-YEDRP 326

RESULT 4

US-07-923-976-2

Sequence 2, Application US/07923976

Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-2

Query Match 12.6%; Score 241; DB 1; Length 837;
Best Local Similarity 28.0%; Pred. No. 5.8e-16;
Matches 89; Conservative 45; Mismatches 112; Indels 72; Gaps 17;

53 LYVGLPEKPYNISCSKNNKDLTCRTPAHGETFLHTVYSIK-YKLR---NYGQDNT 107
118 LHAQPPSPFNLSCLMLTNSLYCQEPSP--ETHLPISFLIKSFSSRADQYQGPETI 175
108 CEYHTVGPNSCHIR-KDLALFTPEIWEATNRLGSRSDVLTLDIDVTTDP-- 163
176 PDCAKKNQNNCSIRKMLLYQVMAIVQAENMLGSESSEPRCLDPPADVYKLEPPMOA 235
163 ---PDVHVSRYVGLGLEDLSVRWVS-PPALADFLQAKYQIYRYE-DSVDMKVVDVY-S 215
236 LDIGDVAVSHQPCGL-----WLSMKWPKRSEYVEQCELTQQLGAWMTLVFHLPS 288
216 NOTSRLAGLKPGTYVFOVRCNPFGIYSKRAKAGIMSEMS-----HPT-AASTPSEBPG 269
289 SKDQELGCLHQAAPYTTLMRC-----IRSLPFGMSRPSRSLQALPIMKAPTILDT-- 342
270 PEGGACEPGEPPSS-----GVRRELKQFLGMLKKAHYCSNLSFRLYDQRRANQ 320
342 ---WCOKQDLPDGTIVSVGLFWKFTPLQEDSDQIQGYL-----LSWNS 380

OY 321 KSHKTRNH---ETRGSC 335
DB 381 PDHQGDHLCNTTQLSC 398

RESULT 5
US-07-923-976-4
Sequence 4, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 836 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-4

Query Match 11.5%; Score 220.5; DB 1; Length 836;
Best Local Similarity 32.0%; Pred. No. 6.7e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

53 LYVGLPEKPYNISCSKNNKDLTCRTPAHGETFLHTVYSIK-YKLRVYGO---DNT 107
117 LRAQYPPAIPNLSCLMLTNSLYCQEPSP--ETHLPISFLIKSFSSRADQYQGPETI 174
108 CEYHTVGPNSCHIR-KDLALFTPEIWEATNRLGSRSDVLTLDIDVY-----T 158
175 LDCVPKQSQSCCIPRKHLLLYQVMAIVQAENMLGSESSEPRCLDPPADVYKLEPPMRT 234
159 TDPPDVHVSRYVGLGLEDLSVRWVS-PPALADFLQAKYQIYRYE-DSVDMKVVDVYNO 217
235 MDPSEAPAPQAGCLQ-----LCW--EPWQPLHINOKCELRLHKKPQRCGASVALYGPPLLE 288
218 T-SCLRLAGLKPGTYVFOVRCNPFGIYSKRAKAGIMSEMS 255

Db 289 ALOYELCGLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 6

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-6

Query Match 11.5%; Score 220.5; DB 1; Length 771;
Best Local Similarity 32.0%; Pred. No. 6e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

QY 53 IYVGLPEKPKVISC-WSKNMDELTCRMTPGAHEFTLHTNSLK-YKLRWQ---DNT 107
DB 117 LRAQVPAIPHLNLSCLMNTTSSLCQMEPGP-ETHLPSTFLSKSRKNGCQOGDSI 174
QY 108 CEHYTVGPHSCHIP-KDIALFTPEIWEATNRLGSARSADVLTLDIDVY-----T 158
DB 175 LDCVPRKDSQSHCCIPRKHLLLYONNGIWOAENALGTSMSPOLCLDPMDVVKLEPMLRT 234
QY 159 TDPPEVHVSRYVGLDELQSLRWVSPALAKDFLOAKYQIRYRE-DSVDMKVVDDVSNQ 217
DB 235 MDPSEAPAPQAGCQ---LCW--EPWQGLHINQKCELRHKPQGEASWALVGPLPLE 288
QY 218 T-SCRLAGLKPGTYVYVQVRCNPFGIYSKRAIGIWEWS 255
DB 289 ALOYELCGLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 7

US-07-923-976-8
Sequence 8, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 863 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-8

Query Match 11.5%; Score 220.5; DB 1; Length 863;
Best Local Similarity 32.0%; Pred. No. 7.1e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

QY 53 IYVGLPEKPKVISC-WSKNMDELTCRMTPGAHEFTLHTNSLK-YKLRWQ---DNT 107
DB 117 LRAQVPAIPHLNLSCLMNTTSSLCQMEPGP-ETHLPSTFLSKSRKNGCQOGDSI 174
QY 108 CEHYTVGPHSCHIP-KDIALFTPEIWEATNRLGSARSADVLTLDIDVY-----T 158
DB 175 LDCVPRKDSQSHCCIPRKHLLLYONNGIWOAENALGTSMSPOLCLDPMDVVKLEPMLRT 234
QY 159 TDPPEVHVSRYVGLDELQSLRWVSPALAKDFLOAKYQIRYRE-DSVDMKVVDDVSNQ 217
DB 235 MDPSEAPAPQAGCQ---LCW--EPWQGLHINQKCELRHKPQGEASWALVGPLPLE 288
QY 218 T-SCRLAGLKPGTYVYVQVRCNPFGIYSKRAIGIWEWS 255
DB 289 ALOYELCGLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 8

RESULT 10
US-08-449-329-2
Sequence 2, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mastrook, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-329-2

Query Match 11.4%; Score 219.5; DB 1; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;
DB 2 LNRRLPELSESRVNSTALALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPPE 60
59 VNGTDLPDL---LNGSQLV---LHGLELGHSGLYACFHRDSMHLRHQVLLHVLGPPR 110
DB 61 KPNISQSKNM-KDLICRM-----TPAHGETFLHNTYSLKYLKRWYQDNTCEEH 112
111 EPLVLSRSMTYKRGYCSWHLPTPTPTPTNTVTLHOSKIM-----VCEKDP 158
DB 113 TVGPHSCHIRKDLALFT--PYEIVEATNRLGSARSDVLTLDLDVTTDPPDVHVSRY 170
159 AL-KNCRHI-RYMHLESTIKYKISIVSNALGH-NATATITDEFITVAKDPPEVAVARV 215
DB 171 GGLDLSVAVSWSPPLKD-FLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLKPCT 229
216 PSNPRRLLEVWQPTSTWPDSEPLKFFLRPLILDQWQH-ELSDGTAHTITDAVAK 274
DB 230 VYFVOYRCNFGIYSGKKAGIWMSESHPTAASPRSER----- 269
275 EYIIQVAAK-----DNEIGTWSQMS-VAHAHPWTEPRHLTTEAQAETTTSTSSLA 327
QY 269 -----GPGGACEP 277

DB 328 PPPTKICDPGEISGGGCPAP 349
RESULT 11
US-08-445-073-2
Sequence 2, Application US/08445073
Patent No. 5848997
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mastrook, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 11.4%; Score 219.5; DB 2; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;
DB 2 LNRRLPELSESRVNSTALALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPPE 60
59 VNGTDLPDL---LNGSQLV---LHGLELGHSGLYACFHRDSMHLRHQVLLHVLGPPR 110
DB 61 KPNISQSKNM-KDLICRM-----TPAHGETFLHNTYSLKYLKRWYQDNTCEEH 112
111 EPLVLSRSMTYKRGYCSWHLPTPTPTPTNTVTLHOSKIM-----VCEKDP 158
DB 113 TVGPHSCHIRKDLALFT--PYEIVEATNRLGSARSDVLTLDLDVTTDPPDVHVSRY 170
159 AL-KNCRHI-RYMHLESTIKYKISIVSNALGH-NATATITDEFITVAKDPPEVAVARV 215
DB 171 GGLDLSVAVSWSPPLKD-FLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLKPCT 229
216 PSNPRRLLEVWQPTSTWPDSEPLKFFLRPLILDQWQH-ELSDGTAHTITDAVAK 274
DB 230 VYFVOYRCNFGIYSGKKAGIWMSESHPTAASPRSER----- 269
275 EYIIQVAAK-----DNEIGTWSQMS-VAHAHPWTEPRHLTTEAQAETTTSTSSLA 327

QY 269 -----GPGGACBP 277
DB 328 PPPTKICDPGELSGSGGCPAC 349

RESULT 12

PCT-US91-03896-2
Sequence 2, Application PC/TUS9103896
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furl, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896
FILING DATE: 19910603
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US91-03896-2

Query Match 11.4%; Score 219.5; DB 3; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;

Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;

QY 2 LNSRRRLPELSESVNASTLALALANLNGSRGSDNLVCHARDOSIAGS-CLYGLPPE 60
DB 59 VNGDLDAPD- -LNSQIV- -LGLGLGSHGLYACHRDSWHLRHQVLLHVGJPPR 110
QY 61 KPVNISCSKMM-KDLTCRW- -TPGAGHETFLHTYSLKTKLWYGODNCEYH 112
DB 111 EPV-LSCRSTYFGFYCSWHLPTPIYPMFTFNTVHSGKIM- - - - -VCKDP 158
QY 113 TVGSHCHIKDLALF- -PYEIVVENTNLGSRSDVLTLDLIDVTTDPPDVHVSRY 170
DB 159 AL-KNRCHI-RYHMLFSTIKYSISVSNALGH-NATAITFDEFTYKPPPENNVARPV 215
QY 171 GGLDOLSVRWSPALKD-FLFOAKQIYRYVEDSVDMKVVDVSNQTSCKLAGLKPPT 229
DB 216 PSNPRRLVETWQPTSTPDPESPFLKFLYRPLILDQWQHV-ELSDGTAHTTDDYAGK 274
QY 230 VYVQVNCNPFGLYSGKAGIEMSEWSPHPTASTPRSERP- - - - - 269
DB 275 EYIIQVAAK- - - - -DNEIGTWSQMS-VAAHATPWEERPHLITTEAQAETTTSTSSLA 347

QY 269 -----GPGGACBP 277
DB 328 PPPTKICDPGELSGSGGCPAC 349

RESULT 13

US-08-419-652-6
Sequence 6, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: CD 9174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..602
OTHER INFORMATION: /note- "Represents residues 98 to
OTHER INFORMATION: 731 of human granulocyte colony-stimulating
factor-receptor."
US-08-419-652-6

Query Match 11.1%; Score 213.5; DB 2; Length 602;
Best Local Similarity 31.8%; Pred. No. 2.1e-13;

Matches 68; Conservative 31; Mismatches 86; Indels 29; Gaps 11;

QY 58 PPKPVNISCSKMM-KDLTCRWTPGAGHETFLHTYSLK-YKLRWYQ- - - - -DNTCEYH 112
DB 3 PPAIPNLSCMLNLTSSICOWEPP-ETHLPSTFLKSRSGNCGTQGSIIIDCV 60
QY 113 TVGPHSCHIP-KDLALFTEIVVENTNLGSRSDVLTLDLIDV- - - - -TTDPP 163
DB 61 KQGSQSCCIPKRLHLYQNGIWOENALGTSMSPOLDIPDVKLEPPMLRTMDPSP 120
QY 164 DVHVSVGLIEDOLSVRWSPALKDFLFOAKQIYRYVE-DSVDMKVVDVSNQTSCK 221
DB 121 EAAPQAGCLQ- - - - -LCW-EPWQGLHINQCELRHKKRQGEASWALVGPLLEALQYE 174

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:10 ; Search time 49.27 Seconds

(without alignments)
284.614 Million cell updates/sec

Title: US-09-037-657-25

Sequence: 1 TLNGRRRLPELRSVLNASTL.....TRGSCPADGAREVLPDKL 350

Scoring table: BLOSUM62

Searched: 122810 segs, 40065486 residues

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	17.3	622	2 A40144	prolactin receptor
2	325.5	17.0	206	2 A57018	prolactin receptor
3	316	16.5	830	2 I50455	prolactin receptor
4	313	16.3	610	2 A34631	lactogen receptor
5	313	16.3	610	2 A36116	prolactin receptor
6	313	16.3	412	2 A41070	prolactin receptor
7	313	16.3	310	2 A29884	prolactin receptor
8	309.5	16.1	303	2 I77524	prolactin receptor
9	309.5	16.1	292	2 I77525	prolactin receptor
10	309.5	16.1	608	2 I53269	prolactin receptor
11	308	16.1	831	2 J01655	prolactin receptor
12	306.5	15.7	581	2 I45971	prolactin receptor
13	306.5	15.7	616	2 A30304	prolactin receptor
14	297	15.5	917	2 I49639	prolactin receptor
15	290.5	15.1	918	2 A36337	prolactin receptor
16	285	14.9	918	2 A44257	glycoprotein 130 -
17	263.5	13.7	918	2 I51086	membrane glycoprot
18	241	12.6	837	2 A34898	interleukin-6 sign
19	226.5	11.8	372	2 I58141	prolactin receptor
20	220.5	11.5	783	2 JH0329	granulocyte colony
21	220.5	11.5	771	2 B38252	granulocyte colony
22	220.5	11.5	863	2 C38252	granulocyte colony
23	219.5	11.4	372	1 UHHCN	granulocyte colony
24	204	10.6	432	2 I48343	ciliary neurotroph
25	203	10.5	422	2 I37891	interleukin-11 rec
26	202	10.5	362	2 S60614	growth promoting a
27	199	10.4	156	2 A32868	hematopoietic grow
28	194	10.1	625	2 S35317	lactogen receptor
29	191	10.0	150	2 B34631	proto-oncogene - m
30	190	9.9	626	2 S37622	MPL-R protein prec
31	188.5	9.8	579	2 B45266	interleukin-6 rece
32	188.5	9.8	635	2 A45266	leukemia inhibitor
33	181	9.4	468	1 A41242	leptin receptor (v
34	176	9.2	1097	2 S17308	leptin receptor (v
35	174.5	9.1	894	2 S68437	leptin receptor (v
36	174.5	9.1	900	2 S68441	leptin receptor (v
37	174.5	9.1	805	2 S68441	leptin receptor (v
38	173.5	9.0	460	2 UJ0145	leptin receptor (v
39	170	8.9	894	2 J04797	leptin receptor pr

40	170	8.9	1162	2 PC4184	leptin receptor, O
41	170	8.9	805	3 JC4897	leptin receptor, O
42	169	8.8	265	2 S14081	erythropoietin rec
43	166	8.7	1092	2 JX0312	differentiation st
44	166	8.7	719	2 JC3181	differentiation st
45	165.5	8.6	440	2 J0144	interleukin-6 rece

ALIGNMENTS

RESULT 1
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
C/Accession: A40144
R/Boutin, J.M.; Edery, M.; Shlitta, M.; Jolicoeur, C.; Lesneux, L.; All, S.; Gould, D
Mol. Endocrinol. 3, 1455-1461, 1989
A/Title: Identification of a cDNA encoding a long form of prolactin receptor in human
A/Reference number: A40144; MUID:90114212
A/Accession: A40144
A/Molecule type: mRNA
A/Residues: 1-622 <BOU>
A/Cross-references: GB:M31661; NID:G190361; PID:G190362
A/Genes: GDB:PLR
A/Map position: 5p13.3-5p13.1
A/Cross-references: GDB:120315; OMIM:176761
C/Keywords: glycoprotein; transmembrane protein
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-622/Product: prolactin receptor, long form #status predicted <MAT>
F/59,104,233/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.38; Score 332; DB 2; Length 622;
Best Local Similarity 37.18; Pred. No. 1.8e-21;

Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

OY 47 ILAAGCLVYG-LPEKPNVISCNKKMDLTCRTFGAHGTFHTNYSKYKLRMGQD 105
Db 15 LFLWTLCLNGQLPGKPEKFCRSPNKEFTFCWVRPPTDG--LPTNYSLYHREGFTLM 72
OY 106 NTCEHYHTVGHPSCHIRPD-LALFPEIWEATNRLGSARSDVLTIDIDVYTTDPPD 164
Db 73 HECDDYITGPNNSCHFGQVYSMTRTIYAMNATNKGSSFSDLYDVYIVQDPDPLE 132
OY 165 VHSRVGGLDQLSVRVV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDDVSNQTS 219
Db 133 LAV-EVQPEDEKRPKRYLWIKNSPPTLLDLKGTGFTLLYELIKPEKAEME-IHFAGQTE 190
OY 220 CRLAGLPGYTFYQVNCNPGTIGSKAGIWESEWSPHTAASP 263
Db 191 FKILSLHPGKTLVQVCRKP-----DHGYWSMSPATRIQIP 227

RESULT 2

A57018
prolactin receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
C/Accession: A57018
R/Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A/Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
A/Reference number: A57018; MUID:95286597
A/Accession: A57018
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-206 <RES>
A/Cross-references: GB:S78505; NID:G999114; PID:G999115

Query Match 17.0%; Score 325.5; DB 2; Length 206;
 Best Local Similarity 37.6%; Pred. No. 1.7e-21;
 Matches 80; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

57 LPPEKPNVISCWKNKMDLTCMTPGAHGELFHTNYSLKYLKMYGODWTCCEHYTGP 116
 2 LPPEKPELFKRSNKEFTCMWPGTDG--LPTNYSLYHNGEFLMHECPYITGCP 59
 117 HSHIPKD-LALTPYEIWEATNRLGSANSVDLTLDIVYTTDPPDVHVSNGLED 175
 60 NSCHFGQKQYTSMTWTYIMVNAINOMGSSFSEDELYVDVTVYVCPDPLELAV--EVKQPED 118
 176 QLSRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCHLAGLKPGTV 230
 119 RKPLWKMSPPPLIDLTGTFWLLYERLKLPERAAEME--IHFAGQOTEFKLSLHFGQK 177
 231 YFVQRCNPFGIYSGKAGIWMSESHPTAASP 263
 178 YLVQVRCKP-----DHGYWSMSPATFIQIP 203

RESULT 3
 150455
 prolactin receptor - pigeon
 C:Species: Columba livia (domestic pigeon)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
 C:Accession: 150455
 R:Chen, X.; Horseman, N.D.
 C:Endocrinology 135, 269-276, 1994
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
 A:Reference number: 150455; MUID:94283267
 A:Accession: 150455
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

Query Match 16.5%; Score 316; DB 2; Length 830;
 Best Local Similarity 36.6%; Pred. No. 6.8e-20;
 Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

58 PPEKPNVISCWKNKMDLTCMTPGAHGELFHTNYSLKYLKMYGODWTCCEHYTGP 116
 231 PPEKPTIKRSPEKETITCMWPGSDG--HPTNYSLYHNGEFLMHECPYITGAP 287
 117 HSHCH-PRDLALTPYEIWEATNRLGSARSDVLTLDIVYTTDPPDV--HYSRVGGL 173
 288 NSCYDKKHTSFMTYINITVKAINEISVSDPLVVDVTVYVCPDPLVNLLEKKTIVNR 347
 174 EDQSVRVNVSPPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCHLAGLKPGTV 230
 348 KPYLVLTW-SPPLADVSGWLLTDEYELRLKPERAEEMETI-FVGOQTHYKFSINPCKK 405
 231 YFVQRCNPFGIYSGKAGIWMSEMS 255
 406 YIVQIHCKP-----DHGWSMS 424

RESULT 4
 A34631
 lactogen receptor 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
 C:Accession: A34631
 R:Zhang, R.; Bucxio, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
 Biochem. Biophys. Res. Commun. 168, 415-422, 1990
 A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
 A:Reference number: A34631; MUID:90241201
 A:Accession: A34631
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <2HA>

A:Cross-references: GB:M34083; NID:g205122; PID:g205123
 A:Note: the authors translated the codon GAG for residue 533 as Gly

Query Match 16.3%; Score 313; DB 2; Length 610;
 Best Local Similarity 35.0%; Pred. No. 8.4e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SLIAGSCLYGLPPEKPNVISCWKNKMDLTCMTPGAHGELFHTNYSLKYLKMYGOD 105
 15 SLKQGS-----PPGRPEIKHCRSPDKETITCMWNGTDG--LPTNYSLYSKE--GEK 65
 106 NT--CEEYHTVGRSHIPKD-LALTPYEIWEATNRLGSANSVDLTLDIVYTTDP 162
 66 TTYECPPYKTSGPSNCSFQKQYTSIMKTYITVNAINOMGSSSDPLVVDVTVYVEPEPP 125
 163 PDVHVSNGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQ 217
 126 RNLT-L-EVKOLNKKKTYLWKMSPPTITDVKTFMTEYERLKLPERAAEME--IHFTHQ 183
 218 TSCRLAGLKPGTVYFVQRCNPFGIYSGKAGIWMSESHPTAASP 263
 184 TQKVFEDLYPGQKYLVTQTRCKP-----DHGYWSMSQSSVEMP 222

RESULT 5
 A36116
 prolactin receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
 C:Accession: A36116
 R:Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, M.L.
 Mol. Endocrinol. 4, 1136-1143, 1990
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A:Reference number: A36116; MUID:91155946
 A:Accession: A36116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <SHL>
 A:Cross-references: GB:M57668; NID:g206366; PID:g206367; GB:M60728

Query Match 16.3%; Score 313; DB 2; Length 610;
 Best Local Similarity 35.0%; Pred. No. 8.4e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SLIAGSCLYGLPPEKPNVISCWKNKMDLTCMTPGAHGELFHTNYSLKYLKMYGOD 105
 15 SLKQGS-----PPGRPEIKHCRSPDKETITCMWNGTDG--LPTNYSLYSKE--GEK 65
 106 NT--CEEYHTVGRSHIPKD-LALTPYEIWEATNRLGSANSVDLTLDIVYTTDP 162
 66 TTYECPPYKTSGPSNCSFQKQYTSIMKTYITVNAINOMGSSSDPLVVDVTVYVEPEPP 125
 163 PDVHVSNGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQ 217
 126 RNLT-L-EVKOLNKKKTYLWKMSPPTITDVKTFMTEYERLKLPERAAEME--IHFTHQ 183
 218 TSCRLAGLKPGTVYFVQRCNPFGIYSGKAGIWMSESHPTAASP 263
 184 TQKVFEDLYPGQKYLVTQTRCKP-----DHGYWSMSQSSVEMP 222

RESULT 6
 A41070
 prolactin receptor NB2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; I55417
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (nb2) expresses a mutant form of pro-

A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALIS>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 J.O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
 A:Reference number: 155417; MUID:95014432
 A:Accession: 155417
 A:Molecule type: mRNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: ND2-11C cell line
 C:Keywords: transmembrane protein

Query Match 16.3%; Score 313; DB 2; Length 412;
 Best Local Similarity 35.0%; Pred. No. 5, 1e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SILAGSCLYVGLPPEKPVNISCNMKDLTCRMTPGAHEFTLHNTSLKTKLRYGOD 105
 15 SLKNGS-----PPKPELHKCRSPDKETFTCMWNPCTDGG--LPTNYSILYSKE--GEK 65
 106 NT--CEEYHTVGPCHIPKD-LALFTPEIWEATNRLGSARSVDLTLDIVYTTDPP 162
 66 TTYECPDYKTSQPNCSFSGKQYTSIMKIYIITVNAITNGSSSDPLYVDYVYIYEPEP 125
 163 PDVHVSRRVGLLEDLSVWV--SPPALKDF--LFQAKYQIRRVEDSVDMKVVDVSNQ 217
 126 RNLLT-EVKQKDKDKTYLWVWSPPTITDVKTGFTMEYELRKPEAEEME-IHFTGHQ 183
 218 TSCRLAGLPGTYVFOVQNCNPGIYSGSKKAGIWMESHPTAASP 263
 184 TORVFDLYPGQKYLIVOTRCKP-----DHGYMSRWMSQESSVEAP 222

RESULT 7
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence, revision 30-Sep-1989 #text, change 20-Mar-1998
 C:Accession: A29884
 R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ebery, M.; Shirota, M.; Banville, Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth hormone receptor family
 A:Reference number: A29884; MUID:88165059
 A:Accession: A29884

A:Keywords: transmembrane protein
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 16.3%; Score 313; DB 2; Length 310;
 Best Local Similarity 35.0%; Pred. No. 3, 5e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SILAGSCLYVGLPPEKPVNISCNMKDLTCRMTPGAHEFTLHNTSLKTKLRYGOD 105
 15 SLKNGS-----PPKPELHKCRSPDKETFTCMWNPCTDGG--LPTNYSILYSKE--GEK 65
 106 NT--CEEYHTVGPCHIPKD-LALFTPEIWEATNRLGSARSVDLTLDIVYTTDPP 162
 66 TTYECPDYKTSQPNCSFSGKQYTSIMKIYIITVNAITNGSSSDPLYVDYVYIYEPEP 125
 163 PDVHVSRRVGLLEDLSVWV--SPPALKDF--LFQAKYQIRRVEDSVDMKVVDVSNQ 217
 126 RNLLT-EVKQKDKDKTYLWVWSPPTITDVKTGFTMEYELRKPEAEEME-IHFTGHQ 183

QY 218 TSCRLAGLPGTYVFOVQNCNPGIYSGSKKAGIWMESHPTAASP 263
 DB 184 TORVFDLYPGQKYLIVOTRCKP-----DHGYMSRWMSQESSVEAP 222

RESULT 8
 A:Accession: I77524
 A:Molecule type: mRNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-303 <RES>
 A:Cross-references: GB:M22958; NID:g200479; PID:g200480

Query Match 16.1%; Score 309.5; DB 2; Length 303;
 Best Local Similarity 31.4%; Pred. No. 6, 9e-20;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVNAATLALANLNGSRQSGDNLVCHARDSILAGSCLYVGLPPEKPVNISCMSK 70
 DB 1 MSSALAYMLVLSISLNGS-----PPGPELHKCRSP 34
 QY 71 NKMDLTCRMTPGAHEFTLHNTSLKTKLRYGODNT--CEEYHTVGPCHIPKD-LAL 127
 DB 35 DKEFTCMWNPCTDGG--LPTNYSILYSKE--GEKNTYECDDYTSQPNCSFSGKQYTSI 90
 QY 128 FTPEIWEATNRLGSARSVDLTLDIVYTTDPPDVHVSRRVGLLEDLSVWV--PP 185
 DB 91 WKIITVNAITNGSSSDPLYVDYVYIYEPEPRLTL-EVKQKDKDKTYLWVWSPPTITDVKTGFTMEYELRKPEAEEME-IHFTGHQ 149
 QY 186 ALKDF--LFQAKYQIRRVEDSVDMKVVDVSNQTSCLAGLPGTYVFOVQNCNPGI 242
 DB 150 TITDVKTGFTMEYELRKPEAEEME-IHFTGHQTFKVFDPYGVQKYLIVOTRCKP--- 206
 QY 243 YGSKKAGIWMESHPTAASP 263
 DB 206 ----DHGYMSRWMSQESSVEAP 222

RESULT 9
 A:Accession: I77525
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:g200481; PID:g200482

Query Match 16.1%; Score 309.5; DB 2; Length 292;
 Best Local Similarity 31.4%; Pred. No. 6, 6e-20;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVNAATLALANLNGSRQSGDNLVCHARDSILAGSCLYVGLPPEKPVNISCMSK 70
 DB 1 MSSALAYMLVLSISLNGS-----PPGPELHKCRSP 34
 QY 71 NKMDLTCRMTPGAHEFTLHNTSLKTKLRYGODNT--CEEYHTVGPCHIPKD-LAL 127

Db 35 DEFTFCWNNPDSG--LPTNYSILYSKE--GEKNTYCPDPIKTSNCSFSPKQYPSI 90
 QY 128 FTFPEIWEATNRLGARSBDVLTLDIVVTDDPPDVHVSRYGLEDOLSTRWVS--PP 185
 Db 91 WRIITVNAINEMGSSSDPLVDVTVIVEPEPRNLTLEVKOLKDKKTYLWVKMLPP 149
 QY 186 ALKDF---LFOAKQIIRYREVEDSVDMKVVDVSNOTSCRLAGLKPGTYFVQVRCNPGI 242
 Db 150 TITDVKTGTFMEYERILKSEADME--IHFGHOTQFRVFDLYGCKTYLVQTRCKP--- 206
 QY 243 YGSKAGIWESESHPTASTP 263
 Db 206 ---DHGWSRWGQEKSEIEIP 222

RESULT 10

153269
 Prolactin receptor, long form - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Jan-1999
 A:Accession: J01655
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A:Reference number: 153269; MUID:93307149
 A:Accession: J01655
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:9293769; PID:9293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J06671; MUID:94085788
 A:Accession: J06671
 A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:9347398; PID:9347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: 534356
 A:Accession: S34356
 A:Molecule type: mRNA
 A:Residues: 1-557, 'F', 559-608 <EDE>
 A:Cross-references: EMBL:X73372; NID:9312696; PID:9312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domain: transmembrane #status predicted <TM>

Query Match 16.1%; Score 309.5; DB 2; Length 608;
 Best Local Similarity 31.4%; Pred. No. 1,7e-19;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVLAATLALANLNGSRQSGDNLVCHARGSTLACSLVGLPEKPVNISCKSK 70
 Db 1 MSSALATVLLVLSISLNGS-----PPGKPEIHKCRSP 34
 QY 71 NMKDLTCRWTPGAGETFLATNYSILKYLKMYGODNT--CEHYTVGPHSHIPKD-LAL 127
 Db 35 DKEFTCWNNPDSG--LPTNYSILYSKE--GEKNTYCPDPIKTSNCSFSPKQYPSI 90
 QY 128 FTFPEIWEATNRLGARSBDVLTLDIVVTDDPPDVHVSRYGLEDOLSTRWVS--PP 185
 Db 91 WRIITVNAINEMGSSSDPLVDVTVIVEPEPRNLTLEVKOLKDKKTYLWVKMLPP 149
 QY 186 ALKDF---LFOAKQIIRYREVEDSVDMKVVDVSNOTSCRLAGLKPGTYFVQVRCNPGI 242
 Db 150 TITDVKTGTFMEYERILKSEADME--IHFGHOTQFRVFDLYGCKTYLVQTRCKP--- 206

QY 243 YGSKAGIWESESHPTASTP 263
 Db 206 ---DHGWSRWGQEKSEIEIP 222

RESULT 11

J01655
 Prolactin receptor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997
 A:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDN.
 A:Reference number: J01655; MUID:93075121
 A:Accession: J01655
 A:Molecule type: mRNA
 A:Residues: 1-831 <TRAN>
 A:Cross-references: DDBJ:D13154; NID:9222848; PID:d1002939; PID:9222849
 A:Experimental source: Kidney
 C:Keywords: glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-831/Product: prolactin receptor #status predicted <MAT>
 F:439-462/Domain: transmembrane #status predicted <TM>
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (con

Query Match 16.1%; Score 308; DB 2; Length 831;
 Best Local Similarity 34.6%; Pred. No. 3.4e-19;
 Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

QY 58 PREKPVNISCKSKMKDLTCRWTPGAGETFLH-TNLSKYLKMYGODNTCEHYTVGP 116
 Db 230 PPEFTLTKCSPEKEFTCWNNPDSG--LPTNYSILYSKE--GEKNTYCPDPIKTSNCSFSPKQYPSI 90
 QY 117 HSCHI-PKDALFPEIWEATNRLGARSBDVLTLDIVVTDDPPDV--HVSRYGGL 173
 Db 287 NSCFDKKHHSFWITVITRATNEMGSSSDPLVDVTVIVEPEPRNLTLEVKOLKDKKTYLWVKMLPP 149
 QY 174 EDOLSVRWSPALKDF---LFOAKQIIRYREVEDSVDMKVVDVSNOTSCRLAGLKPGTV 230
 Db 347 KPYLVLTW-SPPPLADVRSGMLTLEYELRLKPEEGEMETI-FVGQGTQYKMFSLNGK 404
 QY 231 YFVQVRCNPGIYGSKAGIWESESHPTASTP 263
 Db 405 YIIQIRCKP-----DHGWSRWGQEKSEIEIP 222

RESULT 12

145971
 Prolactin receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
 A:Accession: L45971
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992
 A:Title: Molecular cloning of the bovine prolactin receptor and distribution of pro:
 A:Reference number: 145971; MUID:93246019
 A:Accession: L45971
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-581 <SCO>
 A:Cross-references: GB:L02549; NID:9163617; PID:9163618
 C:Genetics: PRLR

Query Match 16.0%; Score 306.5; DB 2; Length 581;
 Best Local Similarity 31.2%; Pred. No. 2.9e-19;
 Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;
 QY 12 LSRVLAATLALANLNGSRQSGDNLVCHARGSTLACSLVGLPEKPVNISCKSK 71
 Db 1 MSSALATVLLVLSISLNGS-----PPGKPEIHKCRSP 34

Db 7 SRVFIILLFLSVSLNGOS-----PPEKPKLVKCRSPG 40

QY 72 MKDLTCHWTFGAGHETFLHNNYSIAKYKLRWGDONTCEHYTHVPHSCHT-PRDLAFTP 130

Db 41 KEFTTCWMEPGADG--LPNNYTLTHKEGFTLHECPDXTGGPNSCYSKKTSIWK 98

QY 131 YEIWEATNRLSGARSVDLTLDIDVTTDPPPVHVSRYVGLSDQSVRW--SPPALK 188

Db 99 YVITVNNINMGSISSDPLVYHYTYIYEPPPNLTL-ELKHPRDKRYLWIKNSPPTMT 157

QY 189 D-----FLFOAKYQIRYVEDSDVMKVVDDVSNQTSCLAGLKGTYFVQVRCNPFQIY 243

Db 158 DVKSGWFIID--YEIRLKPKEATDME-THFLKOTQKIFNLPGQKYLQVIRCKP----- 211

QY 244 GSKKAGIYSEMSHPTASTP 263

Db 211 ---DHGIWSEMSPESSIQIP 227

RESULT 13

A30304

prolactin receptor 2 precursor - rabbit

M:Alternate names: prolactin receptor, mammary gland

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998

C:Accession: A30304; A60380

R:Entry, M.: Jolicoeur, C.; Levt-Meynueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989

A:Title: Identification and sequence analysis of a second form of prolactin receptor by

A:Reference number: A30304; MID:89184578

A:Accession: A30304

A:Molecule type: mRNA

A:Residues: 1-616 <ED>

A:Cross-references: GB:J04510; NID:g165669; PID:g165670

R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I. Int. J. Biochem. 22, 1089-1095, 1990

A:Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor

A:Reference number: A60380; MID:9116782

A:Accession: A60380

A:Molecule type: protein

A:Residues: 41-98, 'X', 90-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108; 150-164, 'XX', 167

A:Note: the amino end of the mature protein was blocked

C:Keywords: blocked amino end; glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-616/Product: prolactin receptor 2 #status predicted <MAT>

F:235-256/Domain: transmembrane #status predicted <TM>

F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 300.5; DB 2; Length 616;

Best Local Similarity 35.4%; Pred. No. 1.4e-18;

Matches 75; Conservative 29; Mismatches 91; Indels 17; Gaps 7;

QY 58 PPEKPNISCSNMKMDLQRTWPTGAGHETFLHNNYSIAKYKLRWGDONTCEHYTHVPH 117

Db 27 PPEKPNISCSNMKMDLQRTWPTGAGHETFLHNNYSIAKYKLRWGDONTCEHYTHVPH 84

QY 118 SCHI-PRDLAFTPYEWEATNRLSGARSVDLTLDIDVTTDPPPVHVSRYVGLSDQ 176

Db 85 SCVFSKSHKHSIMWITITVATINMGSSVSDPRVVDYTYIYEPPPNLTL-EKXHEDR 143

QY 177 LSVRWVS--PPALKDF--LFQAKYQIRYVEDSDVMKVVDDVSNQTSCLAGLKGTY 231

Db 144 KPLVWVKMLPPLVDVSGWLTQYERLKPKEAWE-THFAGQOQOFKILSLXPQKY 202

QY 232 FVQVRCNPFQIYSEMSHPTASTP 263

Db 203 LVQVRCKP-----DHGIWSEMSPESSIQIP 227

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997

C:Accession: I49699; I48370

R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T. J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp

A:Reference number: I48370; MID:9221552

A:Accession: I49699

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: GB:M83336; NID:g193591; PID:g193592

A:Accession: I48370

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:g840816; PID:g840817

C:Genetics:

A:Gene: gp130

C:Keywords: glycoprotein

Query Match 15.5%; Score 297; DB 2; Length 917;

Best Local Similarity 30.5%; Pred. No. 3.6e-18;

Matches 83; Conservative 45; Mismatches 124; Indels 20; Gaps 9;

QY 3 NGRRLPELISRVINASTLALANLNGSRORSQSDNLYCHARDGSIAGSCLYVGLPPEKP 62

Db 70 NHAAPREQVATNRTSSVTFIDVPLVSQVLGNLISFQIDQNYGVYMLSGFPDPK 129

QY 63 VNISCSNMKMDLQRTWPTGAGHETFLHNNYSIAKYKLRWGD-NTCEHYTHVPHSCHT 121

Db 130 TNLTCIYNENKMKMCOMDPCR--EYILEYNTLTKSE--WATERFPDQCKHGT---SCWV 182

QY 122 PKDLAFTPYEWEATNRLSGARSVDLTLDIDVTTDPPPVHVSRYVGLSDQSVRW 181

Db 183 SYMTYVTVNLEWVEANLAKVSSSEINFDVQKAPDPYMLSVTNSELSILKLSW 242

QY 182 VSPPALDPLFOAKYQIRYVEDSDVMKVV--DVSNGTSCLAGLKGTYFVQVRCN 238

Db 243 VSSGL--GGLDLKSDIQYTKRNASWIMQVPLDTPSPRSTFVQDLKPEYVPR-- 299

QY 239 PFGTYSKRAKGISSEMSHPTAST--PRSERP 268

Db 299 --SIKDSGK-GYMSDSEASGTYEDRPSRP 327

RESULT 15

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T. Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MID:91084844

A:Accession: A36337

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:g186353; PID:g186354

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

Query Match 15.1%; Score 290.5; DB 2; Length 918;

Best Local Similarity 28.7%; Pred. No. 1.4e-17;

Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;

RESULT 14

I49699

glycoprotein 130 - mouse

```

OY 7 LPELSRYLNASTLALANLNGSRQSGDNLVCHARDGSLIAGSCLTVGLPPEKPNIS 66
Db 74 IPKEQYTIINRTASSVTFTDIASINIQJTCNILEFGOLEQWYIGITIISGLPPEKPNLS 133
OY 67 CWSKMKDLCRTMPCGAHGETFLHTNYSIAKYKLRWYGODNTCEEHVGPCHIPKDLA 126
Db 134 CIVNCGKMKRCWEGGR--ETHLENTFLKSEMAIHKFADCKAKRDT--PTSCYVYSTV 189
OY 127 LFTPEIWEATNRLGSARSDVLTLDLIDVTTDPPDPVHVSRYVGLEDQLSVRWVSPA 186
Db 190 YFVNIEVWEAENALGKVTSDHINFDPPYKVPNPNHLSVINSELSIILKLTWN-PS 248
OY 187 LKDFLQAKYQIRYRVEDSVDMKVY--DVSNOTSCLAGLAPGTYFVQVRCNPGITY 243
Db 249 IKSUIT-LKINIQRTKDASTWSQIPPEDTASTRSSFTVODLKPFTEYFRIRC----M 302
OY 244 GSKRAGIWEWSHPTASTPRSERP 268
Db 303 KEDKGYSWDSWSEASGIT-YEDRP 326

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 Job time: 5403 sec

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:14 ; Search time 35.09 Seconds
(without alignments)
281.958 Million cell updates/sec

Title: US-09-037-657-25
Effect score: 1919
Sequence: 1 TLNGRRLPELPSRVNASTL.....TNGSCPADGARREVLPRDL 350

Scoring table: BLOSUM62

Database: 77977 seqs, 28268293 residues
SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	17.3	622	1	PLRL_HUMAN
2	316	16.5	830	1	PLRL_COILI
3	313	16.3	610	1	PLRL_RAT
4	309.5	16.1	608	1	PLRL_MOUSE
5	308	16.1	831	1	PLRL_MOUSE
6	307	16.0	831	1	PLRL_MOUSE
7	306.5	16.0	831	1	PLRL_MOUSE
8	304	15.8	581	1	PLRL_MOUSE
9	300.5	15.7	616	1	PLRL_MOUSE
10	297	15.5	917	1	PLRL_MOUSE
11	290.5	15.1	918	1	PLRL_MOUSE
12	285	14.9	918	1	PLRL_MOUSE
13	263.5	13.7	630	1	PLRL_MOUSE
14	241	12.6	837	1	PLRL_MOUSE
15	226.5	11.8	372	1	PLRL_MOUSE
16	220.5	11.5	836	1	PLRL_MOUSE
17	217.5	11.3	372	1	PLRL_MOUSE
18	202	10.5	362	1	PLRL_MOUSE
19	194	10.1	625	1	PLRL_MOUSE
20	188.5	9.8	635	1	PLRL_MOUSE
21	181	9.4	468	1	PLRL_MOUSE
22	176	9.2	1097	1	PLRL_MOUSE
23	174.5	9.1	1162	1	PLRL_MOUSE
24	173.5	9.0	460	1	PLRL_MOUSE
25	171.5	8.9	462	1	PLRL_MOUSE
26	166	8.7	1092	1	PLRL_MOUSE
27	165.5	8.6	638	1	PLRL_MOUSE
28	161.5	8.4	508	1	PLRL_MOUSE
29	161	8.4	1165	1	PLRL_MOUSE
30	158.5	8.3	638	1	PLRL_MOUSE
31	158	8.2	507	1	PLRL_MOUSE
32	156	8.1	507	1	PLRL_MOUSE
33	153	8.0	638	1	PLRL_MOUSE
34	146	7.6	638	1	PLRL_MOUSE
35	145.5	7.6	897	1	PLRL_MOUSE
36	145.5	7.6	897	1	PLRL_MOUSE
37	145	7.6	897	1	PLRL_MOUSE
38	143.5	7.5	897	1	PLRL_MOUSE
39	141.5	7.4	898	1	PLRL_MOUSE
40	141.5	7.4	898	1	PLRL_MOUSE
41	141.5	7.4	898	1	PLRL_MOUSE
42	139.5	7.3	662	1	PLRL_MOUSE
43	138.5	7.2	608	1	PLRL_MOUSE

ALIGNMENTS

RESULT	ID	Query Match	Score	DB	Description
1	PLRL_HUMAN	17.3	332	1	PLRL_HUMAN
2	PLRL_HUMAN	16.5	316	1	PLRL_HUMAN
3	PLRL_HUMAN	16.3	313	1	PLRL_HUMAN
4	PLRL_HUMAN	16.1	309.5	1	PLRL_HUMAN
5	PLRL_HUMAN	16.1	308	1	PLRL_HUMAN
6	PLRL_HUMAN	16.0	307	1	PLRL_HUMAN
7	PLRL_HUMAN	16.0	306.5	1	PLRL_HUMAN
8	PLRL_HUMAN	15.8	304	1	PLRL_HUMAN
9	PLRL_HUMAN	15.7	300.5	1	PLRL_HUMAN
10	PLRL_HUMAN	15.5	297	1	PLRL_HUMAN
11	PLRL_HUMAN	15.1	290.5	1	PLRL_HUMAN
12	PLRL_HUMAN	14.9	285	1	PLRL_HUMAN
13	PLRL_HUMAN	13.7	263.5	1	PLRL_HUMAN
14	PLRL_HUMAN	12.6	241	1	PLRL_HUMAN
15	PLRL_HUMAN	11.8	226.5	1	PLRL_HUMAN
16	PLRL_HUMAN	11.5	220.5	1	PLRL_HUMAN
17	PLRL_HUMAN	11.3	217.5	1	PLRL_HUMAN
18	PLRL_HUMAN	10.5	202	1	PLRL_HUMAN
19	PLRL_HUMAN	10.1	194	1	PLRL_HUMAN
20	PLRL_HUMAN	9.8	188.5	1	PLRL_HUMAN
21	PLRL_HUMAN	9.4	181	1	PLRL_HUMAN
22	PLRL_HUMAN	9.2	176	1	PLRL_HUMAN
23	PLRL_HUMAN	9.1	174.5	1	PLRL_HUMAN
24	PLRL_HUMAN	9.0	173.5	1	PLRL_HUMAN
25	PLRL_HUMAN	8.9	171.5	1	PLRL_HUMAN
26	PLRL_HUMAN	8.7	166	1	PLRL_HUMAN
27	PLRL_HUMAN	8.6	165.5	1	PLRL_HUMAN
28	PLRL_HUMAN	8.4	161.5	1	PLRL_HUMAN
29	PLRL_HUMAN	8.4	161	1	PLRL_HUMAN
30	PLRL_HUMAN	8.3	158.5	1	PLRL_HUMAN
31	PLRL_HUMAN	8.2	158	1	PLRL_HUMAN
32	PLRL_HUMAN	8.1	156	1	PLRL_HUMAN
33	PLRL_HUMAN	8.0	153	1	PLRL_HUMAN
34	PLRL_HUMAN	7.6	146	1	PLRL_HUMAN
35	PLRL_HUMAN	7.6	145.5	1	PLRL_HUMAN
36	PLRL_HUMAN	7.6	145.5	1	PLRL_HUMAN
37	PLRL_HUMAN	7.6	145	1	PLRL_HUMAN
38	PLRL_HUMAN	7.5	143.5	1	PLRL_HUMAN
39	PLRL_HUMAN	7.4	141.5	1	PLRL_HUMAN
40	PLRL_HUMAN	7.4	141.5	1	PLRL_HUMAN
41	PLRL_HUMAN	7.4	141.5	1	PLRL_HUMAN
42	PLRL_HUMAN	7.3	139.5	1	PLRL_HUMAN
43	PLRL_HUMAN	7.2	138.5	1	PLRL_HUMAN

Query Match: 17.38; Score 332; DB 1; Length 622;
Best Local Similarity: 37.18; Pred. No. 4,7e-21;
Matches: 83; Conservative: 28; Mismatches: 95; Indels: 18; Gaps: 8;

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QY 47 ILAAGCLYVG-LPPEKPVNISCSMKMKDLGCRMTGAGHEFFLENTSLAKKLMWYOD 105
DB 15 LELNLCNLGOLPGRKPELFKRSRPNKEFTFCWMPRGDGC--LPTNLSLYHREGETLM 72
QY 106 NTCSEYHYVGPSPHCHIPRD-LALFPPYEIWEATNRIGSARSVDYTLIDLVYTTDPPPD 164
DB 73 HCCPDYITGGPNSCHFGKQYTSMTWTYIMMVAATNMGSSFSDELXYVDTYIVGDPDPLE 132
QY 165 VHVSVAGLEDPOLSVRWV--LSPALKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTS 219
DB 133 LAV-EVKQPEDKPKYLMKWSPPPLIDKTGWFLLYELIRLKPKEAEME-IFHAGQOTE 190
QY 220 CRLGLKPGTYVYQVRCNPFQYSGKAGIMSEWSHPTAATP 263
DB 191 FKILSHGQKXYLVQVRCKP-----DHGWSMSAPTFIOIP 227

RESULT 2
PRLR_COLL1 STANDARD: PRT: 830 AA.
AC 090374;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS COLUMBA LIVIA (DOMESTIC PIGEON).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CROPSNC;
RX MEDLINE: 94283267.
RA CHEN X., HOSSEMAN N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor."
RL ENDOCRINOLOGY 135:269-276(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DB EMBL: U07694; G466382;
DR PROSITE: PS00241; RECEPTOR_CYTORININS_1; 2.
DR PROSITE: PS00340; RECEPTOR_CYTORININS_2; 2.
DR PFAM: PF00041; fn3; 4.
DR HSSP: P16471; 1BP3.
KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT STGNL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112

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FT CARBOHYD 132 132
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
SO SEQUENCE 830 AA; 94507 MW; 5EFA0D51 CRC32;

Query Match 16.5%; Score 316; DB 1; Length 830;
Best Local Similarity 36.6%; Pred. No. 1.6e-19;
Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

QY 58 PPEKPVNISCSMKMKDLGCRMTGAGHEFFLH-TNLSLAKKLMWYODNTCEYHYVGP 116
DB 231 PPEKPTIIRKSPRKEFTFCWMPKPSDGC--HPTNLTLLSKGEERVECPDYKTAGP 287
QY 117 HSCHI-PRDLALFPPYEIWEATNRIGSARSVDYTLIDLVYTTDPPPDV--HYSRNGC 173
DB 288 NSCYFDKKHSTFWIYITKATNEISNVSDFLYVDTYIVOTDPPVNTLELKTQVNR 347
QY 174 EDOLSVRWSPPALKDF--LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPGTV 230
DB 348 KPYLVLTW-SPPPLADYRSGWLTLDYELRLKPEAEAEEMETI-FVGOQTHYKMFSLNKGK 405
QY 231 YFQVRCNPFQYSGKAGIMSEWS 255
DB 406 YIVQIRCKP-----DHHGMSSEWS 424

RESULT 3
PRLR_RAT STANDARD: PRT: 610 AA.
AC P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 91155946.
RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
RT EDERY M., DJIANE J., KELLY P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and rat liver."
RL MOL. ENDOCRINOL. 4:1136-1143(1990).
RN [2]
RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
RX MEDLINE: 90241201.
RA ZHANG R., BUCKKO E., TSAI-MORRIS C.H., HU Z.Z., DUFRU M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen receptor cDNA species."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).
RN [3]
RP SEQUENCE OF 281-610 FROM N.A.
RA BANVILLE D., STOCIO R., MURPHY K.K., BOIE Y., KELLY P.A.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RC TISSUE-LIVER;
RX MEDLINE: 88165059.
RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
RA SHIROTA M., BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of the growth hormone/prolactin receptor gene family."
RL CELL 53:69-77(1988).
RN [5]
RP SEQUENCE FROM N.A. (FORM NB2).
RC TISSUE-LYMPHOMA;

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RX MEDLINE; 92041834.
 RA ALT S., PELLIGRINI I., KELLY P.A.;
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
 of prolactin receptor.";
 RL J. BIOL. CHEM. 266:20110-20117(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RX MEDLINE; 95014432.
 RA O'NEAL R.D., YU-LEE L.Y.;
 RT "Differential signal transduction of the short, Nb2, and long
 prolactin receptors. Activation of interferon regulatory factor-1 and
 cell proliferation.";
 RL J. BIOL. CHEM. 269:26076-26082(1994).
 RN [1]
 RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC [1] SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1] ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING OF THE PRLR GENE.
 CC [1] SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC [1] SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 or send an email to license@isb-sib.ch).

 R EMBL; M57668; G206367; -
 R EMBL; M34083; G205123; -
 R EMBL; L48060; G1019651; -
 R EMBL; U34730; G1223859; -
 R EMBL; M19304; G206365; -
 R EMBL; M74152; G206390; -
 R EMBL; U07567; G641964; -
 R PIR; A29884; A29884.
 R PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 R PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 R PRAM; PF00041; fn3; 2.
 R HSSP; P16471; 1BP3.
 R RECEPTOR_TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 W ALTERNATIVE SPLICING.
 W SIGNAL 1 19
 W CHAIN 20 610
 W DOMAIN 20 229
 W TRANSMEM 230 253
 W DOMAIN 254 610
 W DOMAIN 20 117
 W DOMAIN 119 222
 W DISULFID 31 41
 W DISULFID 70 81
 W CARBOHYD 54 54
 W CARBOHYD 99 99
 W CARBOHYD 127 127
 W VARSPIC 131 130
 W VARSPIC 151 610
 W VARSPIC 281 310
 W VARSPIC 311 610
 W VARSPIC 342 539
 W VARSPIC 236 236
 W VARSPIC 345 345
 W VARSPIC 465 465
 W VARSPIC 466 466
 W VARSPIC 469 469
 W VARSPIC 541 541
 W VARSPIC 555 555
 W SEQUENCE 610 AA; 68599 MW; C579BC43 CRC32;
 POTENTIAL.
 EVKOLDKRTYLMWKSPT -> DYRWESCHQELPKSA
 KLN (IN SHORT FORM).
 MISSING (IN SHORT FORM).
 KGRSELSALGCODEPRTSCEDLYEFL ->
 TGSRSKYVDLYLDPGFGFKLDNAGELYD (IN
 MEDIUM FORM).
 MISSING (IN MEDIUM FORM).
 V -> A (IN REF. 2).
 G -> V (IN REF. 2).
 E -> K (IN REF. 1).
 Q -> E (IN REF. 2).
 A -> G (IN REF. 2).
 T -> M (IN REF. 1).
 O -> K (IN REF. 2).
 C579BC43 CRC32;

Query Match 16.38; Score 313; DB 1; Length 610;
 Best Local Similarity 35.08; Pred. No. 2e-19;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;
 D 46 SILAGSCLYVGLPEPEKPNISCSKNNKDLGCRWTPGAHGEPFHTYSLKIKRWGOD 105
 D 15 SILAGS-----PPGKEIHKCRSPDKETFCWNPFGTDG--LPTVSLYSRE--GEK 65
 Q 106 NT--CEEHYVGHPSCHIPD-LALFPYEIWEATNRLSARSQVLTLDLVYTTDP 162
 D 66 TTYECPPDKTSGPNSCFSSQYTSIMKIYIITVATQMGSSSDPLVYVYTIIVEPEPP 125
 Q 163 PDVYVSVGLEGDLSTRWV--SPALKD---LFOAKYQIRYVEDSYDMKYVDVDSNQ 217
 D 126 RNLTL-EVKOLDKRTYLMWKSPTITDVKTGFTWEYRIELKPEAEWE-IHTGHD 183
 Q 218 TSCLAGLKPQTVYFVQVRNPFGYSKRAGINSESHSTA5TP 263
 D 184 TQFVFPDLYPGKTYIVQTRCP-----DHGYSRWSSQSSVEVP 222
 RESULT 4
 PRLR_MOUSE STANDARD: PRT; 608 AA.
 AC 008501: 062099; P15213; P15212;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RP STRAIN-C3H; TISSUE-MAMMARY GLAND;
 RX MEDLINE; 94085788.
 RA MOORE R.C., OKA T.;
 RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
 long-form prolactin receptor.";
 RL GENE 134:263-265(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RP STRAIN-SWISS WEBSTER; TISSUE-LIVER;
 RX MEDLINE; 93307149.
 RA CLARKE D.L., LINZER D.I.H.;
 RT "Changes in prolactin receptor expression during pregnancy in the
 mouse ovary.";
 RL ENDOCRINOLOGY 133:224-232(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RA SASAKI M.;
 RL SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RP STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
 RA EDERY M., PEZET A., NANDI S., KELLY P.A.;
 RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
 RP STRAIN-SWISS WEBSTER; TISSUE-LIVER;
 RX MEDLINE; 89261824.
 RA DAVIS J.A., LINZER D.I.H.;
 RT "Expression of multiple forms of the prolactin receptor in mouse
 liver.";
 RL MOJ. ENDOCRINOL. 3:674-680(1989).
 CC [1] FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
 CC [1] SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1] ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
 (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
 GENE.
 CC [1] SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

```
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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DR EMBL; L13593; G347842; -
DR EMBL; L14811; G293770; -
DR EMBL; D10214; G220576; -
DR EMBL; X73372; G312697; -
DR EMBL; M22959; G200482; -
DR EMBL; M22958; G200480; -
DR PIR; J10671; J10671.
DR MGI; MGI:97763; PRL.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
DR PFAM; PF00041; fn3; 2.
DR HSSP; P16471; 1BP3.
KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 19
FT CHAIN 20 608
FT DOMAIN 20 229
FT TRANSMEM 230 253
FT DOMAIN 254 608
FT DOMAIN 20 117
FT DOMAIN 119 222
FT DISULFID 31 41
FT DISULFID 70 81
FT CARBOHYD 54 54
FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT VASPLIC 281 292
FT VASPLIC 281 303
FT VASPLIC 304 608
FT CONFLICT 558 558
SQ SEQUENCE 608 AA; 68240 MW; AA401B67 CRC32;

Query Match 16.1%; Score 309.5; DB 1; Length 608;
Best Local Similarity 31.4%; Pred. No. 4e-19;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVNSTALALANLNGSRGSDNVCARHDSGLAGSLYGLPPEKFNISCMK 70
DB 1 MSALAYMLLVSTLSLNGS-----PPGKEIHKCNSP 34

QY 71 NKKDLTCRWTPGAHGETFLHTNYSLKYLKMYGQDNT--CEEYHVGPHSCHIPRD-LAL 127
DB 35 DKETFCWNNPSSDGG--LPTNYSLSYKRE--GEKNTYCPDYKTSGRNSCFSSKQYTSI 90

QY 128 FPPETLWVATNRLGASRSDVLTLDLVYTTDPPDVAVSKVGLDGLSTRVWS--PP 185
DB 91 WKIYITVATNEMSGSTSDPLVDTYIVVEPEPPNLT-L-EVKDLKKKTYLWAKWLP 149

QY 186 ALKDF---LFOAKYQRYRVNEDSVDRKVVVDVSNQTSCLAGLQPTVYFVQVRCNPFQI 242
DB 150 TITDVATGFTMEYERLRKSEADENE-IHFGHQGFVFDLYPQAKLYVTRCKP--- 206

QY 243 YGSKKAGIWEWSHPTAASP 263
DB 206 ---DHGYSRWGOEKSEIEIP 222

RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.

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AC 004594;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DE 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).  
GN PRLR.  
OS GALLUS GALLUS (CHICKEN).  
OC ENKAROT; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;  
NC NOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WHITE LBSHORN; TISSUE-KIDNEY;  
RX MEDLINE; 93075121.  
RA TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;  
RT "Double antenna structure of chicken prolactin receptor deduced from  
RL the cDNA sequence";  
CC BIOCHEM. BIOPHYS. RES. COMMUN. 188:490-496(1992).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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DR EMBL; D13154; G222849; -
DR PIR; J01655; J01655.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PFAM; PF00041; fn3; 4.
DR HSSP; P16471; 1BP3.
KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; B977BE07 CRC32;

Query Match 16.1%; Score 308; DB 1; Length 831;
Best Local Similarity 34.6%; Pred. No. 7.9e-19;
Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

QY 58 PPEKFNISCMKNNKDLTCRWTPGAHGETFLH-TNYSLKYLKMYGQDNTCEEYHYVGP 116
DB 230 PPEKFTIHKCSPEKETFTCWKPKDGG---HPTNYLLSKSEDEGVYECPPYRTAGP 286

QY 117 HSCCH-PRDALLFPPEYELWVATNRLGASRSDVLTLDLVYTTDPPDV--HYSRVGL 173
DB 287 NSCYDKRHTSFMTIYNTVATNEMSGNSSDPRIVDVTYIVQDPVAVTLELKPINR 346

FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SO SEQUENCE 581 AA; 65153 MW; CORCA0A2 CRC32;

Query Match
 Best Local Similarity 31.2%; Score 306.5; DB 1; Length 581;
 Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;

QY 12 SRVLAATLALANLNGSRGSDNLVCHARDGSLAGSCLVGLPPEKPNVSCWSKN 71
 DB 7 SRVVFLLFLFSLVSLNGOS-----PPEKPKLVKCRSPG 40
 QY 72 MKDLTCRWTPGAGETFLHNTYSLAKYKRLRYGDNCEHTYHPSCHI-PKDLALFPP 130
 DB 41 KEFTFTWMEPGADGG--LPTNYTLTYHKEGETLIHPCDPKGTGSPSCFSKHTSIWKA 98
 QY 131 YEIWEATNRLGARSVDLTLDVYTTDPPDVHVSRYVGLDQLSVRW--SSPALK 188
 DB 99 YVTVNAINOMGISSDPLVHTYIYEPEPPANLTL-ELKHEDRKPILMIKSPPTWT 157
 QY 189 D-----FLFOAKYQIRYRVDSVDMKVVDSVNOTSCLAGLPGYTYVQVHCNPFGLT 243
 DB 158 DVKSGMFIQ--YEIRLKPPEKATDME-THTLTKOTLKIRNLYVGOKYLVQIRCKP----- 211
 QY 244 GSKKAGTSEMSHPTASTP 263
 DB 211 ---DHGYTSEMSPESSIOIP 227

RESULT 8
 PRLR_CEREL STANDARD; PRT; 581 AA.
 ID PRLR_CEREL Q28235;

DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

OS CERVUS ELAPHUS (RED DEER).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
 CC CERVUS.

[1]
 RA SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 96030711.
 RA CLARKE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
 RA KELLY P.A., JABBOUR H.N.;

RT "Expression of the prolactin receptor gene during the breeding and
 non-breeding seasons in red deer (Cervus elaphus): evidence for the
 expression of two forms in the testis";
 RL J. ENDOCRINOLOGY, 146:313-321(1995).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DR EMBL; X94953; E218406;
 CC DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
 CC DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
 CC DR PFAM; PF00041; fn3; 2;
 CC DR HSP; P14787; IAN3.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 581 PROLACTIN RECEPTOR.
 FT DOMAIN 25 254 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 238 POTENTIAL.
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 123 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 FT CARBOHYD 233 233 POTENTIAL.
 SO SEQUENCE 581 AA; 65159 MW; 721F0366 CRC32;

Query Match
 Best Local Similarity 33.2%; Score 304; DB 1; Length 581;
 Matches 75; Conservative 37; Mismatches 92; Indels 22; Gaps 8;

QY 44 DGSILAGSCLVGLPPEKPNVSCWSKNKDLTCRWTPGAGETFLHNTYSLKYKRWYG 103
 DB 18 NMSLNGOS-----PGRKRIIKRSPGKETFTCWMEPSDGG--LPTNYTLTYHREGT 70
 QY 104 QDNCEHTYHPSCHI-PKDLALFPEIYVATNRLGARSVDLTLDVYTTDPP 162
 DB 71 LIHECPDYKTGPGNTCYFSKHTSIKIRYIVTVNAINOMGVSSDPLVYDYIYEPEPP 130
 QY 163 PDVHVSRYVGLDQLSVRW--SPALKDF--LFOAKYQIRYRVDSVDMKVVDSVNSQ 217
 DB 131 ANLTL-ELKHEDRKPILMIKSPPTWTDVKSGMFIQYELRKPETADME-IHRAKQ 188
 QY 218 TSCRLAGLPGYTYVQVHCNPFGLTSCRWTPGAGETFLHNTYSLKYKRWYG 263
 DB 189 TQKITSIPVQKRYLVQIRCKP-----DHGYTSEMSPESSIOIP 227

RESULT 9
 PRLR_RABIT STANDARD; PRT; 616 AA.
 ID PRLR_RABIT P14787;

DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

OS ORCTOLOGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC LAGOMORPHA; LEPORIDAE; ORCTOLOGUS.

[1]
 RA SEQUENCE FROM N.A.
 RC TISSUE-MAMMARY GLAND;
 RX MEDLINE; 89184578.
 RA EDERY M., JOLICOEUR C., LEVI-MEYREUETS C., DUSANTER-FOURT I.,
 RA PETRIDOU B., BOOTIN J.M., LESUEUR L., KELLY P.A., DIANE J.,
 RA "Identification and sequence analysis of a second form of prolactin
 receptor by molecular cloning of complementary DNA from rabbit
 mammary gland";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DR EMBL; X94953; E218406;
 CC DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
 CC DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
 CC DR PFAM; PF00041; fn3; 2;
 CC DR HSP; P14787; IAN3.

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EMBL: J04510; G165670; -
 DR PIR: A30304; A30304.
 DR PDB: 1AN3; 03-DEC-97.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 2.
 DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 DR SIGNAL: 1 24
 CHAIN 1 24
 DOMAIN 25 616
 TRANSMEM 25 234
 DOMAIN 25 258
 DOMAIN 259 616
 DOMAIN 25 122
 DOMAIN 124 122
 DISULFID 36 46
 DISULFID 75 86
 CARBOHYD 59 59
 CARBOHYD 104 104
 CARBOHYD 132 132
 SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;
 Query Match 15.7%; Score 300.5; DB 1; Length 616;
 Best Local Similarity 35.4%; Pred. No. 2.4e-18;
 Matches 75; Conservative 29; Mismatches 91; Indels 17; Gaps 7;

58 PEKPVNISCWKNMMDLTCRMTPGAAGETFLHTNYSKYKLMWYGQDNCEHYVGH 117
 27 PGKRFIEFKCRSEPEKTEFCWRRPGADG--LPNTLYLHKGSETTHCCPDYKGGPV 84
 118 SOHI-PKDLATTPYEINVEATNRUGASNSDVLTDLDVYTTDPPDVHVRVGLDQ 176
 85 SCYFSKKTHTSIITIIITVANNOMGSSVSDRYVDVTVIVEDEPPVNLTL-EVKHPDR 143
 177 LSVRWVS--PPALXCF--LPQAKYQIRVSDSDMKVYDVSNQTSCLAGLAFGVY 231
 144 KPYLWKKLPPPLVLRSGWLTLYEIRLKPKEAEME-THRAGQOTQKILSLVGGKY 202
 232 FVOVRCNPFYIGSKKAGISMSHPTASTP 263
 203 LVYRCRP-----DHGFWSVSPSSIQIP 227
 RESULT 10
 L6B_MOUSE
 D IL6B_MOUSE STANDARD; PRT; 917 AA.
 C 000560;
 T 01-FEB-1995 (REL. 31, CREATED)
 T 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 T 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 T INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6- β) (INTERLEUKIN
 T 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 T IL6ST
 S MUS MUSCULUS (MOUSE).
 C EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 C RODENTIA; SCIURGNATHI; MURIDAE; MURINAE; MUS.
 P (1)
 P SEQUENCE FROM N.A.
 P STRAIN-ICR; TISSUE-MACROPHAGE;
 C MEDLINE; 92291532.
 C SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;
 C Molecular cloning of a murine IL-6 receptor-associated signal
 C transducer, gp130, and its regulated expression in vivo.
 C J. IMMUNOL. 148:4066-4071(1992).
 -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING

CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
 CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
 CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CC CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 CC DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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EMBL: X62646; G840817; -
 DR EMBL: M83336; G193592; -
 DR MGI: M96560; IL6ST.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 DR HSSP: P40189; 1B0V.
 DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT.
 KM
 FT SIGNAL: 1 22
 FT CHAIN 1 22
 FT TRANSMEM 23 617
 FT DOMAIN 618 639
 FT DOMAIN 640 917
 FT DOMAIN 26 120
 FT DOMAIN 124 220
 FT DOMAIN 221 322
 FT DOMAIN 323 420
 FT DOMAIN 422 515
 FT DOMAIN 516 611
 FT DOMAIN 723 741
 FT DISULFID 134 144
 FT DISULFID 172 180
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 225 225
 FT CARBOHYD 388 388
 FT CARBOHYD 476 476
 FT CARBOHYD 551 551
 SEQUENCE 917 AA; 102452 MW; ASDCD259 CRC32;

Query Match 15.5%; Score 297; DB 1; Length 917;
 Best Local Similarity 30.5%; Pred. No. 7.8e-18;
 Matches 83; Conservative 45; Mismatches 124; Indels 20; Gaps 9;
 QY 3 NGRRLPPLSLVNLASTLALANLNGSRQSGNLYCHARDGSLAGSCLYGLPPEKP 62
 Db 70 NHAAPVPEQTVINRTSSVYFTDVVLPVSQVLTNCNIIISFGQIEQNVYGVMLSGFPDPKP 129
 QY 63 VNISCWKNMMDLTCRMTPGAAGETFLHTNYSKYKLMWYGQDNCEHYVGH 121
 Db 130 TNLACIYNKGNMCLQNDPGR--ETIYETNYTLSE--WATEKFPDQSKRHGT--SCWV 182
 QY 122 PKDLATTPYEINVEATNRUGASNSDVLTDLDVYTTDPPDVHVRVGLDQSLVVR 181

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DB 103 SYMPYINIEWEAEANALGVSESEINFDPVDKVRKTPPYNLSVTNSELSILKLSW 242
OY 102 VSPPLAKPFLQKQYQIRVEDSDVMKVY---DDVSNQTSCLAGLPGVYFVOVACN 238
DB 243 VSSGL- GGLDLKSDIDYRKDASTWIOVPLEDTMSPTSTVODLKFTEYFRIR-- 299
OY 239 PEGYSGKAGIMSEMSHPTAST--PRSERP 268
DB 299 --SINDSGK-GYWSDMSEASGTTEDRPSRP 327

RESULT 11
ID IL6B_HUMAN STANDARD: PRT: 918 AA.
AC P40189;
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSMARTIN M
DE RECEPTOR) (CDM130) (CD130 ANTIGEN).
GN IL6ST.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELOMA, AND PLACENTA;
RX MEDLINE: 9108484.
RA HIRANO M., MURAKAMI M., SAITO M., HIRANO T., TAGA T., KISHIMOTO T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RT Cell 63:1149-1157(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE: 98169383.
RA BRAVO J., STANTON D., HEATH J.K., JONES E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130."
RT EMBD J. 17:1665-1674(1998).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA BETA) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES.
CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm"
CC
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CC
DR EMBL: M57230; G186354;
DR PIR: A36337; A36337.
DR PDB: 1B0U; 26-AUG-98.
DR MIM: 600694;
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 3.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW REPEAT; 3D-STRUCTURE.

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FT SIGNAL 1 22
FT CHAIN 23 918
FT DOMAIN 23 619
FT TRANSMEM 620 641
FT DOMAIN 642 916
FT DOMAIN 26 120
FT DOMAIN 124 222
FT DOMAIN 223 324
FT DOMAIN 325 423
FT DOMAIN 424 517
FT DOMAIN 518 613
FT DOMAIN 725 755
FT DISULFID 134 144
FT DISULFID 172 182
FT CARBOHYD 43 43
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157
FT CARBOHYD 227 227
FT CARBOHYD 379 379
FT CARBOHYD 383 383
FT CARBOHYD 390 390
FT CARBOHYD 553 553
FT CARBOHYD 564 564
SO SEQUENCE 918 AA; 103522 MW; 7CC06F05 CRC32;

Query Match 15.1% Score 290.5; DB 1; Length 918;
Best Local Similarity 28.7% Pred. No. 2.8e-17;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;

OY 7 LPEELSRVNLSTALALANLNGSRSGDNLVCHARDGSLVGLYGPPEKPVNIS 66
DB 74 IPKEGYTIINFTASSVTTDLASLNIQTLNIFRGLEQNVYGIISGLPEKPKNLS 133
OY 67 CWSKMKKLTCTKATPGANGFELHTNYSLKRLKRYGQDNTCEHYTGPHSCHLPKDLA 126
DB 134 CIVNGKMKREEMOGR--ETHLETFNLKSMWATHKRADCKAKBDT--PTSCVDYSTV 189
OY 127 LETPEIWEATNRLGARSQVLTLDIDVYVTPPDVHVSRYVGLDQLSVRWVSPA 186
DB 130 YFVNIEWEAEANALGKTSDBINDPYKKKPNPHLSVYNSELSILKLTWTN-PS 248
OY 187 LKDFLEQKQYQIRVEDSDVMKVY---DDVSNQTSCLAGLPGVYFVOVACNPFGLY 243
DB 249 IKSVIY-LKYNQYTKDASTWSQIPEDTASTRSSTVQDLKPFTEYFRIR-----M 302
OY 244 GSKKAGIMSEMSHPTASTPRSERP 268
DB 303 KEDGKGYSDWSEASGTT-YEDRP.326

RESULT 12
ID IL6B_RAT STANDARD: PRT: 918 AA.
AC P40190;
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE: 93052397.
RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RT GENOMICS 14:666-672(1992).

```

CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, IL-6, CMF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 CC EMBL: M93340; NOT_ANNOTATED_CDS.
 CC PIR: A44257; A44257.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAM: PF00041; fn3; 3.
 CC DR HSP: P40189; 1BQU.
 CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC REPEAT.
 CC FT SIGNAL 1 22 POTENTIAL.
 CC FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 619 640 POTENTIAL.
 CC FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 124 221 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 222 323 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 324 422 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 423 516 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 517 612 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 724 754 SER-RICH.
 CC FT DISULFID 134 144 BY SIMILARITY.
 CC FT DISULFID 172 181 BY SIMILARITY.
 CC FT CARBOHYD 43 43 POTENTIAL.
 CC FT CARBOHYD 61 61 POTENTIAL.
 CC FT CARBOHYD 83 83 POTENTIAL.
 CC FT CARBOHYD 131 131 POTENTIAL.
 CC FT CARBOHYD 157 157 POTENTIAL.
 CC FT CARBOHYD 205 205 POTENTIAL.
 CC FT CARBOHYD 226 226 POTENTIAL.
 CC FT CARBOHYD 382 382 POTENTIAL.
 CC FT CARBOHYD 389 389 POTENTIAL.
 CC FT CARBOHYD 477 477 POTENTIAL.
 CC FT CARBOHYD 552 552 POTENTIAL.
 CC SQ SEQUENCE 918 AA; 102450 MW; E6EFD00 CRC32;
 CC -----
 CC Query Match 14.9%; Score 285; DB 1; Length 918;
 CC Best Local Similarity 30.5%; Pred. No. 8.4e-17;
 CC Matches 81; Conservative 46; Mismatches 121; Indels 18; Gaps 9;
 CC -----
 CC 7 LPBELSVLNLASTLALALNLUNGSRSGDNLVCHARDGSLIAGSLYGLPCKPVNIS 66
 CC 74 VPEQVTVIRKTSVFTVFNQVOLTCTNLSFGQIEQNVGIIITLSGPPDIPNTLS 133
 CC 67 CWSKNNKMDLTCRWTPGAGETFLHTNYSLSKYLKMYGOD-NTCEYHYVGHSHIRKDL 125
 CC 134 CYNESKNNMLCOLDPR-ETYLENTNTLSE-WATEKPPDCYTKH-GISSCWMTYTP 187
 CC 126 ALTPPEIWEATNRLGARSASDVLTLIDLVVTTDPPDVHVSFVGLDQLSVRWYSP 185
 CC 188 IYFNIEMVWEAEALNANVSSEPIFDPVCKRSPPHNLSVTNSELSILKLAWYNSG 247

CC 186 ALKDLPAKAYRIYRVEDSDVMKY---DVSNOTSCRLAGKGYIVQVQNCNPGCI 242
 CC 248 L--DSLRLKSDIYRTDASTWIVPLEDYPSPTSFVODLKFEYVERIR-----SI 301
 CC 243 YGSKRAGIMSEWSHPTASTPSESP 268
 CC DB 302 KENGR-GVWSMDSE-EASGTYEDNP 325
 CC -----
 CC RESULT 13
 CC PRLR-ORENI STANDARD; PRT: 630 AA.
 CC ID AC 091513;
 CC DT 01-NOV-1997 (REL. 35, CREATED)
 CC DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 CC DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 CC DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 CC GN PRLR.
 CC OS OROCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
 CC CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 CC CC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
 CC CC LARROIDEI; CICHLIDAE; TILAPIA.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE-KIDNEY;
 CC RX MEDLINE; 95320210.
 CC RA SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;
 CC RT "Expression cloning of a cDNA encoding a fish prolactin receptor.";
 CC RL PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
 CC CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L34783; G903847;
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAM: PF00041; fn3; 2.
 CC DR HSP: P16471; 1BP3.
 CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 CC FT SIGNAL 1 23 BY SIMILARITY.
 CC FT CHAIN 24 630 PROLACTIN RECEPTOR.
 CC FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 235 258 POTENTIAL.
 CC FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 124 123 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 124 228 FIBRONECTIN TYPE-III.
 CC FT DISULFID 37 47 BY SIMILARITY.
 CC FT DISULFID 76 87 BY SIMILARITY.
 CC FT CARBOHYD 92 92 POTENTIAL.
 CC FT CARBOHYD 101 101 POTENTIAL.
 CC SQ SEQUENCE 630 AA; 70810 MW; E9AAE553 CRC32;
 CC -----
 CC Query Match 13.7%; Score 263.5; DB 1; Length 630;
 CC Best Local Similarity 32.7%; Pred. No. 3.7e-15;
 CC Matches 70; Conservative 27; Mismatches 94; Indels 23; Gaps 9;
 CC -----
 CC 59 PERPVNCSKSKNNKMDLTCRWTPGAGETFLHTNYSLSKYLKMYGODNCEYHYTVGPHS 118
 CC DB 29 PKRPTLKSKSPKEFTCKMKRGSOG--LPTTALYTRKESDVVHECPDYHTAGKNS 86
 CC 119 CHPKDLAL-FTPEIWEATNRLGARSASDVLTLIDLVVTTDPPDVHVSFVGLDQ- 177

Db 87 CFEKNNLILVSNITIVAFNMGKTYSPDODIVYIOPHPPELEVT---VKMDQG 143
 QY 177 ---LSVRWSPALKDF---LFOAKYQIRYVED-SYDMKVVDDVSNQTCRLAGLPQT 229
 Db 144 WPEFLKWSM-BPPKADTRSGMITLILYELRVKLEDESESEME-NHAGQCKNFENIFLSLSSG 201
 QY 230 VYFVQVNCNPGIYSGKAKIWSMESHPTAASP 263
 Db 202 TYLIQVCKP-----DHGFWSMSTSYKVP 228

RESULT 14
 GCSR_MOUSE STANDARD: PRT; 837 AA.

AC P40223;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 GN CSF3R OR CSFGR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90235283.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor.";
 RL CELL 61:341-350(1990).
 RN [2]

STRUCTURE BY NMR OF 225-333.
 RX MEDLINE: 97333327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WxWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: M58288; G193455;
 DR PIR: A34898; A34898.
 DR PDB: 1GCF; 22-OCT-97.
 DR PDB: 1GTO; 22-OCT-97.
 DR MGD: M8533; CSFGR.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 KN RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT: 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT CHAIN 26 837
 FT DOMAIN 26 626
 FT TRASMEN 627 650
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.

FT DOMAIN 651 837 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 118 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 122 228 FIBRONECTIN TYPE-III.
 FT DOMAIN 229 333 FIBRONECTIN TYPE-III.
 FT DOMAIN 334 431 FIBRONECTIN TYPE-III.
 FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
 FT DOMAIN 529 624 FIBRONECTIN TYPE-III.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 249 296 BY SIMILARITY.
 FT DISULFID 267 310 BY SIMILARITY.
 FT CARBOHYD 51 51 POTENTIAL.
 FT CARBOHYD 34 94 POTENTIAL.
 FT CARBOHYD 129 129 POTENTIAL.
 FT CARBOHYD 186 186 POTENTIAL.
 FT CARBOHYD 279 279 POTENTIAL.
 FT CARBOHYD 392 392 POTENTIAL.
 FT CARBOHYD 408 408 POTENTIAL.
 FT CARBOHYD 474 474 POTENTIAL.
 FT CARBOHYD 487 487 POTENTIAL.
 FT CARBOHYD 582 582 POTENTIAL.
 FT CARBOHYD 613 613 POTENTIAL.
 SO SEQUENCE 837 AA; 93406 MW; D55F8AD4 CRC32;

Query Match 12.6%; Score 241; DB 1; Length 837;
 Best Local Similarity 28.0%; Pred. No. 4.5e-13;
 Matches 89; Conservative 45; Mismatches 112; Indels 72; Gaps 17;

QY 53 LVGLPPEPVPVISC-WSNMMDLTCRTPGAGHETFLTNYSLK-YKLR--WIGDNT 107
 Db 118 LHAGYPPASPSPNLSCLMHLTNSLYCQWEPGP--ETHLPTSLKFSRRAQCQYGDRI 175
 QY 108 CEYHTVGPSSCHIP-KDIALFTPEIYEATNRBSARSADVLTDLVVTDP----- 163
 Db 176 PCVAKKRRNNKSIPKNNLLIYOYAIWQAEMTASSSPKLCIDPMQVVKLEPMLQA 235
 QY 163 ----PDVHYSRVGLLEDQLSVKWS-PPALKDFLQAKYQIRYVE-DSVDMKVVDDV-S 215
 Db 236 LDIGPDVYSHQPGCL-----WLSWKPKWKPSEVMEQEGELNYPQLKGNMTLVPHLHS 288
 QY 216 NOTSRLAGLAKCTYTFVOVRCNPNPGIYSGKAGIWSWS-----HPT-AASTPSRERG 269
 Db 289 SKDFELGLGMAQAPYTLQMR-----IRSSLGFWSPSPQLQRPYKAPLIRLDI-- 342
 QY 270 PGGACPEPGRSPSS-----GPVRELKQFIGNLKKHAYCNSLSPRLDQNRAMQ 320
 Db 342 ----WCQKQLDPGVSVQVLFKPPPLQDSQIOGYL-----LSWNS 380
 QY 321 KSKHTRNCH--RTGSC 335
 Db 381 PDHOGDHLICNTQLSC 398

RESULT 15
 CNTR_RAT STANDARD: PRT; 372 AA.

AC 008406;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA).
 GN CNTFR.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RP SEQUENCE FROM N.A.
 RP TISSUE-BRAIN:
 RC TISSUE-BRAIN:
 RX MEDLINE: 93152175.
 RA IP N.Y., MCCLELLIN J., BARREZUELA N.X., ALDRICH T.H., PAN L., LI Y.,
 RA WIGGAND S.J., FRIEDMAN B., DAVIS S., YANCOPOULOS G.D.;
 RT "The alpha component of the CNTF receptor is required for signaling and defines potential CNTF targets in the adult and during

RT development.";
 RL NEURON 10:89-102(1993).
 RN [2]
 RP SEQUENCE OF 185-277 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 93211934.
 RA CLATTERBUCK R.E., PRICE D.L., KOLATOS V.E.;
 RT "Ciliary neurotrophic factor prevents retrograde neuronal death in
 the adult central nervous system.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:2222-2226(1993).
 CC -1- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
 RECEPTOR SPECIFICITY.
 CC -1- SUBUNIT: HETERODIMER OF THE ALPHA CHAIN, LIFR AND GPI30.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S54212; G265056; -
 DR EMBL; S57711; G299332; -
 DR PIR; A47387; A47387
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 1.
 DR PFAM; PF00047; 19; 1.
 DR RECEPTOR; GPI-ANCHOR: GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 20 POTENTIAL.
 FT FT 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT FT FT ALPHA.
 FT PROPEP 337 372 REMOVED IN MATURE FORM (POTENTIAL).
 FT DOMAIN 39 96 IG-LIKE DOMAIN.
 FT FT 201 302 FIBRONECTIN TYPE-III.
 FT DISULFID 46 89 POTENTIAL.
 FT FT CARBOHYD 60 60 POTENTIAL.
 FT CARBOHYD 70 70 POTENTIAL.
 FT CARBOHYD 142 142 POTENTIAL.
 FT CARBOHYD 190 190 POTENTIAL.
 FT CARBOHYD 261 261 POTENTIAL.
 FT LIPID 336 336 POTENTIAL.
 FT FT 261 261 GPI-ANCHOR (POTENTIAL).
 FT CONFLICT N -> D (IN REF. 2).
 FT Q SEQUENCE 372 AA; 40822 MW; B63000CA CRC32;

Query Match 11.8%; Score 226.5; DB 1; Length 372;
 Best Local Similarity 28.4%; Pred. No. 2.9e-12;
 Matches 90; Conservative 34; Mismatches 128; Indels 65; Gaps 16;

2 LNGRRRLPELSRYLNSTLALANNGSRGSDNYCARAGSIIAGS-CLYVGIPPE 60
 59 VNGTDLAPDL---LNSQLILNSLELGHs-----GLYACFHRSQSWHLRHQVLLHVGILPFR 110
 61 KPVNISGWSKRM-KDLTCRW-----TFGAGETFLHNTYSLKYKLRMWGDONTGEYH 112
 111 EPV-LSCRSNTYPRKGYGCMHLSAPTYINTFNVTYVLHSGSKM-----VGEKDP 158
 113 TVGPHSGCHTPKDLAFT--PYELWEATNRLGARSADVTLTLDVYTTDPPPDVAVSRV 170
 159 AL-KNNCHI-RYMHLFTSTIKYKYSISVSNALGH-NTAITFDEFITVKDPPEPNVYARPV 215
 171 GGLEDDLSYRWVSPPALXD-FLQAKYQIRYREDSDVKVVDVDSNQSCLAGLPGT 229
 216 PSNPRLEVTWOTPTWPDSPFLKFLRYRPLILDQOHV-ELSNGTAAHTTTDAYACK 274

QY 230 VPEVOYRCNPFGLYSSKKGIMSEMS-----HPTASTPSENP 268
 DB 275 EYIIQVAAT-----DNEIGTWSQSWVAHAATPWTEPRHLTTEAOAPETTTSTSSILAP 328
 QY 269 GREGGACERGERGEPSSG 285
 DB 329 PPTTKICDP--GELSSG 343

Search completed: September 17, 1999, 03:10:14
 Job time: 294 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:09 ; Search time 68.96 Seconds
(without alignments)
312.359 Million cell updates/sec

Title: US-09-037-657-25

Sequence: 1 TLNGRRLLPELRLSVLNASTL.....TRGSCPRADGARREVLPLDKL 350

Scoring table: BLOSUM62

Searched: 201082 segs, 61543640 residues

Database:

SPTREMBL_10:.*
1: sp_archea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_podent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1800	93.8	422	4	075462	075462 homo sapien
2	327	17.0	881	13	057519	057519 xenopus lae
3	325.5	17.0	206	4	016354	016354 homo sapien
4	309.5	16.1	581	6	046561	046561 ovis aries
5	306.5	16.0	296	6	018880	018880 bos taurus
6	270.5	14.1	346	13	093404	093404 oreochromis
7	235.5	12.3	217	6	046386	046386 mustela vis
8	231.5	12.1	198	6	018985	018985 cervus elap
9	225.5	11.8	335	6	P79203	P79203 ovis aries
10	217.5	11.3	372	11	088507	088507 mus musculu
11	207.5	10.8	862	4	099665	099665 mus musculu
12	204	10.6	432	11	064385	064385 mus musculu
13	203	10.6	422	4	016542	016542 mus sapien
14	195	10.2	432	11	P70225	P70225 mus sapien
15	193.5	10.1	874	11	P97378	P97378 mus musculu
16	192.5	10.0	710	13	057520	057520 xenopus lae
17	178	9.3	316	11	035545	035545 rattus norv
18	174	9.1	1165	6	002671	002671 mus scrofa
19	165.5	8.6	440	11	000343	000343 mus musculu
20	163.5	8.5	895	11	062960	062960 rattus norv
21	161	8.4	958	4	092920	092920 homo sapien
22	161	8.4	1165	4	092921	092921 homo sapien
23	161	8.4	958	4	013592	013592 homo sapien
24	161	8.4	906	4	013593	013593 homo sapien
25	161	8.4	896	4	013594	013594 homo sapien
26	161	8.4	896	4	092919	092919 homo sapien
27	159.5	8.3	383	11	088786	088786 mus musculu
28	152.5	7.9	229	6	027950	027950 bos indicus
29	152.5	7.9	229	6	028206	028206 bos taurus

ALIGNMENTS

30	149	7.8	1093	11	070535	070535 rattus norv
31	148.5	7.7	228	11	035228	035228 mus musculu
32	148	7.7	229	4	075269	075269 homo sapien
33	146	7.6	279	11	064236	064236 rattus norv
34	141.5	7.4	86	6	018853	018853 mustela put
35	141.5	7.4	890	11	0921A0	0921A0 cavla porce
36	140	7.3	229	4	014213	014213 homo sapien
37	137.5	7.2	634	6	046600	046600 bos taurus
38	137.5	7.2	269	6	P79195	P79195 macaca mula
39	137	7.1	396	4	014631	014631 homo sapien
40	137	7.1	420	4	014633	014633 homo sapien
41	137	7.1	333	4	015459	015459 homo sapien
42	135	7.0	896	11	064146	064146 rattus norv
43	134.5	7.0	427	4	095646	095646 mus musculu
44	133	6.9	971	11	070458	070458 mus musculu
45	133	6.9	970	11	088821	088821 mus musculu

RESULT 1
ID 075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMBLrel, 08, Created)
DT 01-NOV-1998 (TREMBLrel, 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel, 10, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GETTNER D.,
RA MENON D.L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.;
RT CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-1 Receptor Family. ;
RL J. Immunol. 0:0-0(1998).
DR EMBL; AF059293; AAC2835.1; -
DR PRAM; PF00041; fn3; 2.
KW signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 422 AA; 46301 MW; 8779BC9 CRC32;
POTENTIAL.
CYTOKINE-LIKE FACTOR-1.

Query Match 93.8%; Score 1800; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.6e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TLNGRRLLPELRLSVLNASTLALANLNGSRSGDNLVCHARDGSLAGCLYGLPPE	60
DB	77	TLNGRRLLPELRLSVLNASTLALANLNGSRSGDNLVCHARDGSLAGCLYGLPPE	136
QY	61	KPVNISQSKMMDLCFRTPGAHGEFLHTNSLKYKLRWQDNTCEYHVGSHSC	120
DB	137	KPVNISQSKMMDLCFRTPGAHGEFLHTNSLKYKLRWQDNTCEYHVGSHSC	196
QY	121	IPDLDLFPPEYELWEATNRLGARSVDLTLDLVTYTDPPDVHVSRYGLEDLSVR	180
DB	197	IPDLDLFPPEYELWEATNRLGARSVDLTLDLVTYTDPPDVHVSRYGLEDLSVR	256
QY	181	WSPPLKDELTPQAKQIKRYVEDSDYKRVVDVSNQISCRLAGLPGTVYFVQVNCNF	240
DB	257	WSPPLKDELTPQAKQIKRYVEDSDYKRVVDVSNQISCRLAGLPGTVYFVQVNCNF	316
QY	241	GIYSGKAGIWSHPTAASPRSERPGGACPRGGEPSGGVRRLEKQFGLWK	300
DB	317	GIYSGKAGIWSHPTAASPRSERPGGACPRGGEPSGGVRRLEKQFGLWK	376
QY	301	HAYGSNTLSPRLYDQWRAVAMQSKHTRNO	328

Db 377 HAYCSNLSFRLYDQWRAMQKSHTRNQ 404

RESULT 2
ID 057519 PRELIMINARY; PRT; 881 AA.

AC 057519; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
GN GP130P1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN (1)
RA SEQUENCE FROM N.A.
RA CHEN J., GRACE A., CHIEN K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -
DR PFAM; PF00041; fn3; 4.
SQ SEQUENCE 881 AA; 99003 MM; 647E152E CRC32;

Query Match 17.0%; Score 327; DB 13; Length 881;
Best Local Similarity 30.7%; Pred. No. 4.7e-22;
Matches 91; Conservative 39; Mismatches 118; Indels 48; Gaps 10;

QY 2 LNCRLPPELSRYLNASTALALANINGSRQSGDNLVGHARDGSIAGSCLYGUPPER 61
DB 65 VKGVKPEYQELNNTTSVFENLTLLNSPCTCNVMSGVAANTLYGIFLGLPDK 124
QY 62 PVNISCSNMKDLGCRWTPGANGETFLHTNYSLKXKLM-----YGDNTCEHYT 113
DB 125 PNLITCIYNODNLCTWDPGR--PTNLPTNYLSH--RMAHFGANYCGANNSC----- 176
QY 114 VGHSCHPKDLALFTPYEIVWEATNRLGSARSVDLTLDLVYTTDPDVHSHVGL 173
DB 176 ---THSP--GQFYIDTFOVEATNMLGQKSETLITDPVNRKPNPOLSLISSLEL 230
QY 174 EDGLSRWVSPALKDFLFQAKQIYRYEDSVDMKVV---DVSNGTSCRLAGLRPTV 230
DB 231 PNLKLEMKNPIT--NAENLKYNIRYRPVKTQDMEMVPEEDTASHRDFTLQDLIPNTV 287
QY 231 YFVQVRCNPFGIYSGKAGIWSMSHPITASTPSSRSPRGSGACPRGSPSSCP 286
DB 288 YEVSINC-----IHKDGHGFSWMSLKKQVTP--EAP-----PSRGP 323

RESULT 3
ID 016354 PRELIMINARY; PRT; 206 AA.

AC 016354; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiinae; Homo.
RN (1)
RA SEQUENCE FROM N.A.
RA MEDLINE; 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
cancer cell lines."
RT J. Biol. Chem. 270:13133-13137(1995).
DR EMBL; S78505; AAB34470.1; -
DR PFAM; PF00041; fn3; 2.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23950 MM; D7E57266 CRC32;

Query Match 17.0%; Score 325.5; DB 4; Length 206;
Best Local Similarity 37.6%; Pred. No. 1e-22;
Matches 80; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

QY 57 LPPEKPVNISCSNMKDLGCRWTPGANGETFLHTNYSLKXKLMYGADNTCEHYTVP 116
DB 2 LPPEKREIKCRSPNKEFTGMMRPOTDGG--LPTNYSLYHREGFTLHNECPDITGGP 59
QY 117 HSCHPKDLALFTPYEIVWEATNRLGSARSVDLTLDLVYTTDPDVHSHVGLGD 175
DB 60 NSCHFGKQYTSMKRYIMVYNNATINQSSFSDELVDVYIYQPPPLAV--EVKQPED 118
QY 176 QLSVRV--SPALNDF--LFOAKYQIRYREDSVDMKVVDVDSNOTSCRLAGLRPTV 230
DB 119 RKPYLMIKSPPTLIDLRKGNFTLXLEYIKRKAEME--TFAGQOTEFKILSLHPGK 177
QY 231 YFVQVRCNPFGIYSGKAGIWSMSHPITASTP 263
DB 178 YLVQVRCRP-----DHGYWSAMSPATFIQIP 203

RESULT 4
ID 046561 PRELIMINARY; PRT; 581 AA.

AC 046561; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprine; Ovis.
RN (1)
RA SEQUENCE FROM N.A.
RA MEDLINE; 98001468.
RA BIGNON C., BIVART N., ORMANDY C., SCHULER L.A., KELLY P.A.,
RA DJANE J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
RN (2)
RA SEQUENCE FROM N.A.
RA BIGNON C., DJANE J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041257; AAB96795.1; -
DR PFAM; PF00041; fn3; 2.
KW Signal.
FT SIGNAL 1
FT CHAIN 25
FT CHAIN 581
SQ SEQUENCE 581 AA; 65235 MM; 6792A7C7 CRC32;

Query Match 16.1%; Score 309.5; DB 6; Length 581;
Best Local Similarity 32.2%; Pred. No. 1.2e-20;
Matches 83; Conservative 33; Mismatches 99; Indels 43; Gaps 8;

QY 12 SHVLNSTALALANINGSRQSGDNLVGHARDGSIAGSCLYGUPPEKPVNISCSNM 71
DB 7 SNVLTLILFLFASLNGS-----PPKRLIKCRSG 40
QY 72 MDLTCRWTPGANGETFLHTNYSLKXKLMYGADNTCEHYTVPDHPHSHIPD-LALFTP 130
DB 41 KETFCWMEPGADGG--LPTNLTLYRKGEFTLHNECPDYGKGCNSCYFSKXYSIMWM 98
QY 131 YEIWEATNRLGSARSVDLTLDLVYTTDPDVHSHVGLLEQOLSRWV--SPALK 188
DB 99 YIITVSAINQMSISSDPIYDVYTIIVEPEPVNLT-ELKHPEDRKPYLWKMSPPILT 157
QY 189 DE--LFOAKYQIRYREDSVDMKVVDVDSNOTSCRLAGLRPTVYFVQVRCNPFGIYS 245

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Db 158 DVSQMSIYELRLKREKATDWE-THFAPKRLQKLFNFYGGKYLVOIRCKP----- 211
QY 246 KKAQMSWSPHPTAASP 263
    |||||
Db 211 -DHGWSWSPSPSIQIP 227

RESULT 5
ID 018880 PRELIMINARY; PRT; 296 AA.
AC 018880;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE; 97375450.
RA SCHULER L.A., NAGEL R.J., GAO J., HONSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
    tissues."
RT Endocrinology 138:3187-3194(1997).
DR EMBL; AF027403; AAB83999.1;
DR PFM; PF00041; fn3; 2.
SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 16.0%; Score 306.5; DB 6; Length 296;
Best Local Similarity 31.2%; Pred. No. 9.4e-21;
Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;

QY 12 SRVNASLALALANUNGRSGDNLVCHARDGSIAGSCLVGLPPEKPVNISCSKN 71
    |||||
Db 7 SRVAFILLFLFSVSLNGS-----PPEKRLVKRSRG 40

QY 72 MKDLCTMPGAGHGFPLHTNYSLKYLKMYGODNTCEYHYVPHSCHT-PKDALFTFP 130
    |||||
Db 41 KETLCWEPGADGG--LPTNTYLLYHKKEGTLHCECPYKKGSGPYCSYFSKHTSIMK 98

QY 131 YEIWEATNRLGARSVDLTLDLVTTDPPEDVYVSRVGLDOLSRVW--SPALK 188
    |||||
Db 99 YVITVNAINQNGISSDPLVYVTVIVEEPANLTL-ELKHPEDKRYLWKWSPPTMT 157

QY 189 D-----FLFOAKYQIRYVEDSVDRKVVDDVSNQTSCLAGLPGTYVYVQVRCNPFGLY 243
    |||||
Db 158 DVKSGWFIQ--YEIRLKPKEATDWE-THFTLKQTKLFFNLXPQKYLVOIRCKP---- 211

QY 244 GSKKAGISWSPHPTAASP 263
    |||||
Db 211 --DHGWSWSPSPSIQIP 227

RESULT 6
ID 093404 PRELIMINARY; PRT; 346 AA.
AC 093404;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Oecochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percormorpha;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
RN (1)
RP SEQUENCE FROM N.A.
RA SHIRAIISHI K., MATSUDA M., MORI T., TETSUYA H.;

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RT "Expression of prolactin and cortisol receptor gene in early-life
    stages of tilapia (Oecochromis mossambicus)."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF080247; AAC31825.1;
DR PFM; PF00041; fn3; 2.
FT NON_TER 346
SQ SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match 14.1%; Score 270.5; DB 13; Length 346;
Best Local Similarity 32.7%; Pred. No. 2.5e-17;
Matches 70; Conservative 29; Mismatches 92; Indels 23; Gaps 9;

QY 59 PERPVNISCSKNKDDITCMTGARGETFLHTNYSIKYLRYGODNTCEYHYVPHS 118
    |||||
Db 29 PGKPTLETCSRSPKEFTCWKRGSDGG--LPTTALYKESDSVYHEPDDHTGKNS 86

QY 119 CHLPK-DLALFTYELWEATNRLGARSVDLTLDLVTTDPPEDVYVSRVGLDQ- 177
    |||||
Db 87 CFENKNDTLIWSINTVATNALGRTSPVDIDVYIVKPPPERKLEYT--VAKDQ 143

QY 177 --LSYRWSPPALKDF--LFOAKYQIRYVED-SVDRKVVDDVSNQTSCLAGLPGT 229
    |||||
Db 144 WPLRLYVW-EPHKAQTRSGWITLITELRYKLEDESEWE-NHAAQOKWFNIFLSRSG 201

QY 230 VYFVQVRCNPFGLYSGSKAGISWSPHPTAASP 263
    |||||
Db 202 TYLIQVRCRP-----DHGWSWSPSPSIQIP 228

RESULT 7
ID 046386 PRELIMINARY; PRT; 217 AA.
AC 046386;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
RN PRLR.
OS Muscula vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Placentalia; Mustelidae; Mustela.
RN (1)
RP SEQUENCE FROM N.A.
RA DODDAS D.A., SONG J.-H., HONDE A., MURPHY B.D.;
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039294; AAB88899.1;
DR PFM; PF00041; fn3; 1.
FT NON_TER 217
SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 12.3%; Score 235.5; DB 6; Length 217;
Best Local Similarity 32.3%; Pred. No. 2.4e-14;
Matches 61; Conservative 30; Mismatches 81; Indels 17; Gaps 7;

QY 81 PGHGETFLHTNYSIKYLRYGODNTCEYHYVPHSCHT-PKDALFTYELWEATN 139
    |||||
Db 2 PEGDGG--LPTKTYLTYKKEGTLHCEPDYITSGPNSCYFNKHTSIWYITINNTN 59

QY 140 RUGARSVDLTLDLVTTDPPEDVYVSRVGLDOLSRVWV--PPALKDF--LFOA 194
    |||||
Db 60 EMGSSSDPRVYTLTYVEPPPVNLS-ELKQPEDKTYIMIKWYPTPLDVASGWLTL 118

QY 195 KYQIRYVEDSVDRKVVDDVSNQTSCLAGLPGTYVYVQVRCNPFGLYSGSKAGISW 254
    |||||
Db 119 QYERLKPKEATDWE-THFAGLQTKLFFNLXPQKYLVOIRCKP-----DHGWSW 170

QY 255 SHPTAASP 263
    |||||
Db 171 SPKRSIQIP 179

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RESULT 8
 O18985 PRELIMINARY; PRT: 198 AA.
 AC 018985;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE SOLUBLE PROLACTIN RECEPTOR.
 OS Cerus elaphus nelsoni (American elk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA JABOUR H.N.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; J14753; CAA75048.1;
 DR PFM; PF00041; fn3; 1.
 SQ SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match 12.1%; Score 231.5; DB 6; Length 198;
 Best Local Similarity 33.2%; Pred. No. 5e-14; Indels 15; Gaps 7;
 Matches 61; Conservative 32; Mismatches 76;

OY 44 DCSILAGSCLYGLPPEKPVNISCMKMKDLRCMTPGAHGTFHTNYSIKYLRWYG 103
 DB 18 NASLNGS-----PPGRKRIICRSPGKETFTCMWEPSSDG--LPVITLTIRKEGT 70
 OY 104 QNTEERYHTVGPSCHI-PKDLAETPYEIWEATNRLSGASDVLTDIDVYTTDP 162
 DB 71 LIHECPDYTGPGNTCYFSKHKHSIKYIVYTNALNNGVSSDPLDYVYIYEPEP 130
 OY 163 PNYHNRVGLDGLSVKVS--PPLKPF---LPQAKQIKRVEDSYDMKYVDVDSQC 217
 DB 131 ANLTL-ELKHEDRKRYLWKWPPPLTLTVKSGWFMIOYEIRLKPETALDWE-HDLHP 188
 OY 218 TSCR 221
 DB 189 TSCR 192

RESULT 9
 P79203 PRELIMINARY; PRT: 335 AA.
 AC P79203;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-NOV-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-M2/80; TISSUE-ANTERIOR PITUITARY.
 RL TORPONSE D.T., BROOKS J., INGLETON P., MCNEILLY A.S.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; J10518; CAA71597.1;
 DR PFM; PF00041; fn3; 1.
 FT NON-TER 1
 FT NON-TER 335
 SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 11.8%; Score 225.5; DB 6; Length 335;
 Best Local Similarity 30.8%; Pred. No. 3.5e-13;
 Matches 57; Conservative 29; Mismatches 68; Indels 31; Gaps 7;

OY 85 GEFLLHTNYSIKYLRWYGODNCEYHTVGPSCHIPD-LALFTPYEIWEATNRLGS 143

DB 8 GETLIH-----ECPDYKGCNGSCFCSKYSIMKMYITVSAINOMGI 51
 OY 144 ASDVLTLDIDVYTTDPPDVHVSRLGLEQLSVRW--SPALKDF--LFOAKIOI 198
 DB 52 SSSDPLVDVYIVPEPPVNLTL-ELKHEDRKRYLWKWPPPLTLTVKSGWFSIOYPI 110
 OY 199 RYRVEDSYDMKYVDVSNQTSCLAGLPGYTFYQVRCNPGIYSGKAGIWMESHPT 258
 DB 111 RAKPEKADWE-THRAPKITQAKINPLPGQKYLVOIRKP-----DHGIWSEKSPS 162
 OY 259 AASTP 263
 DB 163 FQIIP 167

RESULT 10
 O88507 PRELIMINARY; PRT: 372 AA.
 AC O88507;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
 GN CNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, SKELETAL MUSCLE;
 RA MAEDA M., YAGUCHI N., HANYU C., NAKATA Y., ONODA N., TULIN E.E.,
 RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
 RL "Mouse homolog of human ciliary neurotrophic factor receptor."
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF068615; AAC25711.1;
 DR PFM; PF00041; fn3; 1.
 DR PFM; PF00047; 1g; 1.
 DR SIGNAL.
 KW SIGNAL.
 FT CHAIN 1 20 POTENTIAL.
 FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT CHAIN 21 336 ALPHA.
 SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 11.3%; Score 217.5; DB 11; Length 372;
 Best Local Similarity 27.6%; Pred. No. 2.2e-12;
 Matches 88; Conservative 35; Mismatches 129; Indels 67; Gaps 16;

OY 2 LNGRLPPELSEVLNASTLALANLNGSRQSDNLCVCHARDGSLAGS-CLYGLPPE 60
 DB 59 VNGTDLADL---LNGSOLILRSLGLHS-----GLYACFHDNSHLRQVILLVGLPFR 110
 OY 61 KPVNISCMKKN-KDLTRW-----TPGAGETFLHTNYSIKYLRWYGODNCEYH 112
 DB 111 EPV-LSCRSNTYPRKGYCSWHLPTPTIYPNPNVTLHSGKIM-----VCEKDP 158
 OY 113 TVGPHSCHLPDLAFT--PYEIWEATNRLSGASDVLTDIDVYTTDPPDVHVSRY 170
 DB 159 AL-KNRCHI-RYMLHFSITIKYKVSISVSNAIGH-WTALTDEFTIVKDPENYVARPV 215
 OY 171 GLEDELTVRWVSPALPD-FLFOAKIOIRYVEDSVDMKYVDVSNQTSCLAGLPGT 229
 DB 216 PSNPRRLVYVQTPSTWDPDEFPLKFLRYRPLLDWMQHV-ELSDGTAHITTAAYACK 274
 OY 220 VYFVQVRCNPGIYSGKAGIWMSEW-----HPTAASPTPSERP 268
 DB 275 EYIIQVAAK-----DNEIGTWSDMVSAHAHPTPEBRHLTTEAQAETTTSTSLAP 328
 OY 269 GPGGACGP-----RGSGS 283
 DB 329 PPTTKICDPGELSGGSGPS 347

RESULT 11
ID 099665 PRELIMINARY: PRT: 862 AA.
AC 099665; 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE IL-12 RECEPTOR BETA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
RA GATELY M.K., GUBER U.,
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64198; AAB36675.1;
DR PFM: PF00041; fn3; 3.
SQ SEQUENCE 862 AA; 97134 MW; 5FEAFBD5 CRC32;

Query Match 10.8%; Score 207.5; DB 4; Length 862;
Best Local Similarity 28.9%; Pred. No. 5.4e-11;
Matches 71; Conservative 32; Mismatches 104; Indels 39; Gaps 10;
OY 38 LVCHARDGSLGSCLYVGLPPEKPVNISCWSKMK-DLTCRTPGAHGETFLHTNYSLK 96
DB 103 LACINSDEIQIGAFIFGVAPQNLSCIOKGEGTACWTERGR-DTHLYETITQ 160
OY 97 Y-----KLRWYGO--NNTCEHYHTVG-----PHSCHIKDALPPEIWEATNRLCS 143
DB 161 LSGPNLWQKOCKIYIC-DYDDEFGINLTSPSPESNFTAK-----VYAVNSLCS 208
OY 144 ARSDVLTLDIDVTTDPDPVHVSRGLEQDLSYRWVSPALKEFLQAKQIYRYE 203
DB 209 SSSLEPTFTFDIVAPLPMDIRIFQKASVSRCLTYW-----HDEGLVTLNRLYRFS 262
OY 204 DSVMKVYDDVSNQTSCLAGLPGTGYFVQVRCNPFQIGSKAGIWSWSHPTAASP 263
DB 263 NSRLMNMVNTAKAKRHDLDLKPTEVEYFQI-SSKLHLX-----KGSWSDMESLRAQTP 317
OY 264 RSERPG 269
DB 318 EEEPTG 323

RESULT 12
ID 064385 PRELIMINARY: PRT: 432 AA.
AC 064385; 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11ALPHA) (IL11RA1).
DE IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
RX MEDLINE: 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKR S., HARRISON-SMITH M.,
RA GILGON N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for
gp130 for high affinity binding and signal transduction.";
RL EXBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C AND C57BL/6; TISSUE-EMBRYO;
RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,

RA GUENET J.L., GOSSLER A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C AND C57BL/6;
RA GOSSLER A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 9712900.
RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
RA GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
mouse genome.";
RL Blochem. J. 320:359-363(1996).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
CC BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
CC SIGNAL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMNOGLOBULIN SUPERFAMILY.
CC CONTAINS ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DR EMBL: X74953; CAA52908.1;
DR EMBL: U14412; AAB33248.1;
DR EMBL: X94162; CAA63873.1;
DR EMBL: X94163; CAA63873.1; JOINED.
DR WGI: W07426; IL11RA1.
DR PFM: PF00041; fn3; 2.
DR PFM: PF00047; lg; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
FT SIGNAL 1 23
FT CHAIN 24 432
FT DOMAIN 24 367
FT TRANSMEM 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHYD 127 127
FT CARBOHYD 194 194
SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

Query Match 10.6%; Score 204; DB 11; Length 432;
Best Local Similarity 25.4%; Pred. No. 4.7e-11;
Matches 71; Conservative 43; Mismatches 109; Indels 56; Gaps 13;

OY 39 VCHARDGSLGSCLYVGLPPEKPVNISCWSKMKDLTCRTPGAHGETFLHTNYSLYK 98
DB 93 VCGITDVGSGKVTIKLFPARP-EVSCQAVDEYENFSCWSPGO--VSGLPTRLYTSYR 149
OY 99 LHWGQDNTCEHYHGPSCHIPED-----LALTPYEIWEATNRLGASRD 147
DB 150 KTLPGASQRESPTGWPCC--PDPLASRCVYHGAETSEIRINTEVNPJG-ASTC 206
OY 148 VLTLDIDVTTDPDPVHVSRGLEQDLSYRWVSPALKEFLQAKQIYRYEYED 204
DB 209 SSSLEPTFTFDIVAPLPMDIRIFQKASVSRCLTYW-----HDEGLVTLNRLYRFS 262
OY 204 DSVMKVYDDVSNQTSCLAGLPGTGYFVQVRCNPFQIGSKAGIWSWSHPTAASP 263
DB 263 NSRLMNMVNTAKAKRHDLDLKPTEVEYFQI-SSKLHLX-----KGSWSDMESLRAQTP 317
OY 264 RSERPG 269
DB 318 EEEPTG 323

RESULT 13
ID 016542 PRELIMINARY: PRT: 422 AA.
AC 016542; 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Created)

Query Match	10.6%;	Score 203;	DB 4;	Length 422;
Best Local Similarity	24.6%;	Pred. No. 5.7e-11;		
Matches 70;	Conservative 42;	Mismatches 106;	Indels 66;	Gaps 13

RESULT 14
P70225
ID P70225 PRELIMINARY; PRT; 432 AA

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RP SEQUENCE FROM N.A. -
RC STRAIN-CD1: TISSUE-TESTIS;
RX MEDLINE; 97129000.
RA BLINKSI P., HALL M.A., NEUHAUS H., GISEL C., HEATH J.K.,
RA GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome.";
RL Biochem. J. 320:359-363(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1: TISSUE-TESTIS;
RX MEDLINE; 96278810.
RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
RT "Structural analysis of the gene encoding the murine interleukin-11
RT receptor alpha-chain and a related locus.";
RL J. Biol. Chem. 271:13754-13761(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1: TISSUE-TESTIS;
RX MEDLINE; 97230451.
RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
RT "Identification of a second murine interleukin-11 receptor
RT alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
RL Genomics 40:387-394(1997).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.
CC CONTAINS ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DR EMBL; X94157; CAA63872.1; -
DR EMBL; X94158; CAA63872.1; JOINED.
DR EMBL; X94159; CAA63872.1; JOINED.
DR EMBL; X94160; CAA63872.1; JOINED.
DR EMBL; X94161; CAA63872.1; JOINED.
DR EMBL; X98519; CAA67144.1; -
DR EMBL; U69491; AAC53114.1; -
DR MGD; MG1:109123; IL11RA2.
DR PFM; PFM0041; fn3; 2.
DR PFM; PFM0047; lg; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
FT SIGNAL 1 23
FT CHAIN 24 432
FT DOMAIN 24 367
FT TRANS 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHYD 127 127
FT CARBOHYD 194 194
FT CONFLICT 200 200
FT CONFLICT 384 384
SQ SEQUENCE 432 AA; 46721 MM; CAFP/DEC CRC32;
Query Match 10.2%; Score 195; DB 11; Length 432;
Best Local Similarity 27.0%; Pred. No. 3.2e-10;
Matches 65; Conservative 38; Mismatches 104; Indels 34; Gaps 11.
QY 39 VCHARDSILAGSCLVGLPPKPYNISCWKNMKDLTCRWGAGHGTFLHTNSLYRK 98
DB 93 VQQTLDGVSGGMVTLKTLFPARP- EVSCQAVDENFSCFWSPGQ--VSGLPTRLYTSYR 149
QY 99 LRWIGQDNTCEHNYGVGHSHCHIPRD-----LALTPYIWEATNRGLSASND 147
DB 150 KTLTGAESQRESPTGTGWPCC--PDDPLEASRCVYGAEFWESEYRINTVEVNSLD-ASTC 206
QY 148 VLTLDIDLVVTTDDPPDVHVSRGVLEQDLSVRWVSPALK---DFLQAKYQIYRYED 204
DB 207 LLDVRLGSLIARPDPPGRLVSVGYPRLRLASMTYPAWSKROPHLL--KFRLOIYRQO 264
QY 205 SVDMKRVVDVSNQ--TSCRLAGLRPGTYFVQVACNPGIYSGKSGIWSMSHPTAST 262

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Db 265 HPAMSTVEPIGLEVITDVAGLP-----HAVVSARDF-----LDAGTMSAMS-PEAMGT 314
QY 263 P 263
Db 315 P 315

RESULT 15

P97378 PRELIMINARY; PRT; 874 AA.
AC P97378;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOD C.Y.,
RA GATELY M.K., GUBLER U.;
DR Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64199; AAB36676.1; .
DR MGD: MGI:1270861; IL12RB2.
DR PFM: PFM0041; fn3; 4.
SQ SEQUENCE 874 AA; 98196 MW; 9890EB47 CRC32;

Query Match 10.18; Score 193.5; DB 11; Length 874;

Best Local Similarity 27.68; Pred. No. 1.1e-09;

Matches 75; Conservative 42; Mismatches 110; Indels 45; Gaps 13;

QY 13 RVLNAST-LALALANLNGSR-QRSGDNLYCHARDGSIAGSCLYGLPPEKPVNISCMK 70
Db 98 QVNLSLGMLTFCKLCKNSQKKPVVPC-----GVEISYGAPEPPONISCVQE 148
QY 71 NMK-DLTCRWTPGAHGETFLHTNLSLKYKLRMYGODN-TCE-EYHTVGPHSC-----H 120
Db 149 GENGTVACSMNSGR--VTYLTNTYTLQS-----GPNNTCKQKCPSDNRQNCNRDLGIN 202
QY 121 IPKDLALFTPEYIWEATNRLGARSQVLLDLDVYTTDPPDVHVSRYGLDQLSVR 180
Db 203 LSPDLA-ESRFIVAVTAINDGNSSLPHTFTFDIYIPLPMDIRINFLNAGSRGTLQ 261
QY 181 WSPPALKDFLFQAKYQIRYRVEDSVDMKYVDVSNQTSRLAGLKPQTYFVQVRCNPF 240
Db 262 W-----EDGGVYVLLNQLRYQPLNSTSMNVNATNAKGYDLRDLRPFTEYEFQI----- 311
QY 241 GIYGSK---KAGIMSEWSHPTASTPSEKRG 269
Db 311 ---SKLHLGSGSMNSNSELRTPTPEEPVPG 339

Search completed: September 16, 1999, 20:40:09
Job time: 5560 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:10 ; Search time 53.94 Seconds
(Without alignments)
34.029 Million cell updates/sec

Title: US-09-037-657-29
Perfect score: 1006
Sequence: 1 PFTLLIGSSIQATCSIHGDI.....SHQSPRLSXKCPHTGCGR 186

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database:

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/PCTUS9.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	133.5	13.3	708	1	US-07-797-556-2	Sequence 2, Appl1
2	133.5	13.3	708	2	US-08-308-881-2	Sequence 2, Appl1
3	133.5	13.3	708	3	PCT-US95-06530-2	Sequence 2, Appl1
4	115	11.4	1001	1	US-07-797-556-6	Sequence 6, Appl1
5	115	11.4	1001	1	US-07-943-843-2	Sequence 6, Appl1
6	115	11.4	1097	1	US-07-943-843-6	Sequence 6, Appl1
7	115	11.4	1001	2	US-08-347-003-2	Sequence 2, Appl1
8	115	11.4	1097	2	US-08-347-003-6	Sequence 6, Appl1
9	112.5	11.2	719	1	US-07-943-843-4	Sequence 4, Appl1
10	112.5	11.2	719	2	US-08-347-003-4	Sequence 4, Appl1
11	110.5	11.0	862	2	US-08-685-118-2	Sequence 2, Appl1
12	110.5	11.0	862	2	US-08-915-495-2	Sequence 2, Appl1
13	100	9.9	836	1	US-07-923-976-4	Sequence 4, Appl1
14	100	9.9	771	1	US-07-923-976-6	Sequence 6, Appl1
15	100	9.9	863	1	US-07-923-976-8	Sequence 8, Appl1
16	98	9.7	572	2	US-08-419-652-5	Sequence 5, Appl1
17	92.5	9.2	979	2	US-08-308-881-6	Sequence 6, Appl1
18	92.5	9.2	979	3	PCT-US95-06530-6	Sequence 6, Appl1
19	91	9.0	880	1	US-08-445-640-10	Sequence 10, Appl1
20	91	9.0	388	1	US-08-445-640-12	Sequence 12, Appl1
21	91	9.0	874	2	US-08-456-647b-6	Sequence 6, Appl1
22	91	9.0	874	2	US-08-237-401a-6	Sequence 6, Appl1
23	90.5	9.0	837	1	US-07-923-976-2	Sequence 2, Appl1
24	87.5	8.7	917	1	US-08-245-295-2	Sequence 2, Appl1
25	87.5	8.7	917	2	US-08-481-130-2	Sequence 2, Appl1
26	87.5	8.7	917	2	US-08-656-984a-2	Sequence 2, Appl1
27	87.5	8.7	917	2	US-08-485-604-2	Sequence 2, Appl1
28	87.5	8.7	917	2	US-08-487-595-2	Sequence 2, Appl1
29	85.5	8.5	864	1	US-08-372-892-2	Sequence 2, Appl1
30	85.5	8.5	864	1	US-08-372-892-4	Sequence 2, Appl1
31	85.5	8.5	884	1	US-08-445-640-34	Sequence 34, Appl1
32	81	8.1	372	1	US-07-865-878a-4	Sequence 4, Appl1
33	81	8.1	372	1	US-07-676-647-2	Sequence 2, Appl1
34	81	8.1	547	1	US-08-473-981a-6	Sequence 6, Appl1
35	81	8.1	372	1	US-08-449-329-2	Sequence 2, Appl1
36	81	8.1	602	2	US-08-419-652-6	Sequence 6, Appl1
37	81	8.1	372	2	US-08-445-073-2	Sequence 2, Appl1
38	81	8.1	372	3	PCT-US91-03896-2	Sequence 3, Appl1
39	80	8.0	547	1	US-08-314-615-1	Sequence 1, Appl1

40	80	8.0	547	1	US-08-314-362-1	Sequence 1, Appl1
41	80	8.0	547	1	US-08-433-010-1	Sequence 1, Appl1
42	80	8.0	547	2	US-08-482-882-1	Sequence 2, Appl1
43	80	8.0	547	2	US-08-483-389-1	Sequence 1, Appl1
44	80	8.0	547	2	US-08-487-113D-1	Sequence 1, Appl1
45	80	8.0	547	2	US-08-473-503-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-797-556-2
Sequence 2, Application US/07797556
Patent No. 5262522

GENERAL INFORMATION:
APPLICANT: Gearling, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia Inhibitory Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match 13.3%; Score 133.5; DB 1; Length 708;
Best Local Similarity 27.3%; Pred. No. 8.4e-07;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

QY	2	PFTLLIGSSIQATCSIHG---DTPGATAGLYTFNGRLPSELSRLNTSLALALANLN	58
DB	36	PVQGLHNFPAVCYKAKCDYPRVANNYVWKTNHTTIREQYTIINRTASSVTFTDIA	95
QY	59	GSROQSDNIVCHARDSSILAGSCLYGLPPEKPFENISCSRNKKDLTCWPTGANGETF	118
DB	96	SIMTQLCNILTFGLBQNYGYGITIISGLPPEKPNLSCLVNGSKKRCMDGR--ETH	153
QY	119	LHNTYSK 126	
DB	154	LEHFTLK 161	

RESULT 2
US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672

GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 13.3%; Score 133.5; DB 2; Length 708;
Best Local Similarity 27.3%; Pred. No. 8.4e-07;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

QY 2 PHLIGSSIQATCSIHG---DTPGATAGELVTFNGRRLPSLSRLNTSTLALANLN 58
DB 36 PVOQLHSNFTAVCYLKEKCMDFHVNANVIWKTNHFTIPKEQYTIINRTASSVFTDIA 95
QY 59 GSROOSGDLVCHARDGSLIAGSCLYGLPEKPPNISCWSNMMDLTCRWTPGAGET 118
DB 96 SNIQDITCIIITFGQLEONVIGITISGLPPEKPNLSCLVNEGKMKCEWDGGR--ETH 153
QY 119 LHTNYSLK 126
DB 154 LETNFTLK 161

RESULT 3
PCT-US95-06530-2
Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 13.3%; Score 133.5; DB 3; Length 708;
Best Local Similarity 27.3%; Pred. No. 8.4e-07;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

QY 2 PHLIGSSIQATCSIHG---DTPGATAGELVTFNGRRLPSLSRLNTSTLALANLN 58
DB 36 PVOQLHSNFTAVCYLKEKCMDFHVNANVIWKTNHFTIPKEQYTIINRTASSVFTDIA 95
QY 59 GSROOSGDLVCHARDGSLIAGSCLYGLPEKPPNISCWSNMMDLTCRWTPGAGET 118
DB 96 SNIQDITCIIITFGQLEONVIGITISGLPPEKPNLSCLVNEGKMKCEWDGGR--ETH 153
QY 119 LHTNYSLK 126
DB 154 LETNFTLK 161

RESULT 4
US-07-797-556-6
Sequence 6, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-6

Query Match 11.4%; Score 115; DB 1; Length 1001;
Best Local Similarity 23.4%; Pred. No. 0.00016;

Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQATCSI-----HGDTPGAAGELVTFNGRRLPSELRLNLTSTL 50
258 DKVILVGSDFTCVSGQEKVLSALIGHTNCPILHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEHDLKELTICSMN 354
111 PG-----AHGETFLHNTYSLKYLRLVRSE 135
355 PGRVTAIVGPRATSYTLVE-SFSGKY-VRLKRAE 386

RESULT 5

US-07-943-843-2

Sequence 2, Application US/07943843

Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Beckmann, M. P.
TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/943,843
FILING DATE: 19920911
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
S-07-943-843-2

Query Match 11.4%; Score 115; DB 1; Length 1001;
Best Local Similarity 23.4%; Pred. No. 0.00016;
Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQATCSI-----HGDTPGAAGELVTFNGRRLPSELRLNLTSTL 50
258 DKVILVGSDFTCVSGQEKVLSALIGHTNCPILHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEHDLKELTICSMN 354
111 PG-----AHGETFLHNTYSLKYLRLVRSE 135
355 PGRVTAIVGPRATSYTLVE-SFSGKY-VRLKRAE 386

RESULT 6

US-07-943-843-6

Sequence 6, Application US/07943843

Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Beckmann, M. P.
TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/943,843
FILING DATE: 19920911
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-943-843-6

Query Match 11.4%; Score 115; DB 1; Length 1097;
Best Local Similarity 23.4%; Pred. No. 0.00016;
Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQATCSI-----HGDTPGAAGELVTFNGRRLPSELRLNLTSTL 50
258 DKVILVGSDFTCVSGQEKVLSALIGHTNCPILHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEHDLKELTICSMN 354
111 PG-----AHGETFLHNTYSLKYLRLVRSE 135

Db 355 PGRVATLVGPRAATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 7

US-08-347-003-2

Sequence 2, Application US/08347003

Patent No. 5785967

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,003

FILING DATE: 29-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,843

FILING DATE: 11-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2606-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1001 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-003-2

Query Match 11.4%; Score 115; DB 2; Length 1001;

Best Local Similarity 23.4%; Pred. No. 0.00016; Mismatches 46; Indels 44; Gaps 7;

Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

Db 1 DPTLLIGSSLAQTCSI-----HGDTPGATAGLYMTFNGRRPLPSELRLINTSTL 50

Db 258 DKVILVSDITFCVSOEKVLSALIGHNCPLIHLDG-----ENV 297

QY 51 ALAANLNGSRQSGDNLVCHARDGSLIAGSLYGLPEKPFNISCWRMKDITCWT 110

Db 298 AIKIRINISVS-ASSGTINVTFTEDN--IFGTVIFAGYPPDPQOLNCETHDKKEICSWN 354

QY 111 PG-----AHGETPLHTNYSLKVKRLVRS 135

Db 355 PGRVATLVGPRAATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 8

US-08-347-003-6

Sequence 6, Application US/08347003

Patent No. 5785967

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,003

FILING DATE: 29-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,843

FILING DATE: 11-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2606-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1097 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-003-6

Query Match 11.4%; Score 115; DB 2; Length 1097;

Best Local Similarity 23.4%; Pred. No. 0.00018; Mismatches 46; Indels 44; Gaps 7;

Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

Db 1 DPTLLIGSSLAQTCSI-----HGDTPGATAGLYMTFNGRRPLPSELRLINTSTL 50

Db 258 DKVILVSDITFCVSOEKVLSALIGHNCPLIHLDG-----ENV 297

QY 51 ALAANLNGSRQSGDNLVCHARDGSLIAGSLYGLPEKPFNISCWRMKDITCWT 110

Db 298 AIKIRINISVS-ASSGTINVTFTEDN--IFGTVIFAGYPPDPQOLNCETHDKKEICSWN 354

QY 111 PG-----AHGETPLHTNYSLKVKRLVRS 135

Db 355 PGRVATLVGPRAATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 9

US-07-943-843-4

Sequence 4, Application US/07943843

Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,843
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathlyn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-567-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear

```

QY      105 LTRKWTPEAHGETFLHTNTSLKRYKLVRSEKHXMKGVHCEPSLMPY-----DQGP- 156
      : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      141 VACTWERER--DEHLYTEYLDQ-----LSGPRNLTWQNOCKDICYDYLDGFINLTPESP 193

```

OY 156 ----GPHSLXDLGSHOSP 171
DB 194 SNTAKVTAVNSLGSSSLP 213

RESULT 12

US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 11.0%; Score 110.5; DB 2; Length 862;
Best Local Similarity 21.5%; Pred. No. 0.00042;
Matches 43; Conservative 36; Mismatches 62; Indels 59; Gaps 10;
OY 4 LILGSSLAQATCSHGDTPGATAGLY-----WTF-----NGRRLPSELRL-L 45
DB 41 ILIGSVNTVCSL-----KPGGCFHYSRRNLLIKKDRIRNFHGHSLNSQVGLPL 94
OY 46 NSTLALALANLNGSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCSRMK-D 104
DB 95 GTLFLVCKLACINSDEIQ-----ICGAFIVGVAPEEPONLSICQGEQGT 140
OY 105 LTRKWPFGAGETFLHTNLSLTKRLVNSEKHXMGVPCPESLMPY-----PQGP- 156
DB 141 VACTWRGR--DTHLYTEYLQ-----LSGPKMLTWQCKCKDYCYLDGFINLTPESPE 193
OY 156 ----GPHSLXDLGSHOSP 171
DB 194 SNTAKVTAVNSLGSSSLP 213

RESULT 13

US-07-923-976-4

Sequence 4, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Helwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1508
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-4

Query Match 9.9%; Score 100; DB 1; Length 836;
Best Local Similarity 26.7%; Pred. No. 0.0061;
Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;
OY 2 PLLIGSSLAQATCSHGDTPGATAE-GLYWTNGRRLPSELRLN--TSTLALANLN 58
DB 34 PTVHGDPTTASCIIKONSHLDPEQILMRGAELQPGRGORLSDGOESITLPHLN 93
OY 59 GSRQSGDNLVCHARDG---TLASCLYVGLPPEKPFNISCSRMKMDICRWTPGA 114
DB 94 HTQA---FLSCCLMGNLSLQILDVEYLRAGTPPAIPHLSCIMLTSSLCQWEPGP- 149
OY 115 GETFLHTNYSLK-YKLR--LVKSEKHXMGVP-----HC---EPSLMPYQGPPLHSDX 162
DB 149 -ETHLPSTFLTSFSGRCQSGSILDCVFKDQSHCCIRKHLILY-QNMGITWQAE 206
OY 163 DLGSHOSPRL 173
DB 207 NALGTSMSPOL 217

RESULT 14

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:16 ; Search time 64.1 Seconds

(without alignments)
68.730 Million cell updates/sec

Title: US-09-037-657-29

Perfect score: 1006

Sequence: 1 DPTLLIGSSIQATCSIHGDR.....SHQSPRLSKIXCPHTGCGR 186

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	984	97.8	186	1	W55016	Amino acid sequenc
2	699	69.5	413	1	W55011	Novel haemopoietin
3	699	69.5	425	1	W55012	Novel haemopoietin
4	695	69.1	425	1	W59804	Nucleotide sequenc
5	694	69.0	385	1	W70841	Human Zcyto5 vari
6	694	69.0	425	1	W70862	Rat Zcyto5 protel
7	693	68.9	278	1	W55014	Protein sequence o
8	658	65.4	408	1	W59805	Amino acid sequenc
9	658	65.4	389	1	W70849	Human Zcyto5 vari
10	658	65.4	389	1	W70849	Human Zcyto5 vari
11	658	65.4	389	1	W70850	Human Zcyto5 vari
12	658	65.4	389	1	W70851	Human Zcyto5 vari
13	658	65.4	389	1	W70852	Human Zcyto5 vari
14	658	65.4	389	1	W70853	Human Zcyto5 vari
15	658	65.4	392	1	W70840	Human Zcyto5 vari
16	658	65.4	303	1	W70843	Human Zcyto5 vari
17	658	65.4	389	1	W70844	Human Zcyto5 vari
18	658	65.4	303	1	W70845	Human Zcyto5 vari
19	658	65.4	422	1	W70860	Human Zcyto5 vari
20	658	65.4	435	1	W70861	Human Zcyto5 vari
21	655.5	65.2	389	1	W70847	Human Zcyto5 vari
22	655	65.1	389	1	W70846	Human Zcyto5 vari
23	651	64.7	388	1	W70839	Human Zcyto5 vari
24	651	64.7	385	1	W70842	Human Zcyto5 vari
25	509	50.6	350	1	W55015	Amino acid sequenc
26	144	14.3	937	1	R26334	gpi30. New mouse g
27	133.5	13.3	918	1	R10545	Recombinant human
28	133.5	13.3	708	1	R37804	Human gpi30 N-term
29	133.5	13.3	918	1	R46233	Human soluble glyco
30	133.5	13.3	918	1	R94576	Human gpi30 splice
31	133.5	13.3	918	1	R94576	Human gpi30 splice
32	133.5	13.3	708	1	R85911	Human gpi30 protei
33	133.5	13.3	329	1	W17859	Human gpi30 N-term
34	133.5	13.3	918	1	W17859	Rheumatoid arthrit
35	133.5	13.3	918	1	W17859	Human gpi30-C-gamm
36	133.5	13.3	859	1	W70796	Human gpi30-delta-
37	115	11.4	1001	1	R37806	Human LIF-R N-term
38	115	11.4	1001	1	R49506	Human LIF-R N-term
39	115	11.4	1097	1	R49508	Human LIF-R N-term
40	115	11.4	1001	1	R45774	Human LIF-R N-term
41	115	11.4	1097	1	R45776	Human LIF-R N-term
42	115	11.4	1001	1	R74095	Human leukaemia in
43	115	11.4	1097	1	R74097	Human leukaemia in

ALIGNMENTS

ALIGNMENTS						LIF-R-GBP 130 fused IgG1 Fc region and
RESULT	1					
ID	W55016	standard; Protein; 186 AA.				
AC	W55016;					
DT	29-SEP-1998	(first entry)				
DE	Amino acid sequence of Murine NR6					
KM	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;					
KW	cell survival; therapeutic; neuronal proliferation; drug screening;					
OS	Mus sp.					
FM	Key	Location/Qualifiers				
FT	misc_difference 136	/note= "Stop codon"				
FT	misc_difference 139	/note= "Stop codon"				
FT	misc_difference 162	/note= "Stop codon"				
FT	misc_difference 177	/note= "Stop codon"				
PN	W09811225-A2.					
PD	19-MAR-1998.					
PF	11-SEP-1997; G02479.					
PR	11-SEP-1996; AD-002246.					
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.					
PI	(DZIE/) DZIELEWSKA H E.					
PI	Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,					
PI	Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,					
PI	Zhang J;					
DR	WPI: 98-260970/23.					
DR	N-PSDB: V27145.					
PT	New isolated haemopoietin receptor - used for developing products					
PT	for modulating proliferation, differentiation and survival of cells,					
PT	e.g. neuronal cells					
PS	Claim 19; Page 114-115, 182pp; English.					
CC	The NR6 protein is a novel Haemopoietin receptor (HR). Interaction					
CC	between the novel HR and a ligand facilitates proliferation,					
CC	differentiation and survival of a wide variety of cells. The HR and its					
CC	derivatives can be used for modulating the activity of the receptors e.g.					
CC	to regulate development, maintenance or regeneration in an array of					
CC	different cells and tissues in vitro and in vivo. They can be present in					
CC	therapeutics used for modulating neuronal proliferation, differentiation					
CC	and survival. The products can also be used for detection and diagnosis,					
CC	e.g. for cancers or predisposition to cancers, or for drug screening.					
SO	Sequence 186 AA;					
Query Match						
Best Local Similarity		97.8%; Score 984; DB 1; Length 186;				
Matches 184; Conservative		0; Mismatches 2; Indels 0; Gaps 0;				
QY	1	DPTLLIGSSLOATCSIRHDTPEARTAEGLYTFNGRRRLPSELRLNTSTLALAINLNGS	60			
DB	1	DPTLLIGSSLOATCSIRHDTPEARTAEGLYTFNGRRRLPSELRLNTSTLALAINLNGS	60			
QY	61	ROSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSSRMNKDLTCRMTPGAAGETFLH	120			
DB	61	ROSGDNLYCHARDGSLIAGSCLVGLPPEKPFNISCSSRMNKDLTCRMTPGAAGETFLH	120			
QY	121	TNYSLKATKLVLNSEQHXKXGVPCEPSLMDYPOGPGPLSLXDLGSGHSPRLSKIXCPH	180			
DB	121	TNYSLKATKLVLNSEQHXKXGVPCEPSLMDYPOGPGPLSLXDLGSGHSPRLSKIXCPH	180			
QY	181	TGCGGR 186				
DB	181	TGCGGR 186				

RESULT 2

ID W55011 standard; Protein: 413 AA.

AC W55011;

DT 29-SEP-1998 (first entry)

DE Novel haemopoietin receptor NR6.1 protein.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;

KW Mouse.

OS Mus sp.

PN W09811225-A2.

PD 19-MAR-1998.

PF 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRAD-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T, Zhang J.

PI WPI: 98-260970/23.

DR N-PSDB: V27140.

PT New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.

PS Claim 14; Page 77-81; 182pp; English.

CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.

CC Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and its derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

CC Sequence 413 AA;

Query Match 69.5%; Score 699; DB 1; Length 413;

Best Local Similarity 90.5%; Pred. No. 9.7e-67;

Matches 134; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 60

DB 50 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 109

QY 61 ROOSGDNLVCHARDGSILAGSLVYGLPPEKPFNISCWRNKKDLTCRTPAHGETFLH 120

DB 110 ROOSGDNLVCHARDGSILAGSLVYGLPPEKPFNISCWRNKKDLTCRTPAHGETFLH 169

QY 121 TNYSLKYRL-----VREXMKGVPH 143

DB 170 TNYSLKYRLMYGDNTECEHYTVG-PH 196

RESULT 3

ID W55012 standard; Protein: 425 AA.

AC W55012;

DT 29-SEP-1998 (first entry)

DE Novel haemopoietin receptor NR6.2 protein.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;

KW Mouse.

OS Mus sp.

PN W09811225-A2.

PD 19-MAR-1998.

PF 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRAD-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,

PI Zhang J.

DR WPI: 98-260970/23.

DR N-PSDB: V27141.

PT New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.

PS Claim 15; Page 84-87; 182pp; English.

CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.

CC Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and its derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

CC Sequence 425 AA;

Query Match 69.5%; Score 699; DB 1; Length 425;

Best Local Similarity 90.5%; Pred. No. 1e-66;

Matches 134; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 60

DB 50 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 109

QY 61 ROOSGDNLVCHARDGSILAGSLVYGLPPEKPFNISCWRNKKDLTCRTPAHGETFLH 120

DB 110 ROOSGDNLVCHARDGSILAGSLVYGLPPEKPFNISCWRNKKDLTCRTPAHGETFLH 169

QY 121 TNYSLKYRL-----VREXMKGVPH 143

DB 170 TNYSLKYRLMYGDNTECEHYTVG-PH 196

RESULT 4

ID W59804 standard; Protein: 425 AA.

AC W59804;

DT 26-OCT-1998 (first entry)

DE Nucleotide sequence of the murine U4 protein.

KW Murine; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy.

OS Mus sp.

PN W09831811-A1.

PD 23-JUL-1998.

PF 15-JAN-1998; U00334.

PR 16-JAN-1997; US-784863.

PA (GENY) GENETICS INST INC.

PI Collins M, Donaldson DD, Neben T, Whitters M;

DR WPI: 98-41409/35.

DR N-PSDB: V41688.

PT New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto-immune disease

PS Claim 9; Pages 26-27; 38pp; English.

CC This is the amino acid sequence of the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

CC Sequence 425 AA;

Query Match 69.1%; Score 695; DB 1; Length 425;

Best Local Similarity 89.9%; Pred. No. 2,7e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 109
QY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 110 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 169
QY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 170 TNYSLKYKRLWYGQDNTCEYHTVG-PH 196

RESULT 5

W70841
ID W70841 standard; Protein: 385 AA.
AC W70841;
DT 17-MAR-1999 (first entry)
DE Human Zcytor5 variant.
KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
OS Homo sapiens.
PN MO9849307-81.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI; 99-034662/03.
PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 83-84; 55pp; English.
CC The present sequence represents a Zcytor5 variant protein. Zcytor5
CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
SQ Sequence 385 AA;

Query Match 69.0%; Score 694; DB 1; Length 385;
Best Local Similarity 89.9%; Pred. No. 3e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 10 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 69
QY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 70 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 129
QY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 130 TNYSLKYKRLWYGQDNTCEYHTVG-PH 156

RESULT 6

W70862
ID W70862 standard; Protein: 425 AA.
AC W70862;
DT 17-MAR-1999 (first entry)
DE Rat Zcytor5 protein.
KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand.
OS Rattus sp.
PN MO9849307-81.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI; 99-034662/03.
PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 75-76; 55pp; English.
CC The present sequence represents a protein designated Zcytor5, which is
CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
SQ Sequence 425 AA;

Query Match 69.0%; Score 694; DB 1; Length 425;
Best Local Similarity 89.9%; Pred. No. 3.5e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSHGTPGATAGLTWTFNGRRLPSELRLNTSTLALANLNGS 109
QY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 110 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 169
QY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 170 TNYSLKYKRLWYGQDNTCEYHTVG-PH 196

RESULT 7
W55014
ID W55014 standard; Protein: 278 AA.
AC W55014;
DT 02-OCT-1998 (first entry)
DE Protein sequence of products generated by 5N race of brain cDNA.
KW Haemopoietic receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN MO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIEV) DZIELEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,

Query Match 68.9%; Score 693; DB 1; Length 278;
 Best Local Similarity 90.5%; Pred. No. 2.5e-66;
 Matches 133; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR N-PDB: V27143.
 PT New isolated haemopoietin receptor - used for developing products
 for modulating proliferation, differentiation and survival of cells,
 e.g. neuronal cells
 PS Claim 17; Page 93-95; 182pp; English.
 CC The protein sequence was generated by a 5N RACE of brain cDNA using
 NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 differentiation and survival of a wide variety of cells. The HR and its
 derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 278 AA;

Query Match 68.9%; Score 693; DB 1; Length 278;
 Best Local Similarity 90.5%; Pred. No. 2.5e-66;
 Matches 133; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

OY 2 PTLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGSR 61
 DB 1 PTLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGSR 60
 OY 62 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 121
 DB 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 120
 OY 122 NTSKYKRL-----VRSEKHXKGVPH 143
 DB 121 NTSKYKRLMYGQDNCEHYHTVG-PH 146

RESULT 8
 W59805
 ID W59805 standard; Protein; 408 AA.
 AC W59805;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of the human U4 protein.
 KW Human U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 OS Homo sapiens.
 PN M09831811-A1.
 PF 23-JUL-1998.
 PF 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR WPI: 98-414109/35.
 DR N-PDB: V41689.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and autoimmune disease
 PS Claim 9; Pages 29-30; 38pp; English.
 CC This is the amino acid sequence of the human U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 408 AA;

Query Match 65.4%; Score 658; DB 1; Length 408;
 Best Local Similarity 84.5%; Pred. No. 2.3e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 33 DPTLLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGS 92
 OY 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 120
 DB 93 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 152
 OY 121 NTSKYKRL-----VRSEKHXKGVPH 143
 DB 153 NTSKYKRLMYGQDNCEHYHTVG-PH 179

RESULT 9
 W70848
 ID W70848 standard; Protein; 389 AA.
 AC W70848;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN M09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams KL, Foster DC, Gilbert T, Jeinberg AC, Leher JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 92-93; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and the
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 10 DPTLLIGSSLOATCSIHGDPGATAGLYWTFNGRRLPSELRLNTSTLALANLNGS 69
 OY 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 120
 DB 70 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPNISCSNMKDLTCRMTPGAHGETFLH 129
 OY 121 NTSKYKRL-----VRSEKHXKGVPH 143
 DB 130 NTSKYKRLMYGQDNCEHYHTVG-PH 156

RESULT 10
 ID W70849 standard; Protein; 389 AA.
 AC W70849;
 DT 17-MAR-1999 (first entry)
 DE Human zcytoxin-like receptor.
 KW zcytoxin; cytoxin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PI WPI: 99-034662/03.
 PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
 PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 94-95; 55pp; English.
 CC The present sequence represents a zcytoxin variant protein. zcytoxin
 is a cytoxin-like receptor. Soluble zcytoxin may be administered to
 down-regulate the effects of a growth and/or maintenance factor in
 thyroid, heart, and skeletal muscle for example to lessen the effect
 of cardiostrophin-1 on cardiac pathologies, so preventing heart
 enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
 blood, and to discover other possible zcytoxin ligands. A probe
 comprising zcytoxin DNA or RNA can be used to determine the presence
 and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
 anti-idiotypic antibody could be used to purify zcytoxin and the
 therapeutically to modify zcytoxin ligand effects.
 SO Sequence 389 AA.

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLGSSIAQACSHGDPGATAGELVTFNGRRLPSELSTLNTSTLALANLNGS 60
 DE Human zcytoxin variant.
 DB 10 DPTLLGSSIAQACSHGDPGATAGELVTFNGRRLPSELSTLNTSTLALANLNGS 69
 QY 61 ROOSGNLVCHARDGSLGSCLYVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 120
 DE Human zcytoxin variant.
 DB 70 ROOSGNLVCHARDGSLGSCLYVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 129
 QY 121 TNSLTKYKRL-----VRSEKHXKGVPH 143
 DE Human zcytoxin variant.
 DB 130 TNSLTKYKRLRWGQDWTCEHYHTVG-PH 156
 RESULT 11
 ID W70850 standard; Protein; 389 AA.
 AC W70850;
 DT 17-MAR-1999 (first entry)
 DE Human zcytoxin-like receptor.
 KW zcytoxin; cytoxin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045030.
 PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PI WPI: 99-034662/03.
 PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
 PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a zcytoxin variant protein. zcytoxin
 is a cytoxin-like receptor. Soluble zcytoxin may be administered to
 down-regulate the effects of a growth and/or maintenance factor in
 thyroid, heart, and skeletal muscle for example to lessen the effect
 of cardiostrophin-1 on cardiac pathologies, so preventing heart
 enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
 blood, and to discover other possible zcytoxin ligands. A probe
 comprising zcytoxin DNA or RNA can be used to determine the presence
 and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
 anti-idiotypic antibody could be used to purify zcytoxin and
 therapeutically to modify zcytoxin ligand effects.
 SO Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLGSSIAQACSHGDPGATAGELVTFNGRRLPSELSTLNTSTLALANLNGS 60
 DE Human zcytoxin variant.
 DB 10 DPTLLGSSIAQACSHGDPGATAGELVTFNGRRLPSELSTLNTSTLALANLNGS 69
 QY 61 ROOSGNLVCHARDGSLGSCLYVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 120
 DE Human zcytoxin variant.
 DB 70 ROOSGNLVCHARDGSLGSCLYVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 129
 QY 121 TNSLTKYKRL-----VRSEKHXKGVPH 143
 DE Human zcytoxin variant.
 DB 130 TNSLTKYKRLRWGQDWTCEHYHTVG-PH 156

RESULT 12

ID W70851 standard; Protein; 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)
 DE Human zcytoxin variant.
 KW zcytoxin; cytoxin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PI WPI: 99-034662/03.
 PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
 PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a zcytoxin variant protein. zcytoxin
 is a cytoxin-like receptor. Soluble zcytoxin may be administered to
 down-regulate the effects of a growth and/or maintenance factor in
 thyroid, heart, and skeletal muscle for example to lessen the effect
 of cardiostrophin-1 on cardiac pathologies, so preventing heart
 enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
 blood, and to discover other possible zcytoxin ligands. A probe
 comprising zcytoxin DNA or RNA can be used to determine the presence

CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGDTPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 10 DPTLLIGSSLLATCSVHGDPGATAGLWTLNGRRLPELSRVNASTLALANLNGS 69
 QY 61 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 129
 QY 121 TNSLKYKRLRL-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 13

W70852
 ID W70852 standard; Protein; 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE,
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
 PT down-regulating zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGDTPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 10 DPTLLIGSSLLATCSVHGDPGATAGLWTLNGRRLPELSRVNASTLALANLNGS 69
 QY 61 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 129

QY 121 TNSLKYKRLRL-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 14

W70853
 ID W70853 standard; Protein; 389 AA.
 AC W70853;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE,
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
 PT down-regulating zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 99-100; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGDTPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 10 DPTLLIGSSLLATCSVHGDPGATAGLWTLNGRRLPELSRVNASTLALANLNGS 69
 QY 61 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLVCHARDGSIILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGAHGETFLH 129
 QY 121 TNSLKYKRLRL-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 15

W70840
 ID W70840 standard; Protein; 392 AA.
 AC W70840;
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.

PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR MPI: 99-034662/03
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-Idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 392 AA;

Query Match 65.4%; Score 658; DB 1; Length 392;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGDPGATAGLYTFNGRRPSELRLNTSTALALANLNGS 60
 DB 13 DPTLLIGSSSLATCSYHGDPPGATAGSLYTLNGRRLPPELSRYLNASTALALANLNGS 72
 QY 61 RQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMTPGAHEFELH 120
 DB 73 RQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMTPGAHEFELH 132
 QY 121 TNYSLKYLRL-----VRSEKHXKGVPH 143
 DB 133 TNYSLKYLRLRWYGODNTCEYHTVG-PH 159

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:10 : Search time 49.27 Seconds
(without alignments)
151.252 Million cell updates/sec

Title: US-09-037-657-29
Perfect score: 1006

Sequence: 1 DPTLLIGSSLSQATCSIRHGT.....SHQSPRLSKIXCHTGCPCR 186

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database :
1: PIR_60:*
2: PIR_7:*
3: PIR_3:*
4: PIR_4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	144	14.3	917	2	I49699	glycoprotein 130 -
2	133.5	13.3	918	2	A36337	membrane glycoprot
3	130	12.9	918	2	A44257	interleukin-6 sign
4	115	11.4	1097	2	S17308	leukemia inhibitor
5	112.5	11.2	1092	2	JX0312	differentiation-st
6	112.5	11.2	719	2	JC2181	differentiation-st
7	107.5	10.7	422	2	I37891	interleukin-11 rec
8	101.5	10.1	622	2	A40144	prolactin receptor
9	100	9.9	783	2	JH0329	granulocyte colony
10	100	9.9	771	2	B38252	granulocyte colony
11	100	9.9	863	2	C38252	granulocyte colony
12	98	9.7	581	2	I45971	prolactin receptor
13	95	9.4	206	2	A57018	prolactin receptor
14	95	9.4	616	2	A30304	prolactin receptor
15	95	9.4	97	2	I57699	pseudo-prolactin r
16	93.5	9.3	432	2	I48343	interleukin-11 rec
17	93	9.2	460	2	JL0145	interleukin-6 rece
18	93	9.2	440	2	JL0144	interleukin-6 rece
19	91.5	9.1	856	2	I58411	protein-tyrosine k
20	91	9.0	880	2	B53743	protein-tyrosine k
21	91	9.0	876	2	I49152	protein-tyrosine k
22	90.5	9.0	837	2	A34898	granulocyte colony
23	89	8.8	462	1	A37986	interleukin-6 rece
24	89	8.8	830	2	I50455	prolactin receptor
25	88	8.7	880	2	JC4166	prolactin receptor
26	88	8.7	303	2	I77524	protein-tyrosine k
27	88	8.7	292	2	I77525	prolactin receptor
28	87	8.6	608	2	I53269	prolactin receptor
29	87	8.6	831	2	J01655	prolactin receptor
30	85.5	8.5	894	1	A41527	protein-tyrosine k
31	85.5	8.5	610	2	A34631	lactogen receptor
32	85.5	8.5	150	2	B34631	lactogen receptor
33	85.5	8.5	610	2	A34631	lactogen receptor
34	85.5	8.5	412	2	A41070	prolactin receptor
35	85.5	8.5	310	2	A29884	prolactin receptor
36	82.5	8.2	754	2	S35503	finger protein neu
37	81	8.1	372	1	UHHUCN	cellular neurotroph
38	81	8.1	547	1	S28904	intercellular adhe
39	81	8.1	372	2	I58141	cellular neurotroph

40	80	8.0	468	1	A41242	interleukin-6 rece
41	79.5	7.9	834	2	S66498	M-sema F protein p
42	79.5	7.9	894	2	JC4797	leptin receptor pr
43	79.5	7.9	1162	2	PC4184	leptin receptor, O
44	79.5	7.9	805	3	JC4897	leptin receptor, O
45	79	7.9	630	2	I51086	prolactin receptor

ALIGNMENTS

RESULT 1
I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text_change 07-Feb-1997
C/Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A>Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
A/Reference number: I48370; MVID:92291532
A/Accession: I49699
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:9193591; PID:9193592
A/Accession: I48370
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: EMBL:X62646; NID:9840816; PID:9840817
C/Genetics:
A:Gene: gp130
C/Keywords: glycoprotein

Query Match 14.3%; Score 144; DB 2; Length 917;
Best local similarity 26.5%; Pred. No. 3e-06;
Matches 39; Conservative 26; Mismatches 70; Indels 12; Gaps 3;

QY 2 PTLIGSSLSQATCSIRHGT---DTGATREGIYTFNGRRLESESLRLNTSTLALANLN 58
DB 36 PVARQSGNFTALCVLKEACIQHYTVNASTYVWNTNAAVREQVYINRTSTVTEDVV 95
QY 59 GSRQSGDNLVCHARDGSIAGSLYGLPPEKPFNISCWRMKNDTCWTEGANGETP 118
DB 96 LPVQGLCNLTLSRGQIEQNYGYTLMASGFPDPKPTNITLCIVNEGKNLACWDGR--ETI 153
QY 119 LHTNYSIKYRLRLVRSEKXMXGVPHCE 145
DB 154 LEMNYTLK-----SEWATEKFPDQ 173

RESULT 2
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1991 #sequence, revision 12-Apr-1991 #text_change 24-Sep-1998
C/Accession: A36337
R:Hibi, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A/Reference number: A36337; MVID:91084844
A/Accession: A36337
A>Status: preliminary
A/Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:9186353; PID:9186354
C/Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A/Map position: 5q11-5q11
C/Keywords: glycoprotein; membrane protein

1990

;/Cross-references: GB:D17444; NID:g441493; PID:d1004778; PID:g441494

;/Cross-references: GB:D17444; NID:g441493; PID:d1004778; PID:g441494

C:Keywords: receptor

Query Match 11.2%; Score 112.5; DB 2; Length 719;

Best Local Similarity 25.4%; Pred. No. 0.0028;

Matches 29; Conservative 27; Mismatches 41; Indels 17; Gaps 5;

DB 1 DPTLLIGSLQATCSHGDTPGATAEGLYWTFNGRRRLPSELRLINT--STLALALANLN 58

DB 253 DKVYLAASNNITICM-----SPTKVLSC-----QIGNTLRPLHLHYGTVVAHLINIP 300

DB 59 GSRQSGDNLYCHARDGSIAGSCLVGLPPEKFPNISCWSRNMKDLTCRWTPG 112

DB 301 VS-ENSGTNIIFITDD--VYGVTFAGYPPDPVQKISCETHDIKEITCSWNP 351

RESULT 7

Interleukin-11 receptor alpha chain - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Dec-1998

C:Accession: I37891; G01970; G01971

A:Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cy

A:Reference number: I37891; PMID:95399754

A:Accession: I37891

A:Molecule type: mRNA

A:Residues: 1-422 <RES>

A:Cross-references: EMBL:238102; NID:9995653; PID:9995654

A:Reference number: G08959

A:Accession: G01970

A:Molecule type: DNA

A:Residues: 1-422 <VAN>

A:Cross-references: EMBL:032323; NID:9975334; PID:9975335

A:Reference number: G08961

A:Accession: G01971

A:Molecule type: mRNA

A:Residues: 1-422 <VAZ>

A:Cross-references: EMBL:032324; NID:9975336; PID:9975337

A:Reference number: G08961

A:Accession: G01971

A:Molecule type: mRNA

A:Residues: 1-422 <VAZ>

A:Cross-references: EMBL:032324; NID:9975336; PID:9975337

A:Reference number: G08961

A:Accession: G01971

A:Molecule type: mRNA

A:Residues: 1-422 <VAZ>

A:Cross-references: EMBL:032324; NID:9975336; PID:9975337

A:Reference number: G08961

A:Accession: G01971

A:Molecule type: mRNA

A:Residues: 1-422 <VAZ>

A:Cross-references: EMBL:032324; NID:9975336; PID:9975337

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C:Accession: A40144

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A:Reference number: A40144; PMID:90114212

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Reference number: G08961

A:Accession: G01970

RESULT 10

B38252
 C:Species: Homo sapiens (man)
 C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 31-Oct-1997
 C/Accession: B38252
 R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
 A>Title: Three different mRNAs encoding human granulocyte colony-stimulating factor receptor
 A/Reference number: A38252; M0ID:91062348
 A/Accession: B38252
 A>Status: preliminary
 A:Molecule type: mRNA
 A/Residues: 1-771 <PUK>
 A/Cross-references: GB:M59819; GB:M38026; NID:9485363; PID:9485364

Query Match 9.9%; Score 100; DB 2; Length 771;
 Best Local Similarity 26.7%; Pred. No. 0.05;
 Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;

QY 2 PTLIGSSLOATCSIHSDTPGATAE-GLYTFNGRRLPSLSRLN--TSTLALANLN 58
 DB 34 PIVHLDGPITASCIIKONCSHLDPEPQILMRGAEIQPGRGQRRLSDQTESITIPHLN 93
 QY 59 GSRQSGDNLVCHARDG---ILAGSCLYVGLPEPEFNFISC-WSRNMKDLTCRWTPGAR 114
 DB 94 HTQ-----FLSCCLMNGNSLIQIDQVELRAGYPPALPHNLSCIMNLTSSLIQWEPGP- 149
 QY 115 GETFLHTNYSK-YKLR---LVRSXHKMGVP-----HC---EPSLMPYQGGPPLSLX 162
 DB 149 -ETHLPTSTLSEKSRGNCQTGDSILDCVPKDGSHCCIPKHHLLY-QNNGIWOAE 206
 QY 163 DLGSGHSPRL 173
 DB 207 NALGTSMSPOL 217

RESULT 11

C38252
 N:Contains: granulocyte colony-stimulating factor precursor, long form - human
 C/Species: Homo sapiens (man)
 C/Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 17-Mar-1999
 C/Accession: C38252; A38252; JH0330; A46486; S68332; S21607
 R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
 A>Title: Three different mRNAs encoding human granulocyte colony-stimulating factor receptor
 A/Reference number: A38252; M0ID:91062348
 A/Accession: C38252
 A>Status: preliminary
 A:Molecule type: mRNA
 A/Residues: 1-863 <PUK>
 A/Cross-references: GB:M59820; GB:M38027; NID:9183046; PID:9183049
 A/Note: clones PHG11 and PHG5
 A/Accession: A38252
 A>Status: preliminary
 A:Molecule type: mRNA
 A/Residues: 1-680/708-863 <FU2>
 A/Cross-references: GB:M59818; GB:M38025; NID:9183046; PID:9183047
 A/Note: clone PH03
 R:Parsons, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son
 J. Exp. Med. 172, 1559-1570, 1990
 A>Title: Expression cloning of a human granulocyte colony-stimulating factor receptor:
 A/Reference number: JH0329; M0ID:91079757
 A/Accession: JH0330
 A:Molecule type: mRNA
 A/Residues: 1-680/708-863 <LAR>
 A/Cross-references: GB:X55721; NID:931696; PID:931697
 A/Note: clone 25-1; placenta
 R:Seto, Y.; Fukunaga, R.; Nagata, S.

J. Immunol. 148, 259-266, 1992

A/Title: Chromosomal gene organization of the human granulocyte colony-stimulating
 A/Reference number: A46486; M0ID:92091782
 A/Accession: A46486
 A>Status: preliminary
 A:Molecule type: DNA
 A/Residues: 855-863 <SET>
 A/Cross-references: GB:S71484; NID:9240883; PID:9240884
 A/Experimental source: granulocyte
 A/Note: sequence extracted from NCBI backbone (NCBI:71484, NCBI:71485)
 R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
 Arch. Biochem. Biophys. 324, 344-356, 1995
 A>Title: Extracellular domain of granulocyte colony-stimulating factor receptor.
 A/Reference number: S68331; M0ID:96132662
 A/Accession: S68332
 A:Molecule type: protein
 A/Residues: 234-269 <HAN>
 A/Genetics:
 A:Gene: GDB:CSF3R
 A/Cross-references: GDB:126430; OMIM:138971
 A/Map position: 1p35-1p34.3
 A/Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence status predicted <SIG>
 F:25-663/Product: granulocyte colony-stimulating factor receptor, long form #status
 F:25-680/708-863/Product: granulocyte colony-stimulating factor receptor, short form
 F:25-627/Domain: extracellular #status predicted <EXT>
 F:628-653/Domain: transmembrane #status predicted <TM>
 F:654-863/Domain: intracellular #status predicted <INT>
 F:93/128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 9.9%; Score 100; DB 2; Length 863;
 Best Local Similarity 26.7%; Pred. No. 0.057; 87; Indels 26; Gaps 11;
 Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;

QY 2 PTLIGSSLOATCSIHSDTPGATAE-GLYTFNGRRLPSLSRLN--TSTLALANLN 58
 DB 34 PIVHLDGPITASCIIKONCSHLDPEPQILMRGAEIQPGRGQRRLSDQTESITIPHLN 93
 QY 59 GSRQSGDNLVCHARDG---ILAGSCLYVGLPEPEFNFISC-WSRNMKDLTCRWTPGAR 114
 DB 94 HTQ-----FLSCCLMNGNSLIQIDQVELRAGYPPALPHNLSCIMNLTSSLIQWEPGP- 149
 QY 115 GETFLHTNYSK-YKLR---LVRSXHKMGVP-----HC---EPSLMPYQGGPPLSLX 162
 DB 149 -ETHLPTSTLSEKSRGNCQTGDSILDCVPKDGSHCCIPKHHLLY-QNNGIWOAE 206
 QY 163 DLGSGHSPRL 173
 DB 207 NALGTSMSPOL 217

RESULT 12

I45971
 prolactin receptor - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
 C/Accession: I45971
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992
 A>Title: Molecular cloning of the bovine prolactin receptor and distribution of pro
 A/Reference number: I45971; M0ID:9346019
 A/Accession: I45971
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A/Residues: 1-581 <SCO>
 A/Cross-references: GB:I02549; NID:9163617; PID:9163618
 A/Genetics:
 A:Gene: PRLR

Query Match 9.7%; Score 98; DB 2; Length 581;
 Best Local Similarity 33.7%; Pred. No. 0.057;

Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;

OY 42 SRLNTSLALALANNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISCSMSN 101
 Db 7 SRVVFILLFLFSLVSLNG---QS-----PPKPKLVKCRSPG 40

OY 102 MKDLTCMTPPAGHGETFLHTNYSKY 127
 Db 41 KETFCWMEPGADG--LPTNYTLTY 64

RESULT 13
 A57018
 prolactin receptor - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
 C/Accession: A57018
 R/Ref: G. Wells, J.A.
 J. Biol. Chem. 270, 13133-13137, 1995
 A/Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell lines
 A/Reference number: A57018; MUID:95286597
 A/Accession: A57018
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-206 <RES>
 A/Cross-references: GB:578505; NID:g999114; PID:g999115

Query Match
 Best Local Similarity 9.4%; Score 95; DB 2; Length 206;
 Matches 21; Conservative 1; Mismatches 17; Indels 2; Gaps 1;

OY 87 LPPEKPNISCSMSNMDLTCMTPPAGHGETFLHTNYSKY 127
 Db 2 LPPEKPNISCSMSNMDLTCMTPPAGHGETFLHTNYSKY 127

RESULT 14
 A30304
 prolactin receptor 2 precursor - rabbit
 N/Alternate names: prolactin receptor, mammary gland
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
 C/Accession: A30304; A60380
 R/Ref: M. Jolicoeur, C. LeVeyne, C. Dusanter-Fourt, I. Petridou, B. Boutin,
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A/Title: Identification and sequence analysis of a second form of prolactin receptor by
 A/Reference number: A30304; MUID:89184578
 A/Accession: A30304
 A/Molecule type: mRNA
 A/Residues: 1-616 <EDE>
 A/Cross-references: GB:J04510; NID:g165669; PID:g165670
 R/Waters, M.J.; Spencer, S.A.; Hanlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A/Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
 A/Reference number: A60380; MUID:91146782
 A/Accession: A60380
 A/Molecule type: protein
 A/Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167
 A/Note: the amino end of the mature protein was blocked
 A/Keywords: blocked amino end; glycoprotein; transmembrane protein
 A/1-24/Domain: signal sequence #status predicted <SIG>
 A/25-616/Product: prolactin receptor #status predicted <MAT>
 A/235-258/Domain: transmembrane #status predicted <TM>
 A/159, 104, 132, 347, 389, 411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
 Best Local Similarity 9.4%; Score 95; DB 2; Length 616;
 Matches 20; Conservative 2; Mismatches 16; Indels 2; Gaps 1;

OY 88 LPPEKPNISCSMSNMDLTCMTPPAGHGETFLHTNYSKY 127
 Db 1 LPPEKPNISCSMSNMDLTCMTPPAGHGETFLHTNYSKY 127

Db 27 PPKPPIFKCRSPKETFICWMPGADG--LPTNYTLTY 64

RESULT 15
 157699
 pseudo-prolactin receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C/Accession: 157699
 R/Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A/Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A/Reference number: 157699; MUID:89261824
 A/Accession: 157699
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-97 <RES>
 A/Cross-references: GB:M2957; NID:g200477; PID:g200478

Query Match
 Best Local Similarity 9.4%; Score 95; DB 2; Length 97;
 Matches 30; Conservative 9; Mismatches 20; Indels 32; Gaps 4;

OY 37 LPSELRLNTSLALANNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNIS 96
 Db 1 MPSALAYL---LVLSISLNG---QS-----PPKPKPIHK 30

OY 97 CWSRNMDLTCMTPPAGHGETFLHTNYSKY 127
 Db 31 CRSPDKETFCWMPGSDG--LPTNYSITY 59

Search completed: September 16, 1999, 20:42:11
 Job time: 5404 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:14 ; Search time 35.09 Seconds

(without alignments)
149,840 Million cell updates/sec

Title: US-09-037-657-29

Sequence: 1 DPTLLIGSSLIQATCSIHGDT.....SHQSPRLSKIXCPHTGCPGR 186

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	14.3	917	1	IL6B_MOUSE
2	133.5	13.3	918	1	IL6B_HUMAN
3	130	12.9	918	1	IL6B_RAT
4	115	11.4	1097	1	LIFR_HUMAN
5	112.5	11.2	1092	1	LIFR_MOUSE
6	101.5	10.1	632	1	PRLR_HUMAN
7	100	9.9	836	1	GCGR_HUMAN
8	98	9.7	881	1	PRLR_BOVIN
9	95	9.4	461	1	PRLR_RABIT
10	93	9.2	460	1	IL6A_MOUSE
11	91	9.0	880	1	TYO3_MOUSE
12	90.5	9.0	837	1	GCGR_MOUSE
13	89	8.8	462	1	IL6A_RAT
14	89	8.8	830	1	PRLR_COLL
15	88.5	8.8	581	1	PRLR_CEREL
16	88	8.7	608	1	PRLR_MOUSE
17	88	8.7	880	1	TYO3_RAT
18	87	8.6	831	1	PRLR_CHICK
19	85.5	8.5	610	1	PRLR_RAT
20	85.5	8.5	887	1	PRLR_MELGA
21	82	8.2	831	1	CNTR_HUMAN
22	81	8.1	372	1	CNTR_MOUSE
23	81	8.1	372	1	CNTR_RAT
24	81	8.1	547	1	ICAJ_HUMAN
25	80	8.0	468	1	IL6A_HUMAN
26	79	7.9	630	1	PRLR_ORENT
27	77.5	7.7	270	1	YFHX_ECOLI
28	76.5	7.6	704	1	CRAR_MOUSE
29	76.5	7.6	1363	1	ILPR_BRALLA
30	75.5	7.5	550	1	DCOL_STRCI
31	74.5	7.4	1220	1	DEPOL_HSVB
32	74	7.4	437	1	AFLR_ASPL
33	74	7.4	362	1	CNTR_CHICK
34	74	7.4	1165	1	LPRR_HUMAN
35	73.5	7.3	1162	1	LPRR_MOUSE
36	73	7.3	515	1	NEF2_DROME
37	73	7.3	1805	1	NEF2_RAT
38	72	7.2	444	1	AFLR_ASPL
39	72	7.2	532	1	SREP_PENCH
40	71.5	7.1	2481	1	UN52_CAREL
41	71	7.1	854	1	ENV2_SIVCZ
42	71	7.1	1038	1	IT4A_HUMAN
43	71	7.1	367	1	NAR3_HUMAN

ALIGNMENTS

RESULT	ID	IL6B_MOUSE	STANDARD:	PRT:	917 AA.
44	71	7.1	1127	1	POLG_DEN2D
45	71	7.1	1056	1	RIC1_YEAST
1	IL6B_MOUSE				
AC	000560				
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).				
GN	IL6ST.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	RODENTIA; SCIOGONATHI; MORIDAE; MORINAE; MUS.				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ICR; TISSUE-MACROPHAGE;				
RX	MEDLINE: 92291532.				
RA	SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;				
RT	Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo.				
RT	J. IMMUNOL. 148:4066-4071(1992).				
CC	1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6-BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.				
CC	1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAW-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.				
CC	1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES DURING THE REST OF EMBRYOGENESIS.				
CC	1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.				
CC	1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
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CC	EMBL: X62646; G840817; .				
DR	EMBL: M83336; G193592; .				
DR	MGI: 96560; IL6ST.				
DR	PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.				
DR	PIRAT: P40189; IBOU.				
DR	HSSP: P40189; IBOU.				
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT.				
FT	SIGNAL	1	22		
FT	CHAIN	23	917		POTENTIAL.
FT	DOMAIN	23	617		INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	TRANSMEM	618	639		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	640	917		POTENTIAL.
FT	DOMAIN	26	120		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	124	220		IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	221	322		FIBRONECTIN TYPE-III.
FT	DOMAIN	323	420		FIBRONECTIN TYPE-III.


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CC CC      ONE IG-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC CC      -1- DATABASE: NAME=PROM; NOTE=CD guide C030 entry;
CC CC      WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cdl30.htm".
CC CC
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CC CC      MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC CC      ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB.SLB.CH/ANNOUNCE/
CC CC      OR SEND AN EMAIL TO LICENSE@SLB.SLB.CH).
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DR DR      EMBL, M57230; G186354; .
DR DR      PIR; A36337; A36337.
DR DR      PDB; 1BDJ; 26-AUG-98.
DR DR      MIR; 600694; .
DR DR      PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
DR DR      PRFM; PF00041; fn3; 3.
RW RW      RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW KW      REPEAT; 3D-STRUCTURE.
FT FT      SIGNAL          1       22
FT FT      CHAIN           23      918    POTENTIAL.
FT FT      DOMAIN         23      619    INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT FT      TRANSEM        620     641    EXTRACELLULAR (POTENTIAL).
FT FT      DOMAIN         26      918    POTENTIAL.
FT FT      DOMAIN         26      120    CYTOPLASMIC (POTENTIAL).
FT FT      DOMAIN         124     222    IG-LIKE C2-TYPE DOMAIN.
FT FT      DOMAIN         223     324    FIBONECTIN TYPE-III.
FT FT      DOMAIN         424     517    FIBONECTIN TYPE-III.
FT FT      DOMAIN         518     613    FIBONECTIN TYPE-III.
FT FT      DOMAIN         725     755    SER-RICH.
FT FT      DISULFID       132     144
FT FT      CARBOHYD       43       43    POTENTIAL.
FT FT      CARBOHYD       83       83    POTENTIAL.
FT FT      CARBOHYD      121      131    POTENTIAL.
FT FT      CARBOHYD      157      157    POTENTIAL.
FT FT      CARBOHYD      227      227    POTENTIAL.
FT FT      CARBOHYD      379      379    POTENTIAL.
FT FT      CARBOHYD      383      383    POTENTIAL.
FT FT      CARBOHYD      390      390    POTENTIAL.
FT FT      CARBOHYD      553      553    POTENTIAL.
FT FT      CARBOHYD      564      564    POTENTIAL.
SQ SQ      SEQUENCE      918 AA; 103522 MW; 7C0C06F05 CRC32;

Query Match             13.3%; Score 133.5; DB 1; Length 918;
Best Local Similarity   27.3%; Pred. No. 1.6e-05;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2

QY      2 PTLLIGSSLOATGSIHG---DPGAFAEGLYWTFNGRRRLSPSELSRLNLTALALANLN 58
DB      36 PVVQLHNFAYCYLVKXCKMDYFNVANNTIWKMTNHETLPKEGYTLIIIRASSVTFLDIA 95
QY      59 GSRSOSGDNYCHARGDSIIAGSCLYGLPPERPFINISCRMKKKDLTCWTGCANGGEFF 118
DB      96 SLNLQLCNLIITLGOLBNONYGITLIISGLPPEPKRNKLSCIYNKGKRKCWDGGR--ETH 153
QY      119 LHTYTSIK 126
DB      154 LETNETLK 161

RESULT      3
ID ID IL6B_RAT IL6B_RAT STANDARD; PROT; 918 AA.
AC PA0190;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE).
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATTUS NOVEGICUS (RAT).
OC EURARCTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ROENTLIA; SCUROGNATHI; MORIDAE; MORINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER:
RX MEDLINE: 93052397.
RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130."
RL GENOMICS 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: M92340; -1 NOT_ANNOTATED_CDS.
DR PIR: A44257; A44257.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 3.
DR HSSP: P40189; IBOU.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW REPEAT.
FT SIGNAL: 1 22
FT CHAIN: 23 918
FT DOMAIN: 23 918
FT TRANSMEM: 619 640
FT DOMAIN: 641 918
FT DOMAIN: 26 120
FT DOMAIN: 124 221
FT DOMAIN: 222 323
FT DOMAIN: 324 422
FT DOMAIN: 423 516
FT DOMAIN: 517 612
FT DOMAIN: 724 754
FT DISULFID: 134 144
FT DISULFID: 172 181
FT CARBOHYD: 43 43
FT CARBOHYD: 61 61
FT CARBOHYD: 83 83
FT CARBOHYD: 131 131
FT CARBOHYD: 157 157
FT CARBOHYD: 205 205
FT CARBOHYD: 226 226
FT CARBOHYD: 382 382
FT CARBOHYD: 389 389
FT CARBOHYD: 477 477
FT CARBOHYD: 552 552
SQ SEQUENCE 918 AA; 102450 MW; 66EDFCD0 CRC32;

Query Match

12.9%; Score 130; DB 1; Length 918;

Best Local Similarity 26.0%; Pred. No. 3,6e-05;
Matches 38; Conservative 24; Mismatches 72; Indels 12; Gaps 3;
OY 2 PTLIGSSLCATCSHG---DTPGATAGLWYNGRRLPELSLNTSLTALANLN 58
DB 36 PVVRSNFTVCKLREKQCLQVSYNAVYIWKTHVAVPEQVIVNRTASSVFTDV 95
OY 59 GSROSGDNLYCHARDGSIAGSLCYLVGPEKFNISCSWRNMKDLCTRTPGARGETF 118
DB 96 FQNVOLCNITSPQIEQNVYGITITLSCYPPDIPNLSICVNEGKMLCDLPPGR--ETV 153
OY 119 LHTNYSKRYKLRLVRSEKHXMGVPHC 144
DB 154 LETNYTLK-----SEWATEKEFPDC 172
RESULT 4
LIFR_HUMAN
ID LIFR_HUMAN STANDARD; PRT; 1097 AA.
AC P42702;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R).
GN LIFR.
OS HOMO SAPIENS (HUMAN).
OC EURARCTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE: 92007727.
RA GEARING D.P., THUT C.J., VANDENBOS T., GIMPEL S.D., DEANEX P.B.,
RA KING J., PRICE V., COSMAN D., BECKMANN M.P.;
RT "Leukemia inhibitory factor receptor is structurally related to the
IL-6 signal transducer, gp130."
RL EMBL J. 10:2839-2848(1991).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
MEMBRANE-BOUND AND A SECRETED FORM.
CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
MAY ARISE BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: X61615; G34366; -
DR MIM: 151443; -
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PFAM: PF00041; fn3; 4.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW ALTERNATIVE SPLICING; REPEAT.
FT SIGNAL: 1 44
FT CHAIN: 45 1097
FT DOMAIN: 45 833
FT TRANSMEM: 834 858
FT DOMAIN: 859 1097
FT DISULFID: 55 65
FT DISULFID: 64 64
FT CARBOHYD: 85 85
FT CARBOHYD: 131 131
SQ SEQUENCE 131 AA; 131 MW; 66EDFCD0 CRC32;

FT CARBOHYD 143 143 POTENTIAL.
 FT CARBOHYD 191 191 POTENTIAL.
 FT CARBOHYD 243 243 POTENTIAL.
 FT CARBOHYD 303 303 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 407 407 POTENTIAL.
 FT CARBOHYD 426 426 POTENTIAL.
 FT CARBOHYD 445 445 POTENTIAL.
 FT CARBOHYD 481 481 POTENTIAL.
 FT CARBOHYD 489 489 POTENTIAL.
 FT CARBOHYD 572 572 POTENTIAL.
 FT CARBOHYD 652 652 POTENTIAL.
 FT CARBOHYD 663 663 POTENTIAL.
 FT CARBOHYD 680 680 POTENTIAL.
 FT CARBOHYD 729 729 POTENTIAL.
 FT CARBOHYD 787 787 POTENTIAL.
 SO SEQUENCE 1097 AA; 123742 MW; 4120A634 CRC32;

Query Match 11.4%; Score 115; DB 1; Length 1097;
 Best Local Similarity 23.4%; Pred. No. 0.0013;
 Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

OY 1 DPTLLGSSIAATCSI-----HGDPGATAGLWTFNGRRLPSELRLNTSTL 50
 DB 258 DRYVLAGSDITFCVSOEKVLSALIGHTNCPILHDE-----ENV 297
 OY 51 ALALANLNGSROSGDNLVCHARDGSLAGSLVGLPPEKPFNSCWSRNKDKLTCTMT 110
 DB 258 AIKINISVS-ASSTGNTVFTEDN--IGTVIFAGYPPDPTQQLNCEHDLKEICSWN 354
 OY 111 PG-----AHGETFLTNVSLKYLKLVASE 135
 DB 355 PGRVATLVGRPRATSYTLVE-SESGRY-VRLKRAE 386

RESULT 5
 LIFR_MOUSE STANDARD; PRT: 1092 AA.
 AC P42703;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R) (D-FACTOR/LIF RECEPTOR).
 GN LIFR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A. (SECRETED FORM).
 RX MEDLINE: 92007727.
 RA GEARING D.P., THUT C.J., VANDENBOS T., GIMPEL S.D., DELANEY P.B., KING J., PRICE V., COSMAN D., BECKMANN M.P.;
 RT Leukemia inhibitory factor receptor is structurally related to the IL-6 signal transducer, gp130.;
 RT EMBO J. 10:2839-2848(1991).
 RL (12)
 RN SEQUENCE FROM N.A. (SECRETED FORM).
 RC SPRAIN-ICR: TISSUE-LAYER;
 RX MEDLINE: 94039833.
 RA TOMIDA M., YAMAMOTO-YAMAGUCHI Y., HOZUMI M.;
 RT receptor in mouse liver.;
 RT "Pregnancy associated increase in mRNA for soluble D-factor/LIF
 FEBS LETT. 334:193-197(1993).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94334302.
 RA TOMIDA M., YAMAMOTO-YAMAGUCHI Y., HOZUMI M.;
 RT "Three different cDNAs encoding mouse D-factor/LIF receptor.";
 RT J. BIOCHEM. 115:557-562(1994).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF

CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
 CC MEMBRANE-BOUND AND A SECRETED FORM.
 CC -1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,
 CC AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF
 CC THE SECRETED FORM.
 CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
 CC MAY ARISE BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: S73496; G688386;
 DR EMBL: S73495; G688384;
 DR EMBL: D26177; G825506;
 DR EMBL: D17444; G441494;
 DR MGD: MGI:96788; LIFR.
 DR PROSITE, PS00241: RECEPTOR_CYTOKINES_1; FALSE_NEG.
 DR PFAM: PF00041; fn3; 4.
 DR RECEPTOR_TRANSMEMBRAN; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW ALTERNATIVE_SPLICING; REPEAT.
 FT SIGNAL 1 43
 FT CHAIN 44 1092
 FT DOMAIN 44 828
 FT TRANSMEM 829 853
 FT DOMAIN 854 1092
 FT DISULFID 53 63
 FT CARBOHYD 164 164
 FT CARBOHYD 199 199
 FT CARBOHYD 228 238
 FT CARBOHYD 261 261
 FT CARBOHYD 385 385
 FT CARBOHYD 402 402
 FT CARBOHYD 421 421
 FT CARBOHYD 440 440
 FT CARBOHYD 453 453
 FT CARBOHYD 476 476
 FT CARBOHYD 567 567
 FT CARBOHYD 647 647
 FT CARBOHYD 658 658
 FT CARBOHYD 675 675
 FT CARBOHYD 724 724
 FT CARBOHYD 782 782
 FT CARBOHYD 718 718
 FT VARSPLIC 720 1092
 FT VARSPLIC 1092 122573 MW; 07DC092F CRC32;
 SO SEQUENCE

Query Match 11.2%; Score 112.5; DB 1; Length 1092;
 Best Local Similarity 25.4%; Pred. No. 0.0024;
 Matches 29; Conservative 27; Mismatches 41; Indels 17; Gaps 5;

OY 1 DPTLLGSSIAATCSIHGDPGATAGLWTFNGRRLPSELRLNTSTLALANLN 58
 DB 253 DRYVLAGSDITFCVSOEKVLSALIGHTNCPILHDE-----ENV 300
 OY 59 GSROSGDNLVCHARDGSLAGSLVGLPPEKPFNSCWSRNKDKLTCTMTG 112
 DB 301 VS-ENSGTNIIFITDD--YGVTVFAGYPPDVPRKLSCTETHDLKEICSWNG 351

RESULT 6
 PRLR_HUMAN

ID PRLR_HUMAN STANDARD: PRT: 622 AA.
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90114212.
 RA BOUTIN J.-M., EDERY M., SHIROTA M., JOLICOEUR C., LESUEUR L.,
 RA ALI S., GOULD D., DJIANE J., KELLY P.A.;
 RT "Identification of a cDNA encoding a long form of prolactin receptor
 RT in human hepatoma and breast cancer cells."
 RL MOL. ENDOCRINOL. 3:1455-1461(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
 RX MEDLINE; 95075462.
 RA SOMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;
 RT "The x-ray structure of a growth hormone-prolactin receptor complex."
 RL NATURE 372:478-481(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC EMBL; M31661; G190362;
 DR PIR; A40144; A40144.
 DR PDB; 1BP3; 23-SEP-98.
 DR MIM; 176761.
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 2.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 1 24
 FT DOMAIN 25 622
 FT TRANSMEM 25 234
 FT TRANSMEM 259 258
 FT DOMAIN 259 622
 FT DOMAIN 25 122
 FT DOMAIN 123 227
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 104 104
 FT CARBOHYD 233 233
 FT SEQUENCE 622 AA; 69505 MW; 6924E155 CRC32;
 SO
 Query Match 10.1%; Score 101.5; DB 1; Length 622;
 Best Local Similarity 46.2%; Pred. No. 0.015;
 Matches 24; Conservative 3; Mismatches 22; Indels 3; Gaps 2;
 QY 77 ILASGLYVG-LPPEKPNISWNSMMDLTCRWTPGANGELFTNTSLKY 137
 DB 15 LFLNLTCLNGQLPCKPKEIFKCRSPNKEFTCMWRPRTDGG--LPTNLSLY 64

AC 099062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 11-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 GN CSF3R OR GCSFR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA.
 RX MEDLINE; 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMBEL S., SIMS J.E., COSMAN D.,
 RA PARK L., SORESENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein."
 RL J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA.
 RX MEDLINE; 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor."
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor."
 RL J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RX MEDLINE; 92007729.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor."
 RL EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RX MEDLINE; 97331327.
 RA YAMASAKI R., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WxWxS
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand."
 RL NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELLING OF 125-331.
 RX MEDLINE; 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis."
 RL J. BIOL. CHEM. 272:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
 CC EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC BONE MARROW LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER),
 CC GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;

FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SQ SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 9.7%; Score 98; DB 1; Length 581;
 Best Local Similarity 33.7%; Pred. No. 0.03;
 Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;

OY 42 SRLNLTALANINGSGSDNLYCHARGSLAGSCLVGLPPEKPNISGMSRN 101
 DB 7 SRVFFLLFLSVSLNG--QS-----PPEKPLVKKCRSPG 40
 OY 102 MKDLTCRWTPGAGETFLHTNYSKY 127
 DB 41 KEFTCWMERGADG--LPTNTLTLY 64

RESULT 9
 PRLR RABIT STANDARD; PRT; 616 AA.
 AC P14787;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS ORYCTOLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-MAMMARY GLAND;
 RX MEDLINE: 89184578.
 RA EDERER M., JOLICOEUR C., LEVI-MEYREIS C., DUSANTER-FOURT I.,
 RA PETRIDOU B., BOUTIN J.M., LESDEUR L., KELLY P.A., DJIANE J.;
 RT "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
 RN (2)
 RP 3D-STRUCTURE MODELLING OF 30-228.
 RA HALABY D., THOREAU E., DJIANE J., MORNON J.P.;
 RX MEDLINE: 97248733.
 RT "Homology modeling of rabbit prolactin hormone complexed with its
 RT receptor.";
 RL PROTEINS 27:459-468(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC or send an email to license@isb-sdb.ch).
 CC EMBL: J04510; GI65670;
 DR PIR: A30304; A30304.
 DR PDB: 1AN3; 03-DEC-97.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 2.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 616 PROLACTIN RECEPTOR.
 FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 258 POTENTIAL.
 FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 104 104 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SQ SEQUENCE 616 AA; 68840 MW; FB8170B1 CRC32;

Query Match 9.4%; Score 95; DB 1; Length 616;
 Best Local Similarity 50.0%; Pred. No. 0.064;
 Matches 20; Conservative 2; Mismatches 16; Indels 2; Gaps 1;

OY 88 PPEKPNISGMSRNKMDLTCRWTPGAGETFLHTNYSKY 127
 DB 27 PGKPFIFKCRSPKETFTCWMRPGADG--LPTNTLTLY 64

RESULT 10
 IL6A MOUSE STANDARD; PRT; 460 AA.
 ID IL6A_MOUSE
 AC P22272;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
 GN IL6RA OR IL6R.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCITROGNATHI; MORIDAE; MORINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-SPLEEN;
 RX MEDLINE: 90278354.
 RA KISHIMOTO T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
 RA KISHIMOTO T.;
 RT "Functional murine interleukin 6 receptor with the intracellular A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis.";
 RL J. EXP. MED. 171:2001-2009(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-C3H; TISSUE-LIVER;
 RA FIORILLO M.T., CILIBERTO G., DENTE L.;
 RL SUBMITTED (JUL-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sdb.ch).
 CC EMBL: X51975; G49726;
 DR EMBL: X53802; G52693;
 DR PIR: J10145; J10145.
 DR PIR: S14543; S14543.
 DR MCD: MGI:105304; IL6RA.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 1.
 DR PFAM: PF00047; lg; 1.
 DR HSSP: P16471; 1BP3
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.

FT SIGNAL 1 19
 FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 21 357 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 358 385 POTENTIAL.
 FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 47 92 POTENTIAL.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 162 173 BY SIMILARITY.
 FT CARBOHYD 32 32 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 150 150 POTENTIAL.
 FT CARBOHYD 374 374 A -> R (IN REF. 2).
 FT CONFLICT 374 374
 SQ SEQUENCE 460 AA; 50454 MW; 0B9F5F46 CRC32;

Query Match 9.2%; Score 93; DB 1; Length 460;
 Best Local Similarity 29.3%; Pred. No. 0.072;
 Matches 34; Conservative 22; Mismatches 38; Indels 22; Gaps 9;

DB 36 TSLPGATVTLIC-----PGKEAAGNTIHHVYSGSQ-----NREWTGTGTLVLRDVL 84
 QY 3 TLIGSSIAQTCISIHGDTPGATAEG---LYWTNGRRLPELSLTLALANLNG 59
 DB 60 SROSGNLYCHARDGSIAGSC-LYVGLPPEKPFNSCHSRN-MKDLGCRWEGA 113
 QY 85 S-DTGDYL-CSLNDH--LVGTVPVLVDVPEEP-KLSCEKPNLVNAICWRPSS 134

RESULT 11
 TYO3_MOUSE STANDARD; PRT; 880 AA.

AC P5144;
 ID TYO3_MOUSE
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).
 OS TYRO3 OR DTK OR RSE.
 OS MUS MUSCULUS (MUSCLE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIURIFORMIA; MURIDAE; MURINAE; MUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RC MEDLINE; 94193774.
 RX MARK M.R., SCADDEN D.T., WANG Z., GU Q., GODDARD A., GODOMSKI P.J.;
 RA "RSE, a novel receptor-type tyrosine kinase with homology to Axl/Tyfo, is expressed at high levels in the brain."
 RT J. BIOL. CHEM. 269:10720-10728(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RC MEDLINE; 95161079.
 RX CROSIER P.S., LEWIS P.M., HALL L.R., VITAS M.R., MORRIS C.M.,
 RA BEIER D.R., WOOD C.R., CROSIER K.E.;
 RT "Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: structure, genetic mapping and analysis of expression."
 RL GROWTH FACTORS 11:125-136(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6;
 RX MEDLINE; 94336210.
 RA LAI C., GORE M., LEMKE G.;
 RT "Structure, expression, and activity of Tyro 3, a neural adhesion-related receptor tyrosine kinase."
 RT ONCOGENE 9:2567-2578(1994).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 95240399.
 RA SCHULZ N., PAULHIC C., LEE L., ZHOU R.;
 RT "Isolation and expression analysis of tyro3, a murine growth factor

RT receptor tyrosine kinase preferentially expressed in adult brain."
 RL BRAIN RES. MOL. BRAIN RES. 28:273-280(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX SASAKI M.;
 RT SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY IN THE CENTRAL NERVOUS SYSTEM.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN OTHER TISSUES.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE EXTRACELLULAR DOMAINS CONTAINS 2 IG-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC
 CC EMBL; U05683; G469519; -
 CC EMBL; U18933; G622983; -
 CC EMBL; X78103; G473097; ALT_INIT.
 CC EMBL; U18342; G687626; ALT_INIT.
 CC EMBL; AB000828; D1019943; -
 CC MGD; MG1:104294; TYRO3.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PRAM; PF00041; fn3; 2.
 DR PRAM; PF00047; fn3; 2.
 DR PRAM; PF00069; pkinase; 1.
 DR HSP; P11362; IFGI.
 DR RECEPTOR; GLYCOPROTEIN; TYROSINE-PROTEIN KINASE; ATP-BINDING;
 KW TRANSFERASE; PHOSPHORYLATION; TRANSMEMBRANE; SIGNAL; REPEAT;
 KW IMMUNOGLOBULIN FOLD.
 FT SIGNAL 1 30
 FT CHAIN 31 880
 FT DOMAIN 31 419
 FT TRANSMEM 420 440
 FT DOMAIN 441 880
 FT DOMAIN 34 115
 FT DOMAIN 131 200
 FT DOMAIN 214 301
 FT DOMAIN 305 401
 FT DOMAIN 508 785
 FT NP_BIND 514 522
 FT BINDING 540 540
 FT ACT_SITE 645 645
 FT MOD_RES 676 676
 FT CARBOHYD 53 53
 FT CARBOHYD 75 75
 FT CARBOHYD 181 181
 FT CARBOHYD 220 220
 FT CARBOHYD 230 230
 FT CARBOHYD 283 283
 FT CARBOHYD 356 356
 FT CARBOHYD 370 370
 FT CONFLICT 630 630
 FT CONFLICT 811 811
 SQ SEQUENCE 880 AA; 96222 MW; 476973C9 CRC32;

Query Match 9.0%; Score 91; DB 1; Length 880;
 Best Local Similarity 22.0%; Pred. No. 0.24;
 Matches 41; Conservative 18; Mismatches 53; Indels 74; Gaps 7;

QY 11 QATCSHGDTPGATAGLTW---TENGRLPSELSRLNTSLALALANLNGSSQSD 66
 DB 147 QLSCEAVGPPEPVT---ITWNRGLTKVGGPAPSP-----SYLNTVGTQRT-- 190
 QY 67 NIVCHAROGSILAGS---CLVGLGPEKPFNISCNRNKKDLTCMTGPAHEFTLH--- 121
 DB 190 EESCEARNKGLATSRPAIVRLQAPPAEFNTVTITSSYNASVAMVPGADLALLHSGT 249
 QY 121 -----TNTSLKTKLRLVSEKHXMKGVPCPEPL 148
 DB 250 VGVNAPGEMALAVVVPPTCLLRNAPATNTSLNR-----CANAL 294
 QY 149 MEYPOG 154
 DB 295 GPSPYG 300

RESULT 12
 GCSR_MOUSE STANDARD; PRT; 837 AA.

AC P40223;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 GN CSF3R OR CSF3R.
 OS MUS MUSCULUS (MOUSE).
 OC EURARVOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90235283.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor.";
 RL CELL 61:341-350(1990).
 RN (2)
 RP STRUCTURE BY NMR OF 225-333.
 RX MEDLINE; 97331327.
 RA YANASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WXXS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 or send an email to license@slb-slb.ch).
 CC
 CC EMBL; M58288; G193455; -
 DR PIR; A34898; A34898.
 DR PDB; 1GCF; 22-OCT-97.
 DR MGI; MGI:88533; CSFGR.
 DR PROSITE; PS00241; RECEPTOR CYTOKINES 1; 1.
 DR PROSITE; PS00340; RECEPTOR CYTOKINES 2; 1.
 DR PFM; PF00041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 REPEAT; 3D-STRUCTURE.

FT SIGNAL 1 25
 FT CHAIN 26 837
 FT
 FT DOMAIN 26 626
 FT TRANSMEM 627 650
 FT DOMAIN 651 837
 FT DOMAIN 122 228
 FT DOMAIN 122 228
 FT DOMAIN 334 431
 FT DOMAIN 432 528
 FT DOMAIN 529 624
 FT DISULFID 132 143
 FT DISULFID 249 296
 FT DISULFID 267 310
 FT CARBOHYD 51 51
 FT CARBOHYD 94 94
 FT CARBOHYD 129 129
 FT CARBOHYD 186 186
 FT CARBOHYD 279 279
 FT CARBOHYD 392 392
 FT CARBOHYD 408 408
 FT CARBOHYD 474 474
 FT CARBOHYD 487 487
 FT CARBOHYD 582 582
 FT CARBOHYD 613 613
 SO SEQUENCE 837 AA; 93406 MW; D55F84D4 CRC32;

Query Match 9.08; Score 90.5; DB 1; Length 837;
 Best Local Similarity 23.88; Pred. No. 0.26; Indels 21; Gaps 8;
 Matches 45; Conservative 26; Mismatches 95;

QY 2 PTLIGSLQATCSHGDTPGATAEG-LYTFNGRLT-PSELSRL--NTSLALALANL 57
 DB 34 PVRRLGDEVLASCTISPCSKIDQAKILMLRDEPIQGRDQHLLPDTQESLITPLRL 93
 QY 58 NGSQSSQSDNIVCHAROGSILAGSCLVGLGPEKPFNISCNR-NKKDLTCMTGANGCE 116
 DB 94 NYT-QALFELCPWEDSVQLLDOALANGYPASPNSLCLMLTNSLYCOMEGP--E 150
 QY 117 TFLATNYSKTKLRLVSEKHXMKGVPC-----EPSLWPGPGPLSLXDL 164
 DB 151 THLPSTFLKFSRBRADQYGGDTIPDCVAKRKNCSIPKRNLLI-QYMAIYQAEEM 209
 QY 165 GGSQSPRL 173
 DB 210 LGSSSPRL 218

RESULT 13
 IL6A_RAT STANDARD; PRT; 462 AA.

AC P22273;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
 GN IL6R.
 OS RATTUS NORVEGICUS (RAT).
 OC EURARVOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATTUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-FISHER 344; TISSUE-LIVER;
 RX MEDLINE; 91060602.
 RA BAUMANN M., BAUMANN H., FEY G.H.;
 RT "Molecular cloning, characterization and functional expression of the
 rat liver interleukin 6 receptor.";
 RL J. BIOL. CHEM. 265:19853-19862(1990).
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
 RA GIBSON T.;


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RA CHEN X., HORSEMAN N.D.;
RT Cloning, expression, and mutational analysis of the pigeon prolactin
CC receptor."
CC RT ENDOCRINOLOGY 135:269-276(1994).
CC -I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; U07694; G466382;
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PIRAM; PF00041; fn3; 4.
DR HSSP; P16471; 1BP3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 830 PROLACTIN RECEPTOR.
FT DOMAIN 24 439 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 440 460 POTENTIAL.
FT DOMAIN 461 830 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 123 122 FIBRONECTIN TYPE-III.
FT DOMAIN 123 226 FIBRONECTIN TYPE-III.
FT DOMAIN 229 326 FIBRONECTIN TYPE-III.
FT DOMAIN 327 429 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 91 91 POTENTIAL.
FT CARBOHYD 100 100 POTENTIAL.
FT CARBOHYD 112 112 POTENTIAL.
FT CARBOHYD 132 132 POTENTIAL.
FT CARBOHYD 163 263 POTENTIAL.
FT CARBOHYD 304 304 POTENTIAL.
FT CARBOHYD 316 316 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
SQ SEQUENCE 830 AA; 94507 MW; 5EPAD51 CRC32;

Query Match 8.8%; Score 89; DB 1; Length 830;
Best local similarity 48.8%; Pred. No. 0.36;
Matches 20; Conservative 3; Mismatches 14; Indels 4; Gaps 2

Qy 88 PEKEPFNISCWSRNMKDLTCRTPGAHGFTFLH-TWYSIKY 127
Db 231 PEKPITIKCRSPKETETCWMKPSDSG---HPNTVITLY 268
||||| :|||: |||: |
PEKEPFNISCWSRNMKDLTCRTPGAHGFTFLH-TWYSIKY 127
PEKPITIKCRSPKETETCWMKPSDSG---HPNTVITLY 268

RESULT 15
ID ID PRLE_CEREL STANDARD; PRF; 581 AA.
AC 028235;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS CERUUS ELAPHUS (RED DEER).
OC EURKYOTA; MEPAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EDUTHERIA;
OC ARTIODACTYLIA; RUMINANTIA; PECORA; CEROVIDEA; CERVINDAE; CERVINAIE;
OC CERUUS.
CN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 96030711.
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:09 ; Search time 68.96 seconds
(without alignments)
165.996 Million cell updates/sec

Title: US-09-037-657-29

Sequence: 1 DPTLLIGSSLOANCISIHGDT.....SHOSPRLSXICPHGTGCGR 186

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	658	65.4	422	4	075462	075462 homo sapien
2	167.5	16.7	881	13	057519	057519 xenopus lae
3	110.5	11.0	862	4	099665	099665 homo sapien
4	108	10.7	971	11	070458	070458 mus musculu
5	107.5	10.7	970	11	088821	088821 mus musculu
6	107.5	10.7	422	4	016542	016542 homo sapien
7	107.5	10.7	1093	11	070535	070535 rattus norv
8	99.5	9.9	581	6	046561	046561 ovis aries
9	98	9.7	266	6	018880	018880 bos taurus
10	95	9.4	206	4	016354	016354 homo sapien
11	93.5	9.3	432	11	064385	064385 mus musculu
12	93.5	9.3	432	11	P70225	P70225 mus musculu
13	93	9.2	440	11	000343	000343 mus musculu
14	92.5	9.2	979	4	099650	099650 homo sapien
15	91.5	9.1	866	11	062121	062121 mus musculu
16	91	9.0	876	11	060752	060752 mus musculu
17	90	8.9	874	11	P97378	P97378 mus musculu
18	88.5	8.8	188	6	018985	018985 cervus elap
19	86.5	8.6	340	12	086893	086893 marte dwarf
20	83.5	8.3	6658	5	076281	076281 drosophila
21	83	8.3	1886	4	060468	060468 homo sapien
22	83	8.3	1571	4	060469	060469 homo sapien
23	82.5	8.2	754	5	027273	027273 drosophila
24	81.5	8.1	1395	5	044924	044924 drosophila
25	81	8.0	372	11	088507	088507 mus musculu
26	80.5	8.0	1165	6	002671	002671 sus scrofa
27	80	7.9	346	13	093404	093404 oreochromis
28	79.5	7.9	834	11	064151	064151 mus musculu
29	78.5	7.8	1180	4	015051	015051 homo sapien

30	78.5	7.8	917	11	060625	060625 mus musculu
31	78	7.7	1299	4	015179	015179 homo sapien
32	77.5	7.7	270	2	P76995	P76995 escherichia
33	77.5	7.7	1299	4	092823	092823 homo sapien
34	77.5	7.7	753	5	026306	026306 drosophila
35	77	7.7	1127	12	P89532	P89532 dengue viru
36	76.5	7.6	1404	4	015080	015080 homo sapien
37	76.5	7.6	2222	5	097394	097394 drosophila
38	76	7.6	313	12	088195	088195 sugarcane m
39	75	7.5	1241	4	060500	060500 homo sapien
40	75	7.5	310	12	088198	088198 sugarcane m
41	75	7.5	313	12	088199	088199 sugarcane m
42	75	7.5	515	12	09YTX2	09YTX2 sugarcane m
43	74.5	7.4	262	4	043561	043561 homo sapien
44	74.5	7.4	233	4	043919	043919 homo sapien
45	74	7.4	958	4	092920	092920 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	422 AA.
ID	075462			
AC	075462:			
DT	01-NOV-1998 (TRENBLREL.08, Created)			
DT	01-NOV-1998 (TRENBLREL.08, Last sequence update)			
DT	01-MAY-1999 (TRENBLREL.10, Last annotation update)			
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.			
GN	CLF-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREYNER D.,			
RA	MENOLD L.N., WELLS T.N.C., ROSCO-VILBOIS M.H., GAUCHAT J.F.;			
RT	CLF-1, a Novel Soluble Protein Shares Homology with Members of the			
RT	Cytokine Type-1 Receptor Family."			
RL	J. Immunol. 0:0-0(1998).			
DR	EMBL; AF059293; AAC2835.1;			
DR	PFAM; PF00041; fn3. 2.			
KW	Signal.			
FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	422	CYTOKINE-LIKE FACTOR-1.
SQ	SEQUENCE	422 AA;	46301 MW;	877F9BC9 CRC32.
Query Match				
Best Local Similarity 84.5%; Score 658; DB 4; Length 422;				
Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;				
QY	1 DPTLLIGSSLOANCISIHGDPGAREGLYTFNGRRRLPSELRLNSTALAINNGS 60			
DB	47 DPTLLIGSSLOANCISIHGDPGAREGLYTFNGRRRLPSELRLNSTALAINNGS 106			
QY	61 ROOSGDMVCHARDGSLIAGSCLVGLPPEKPFNISCWSRNMDDTCRTPGAAGETFLH 120			
DB	107 ROOSGDMVCHARDGSLIAGSCLVGLPPEKPFNISCWSRNMDDTCRTPGAAGETFLH 166			
QY	121 TNYSLAKTKRL-----VRSEKMKGVPH 143			
DB	167 TNYSLAKTKRLMYGQDNTCEYHTVG-PH 193			
RESULT 2				
ID	057519	PRELIMINARY:	PRT:	881 AA.
AC	057519:			
DT	01-JUN-1998 (TRENBLREL.06, Created)			
DT	01-JUN-1998 (TRENBLREL.06, Last sequence update)			
DT	01-MAY-1999 (TRENBLREL.10, Last annotation update)			
DE	GP130P1.			


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OY 50 LALALANLNGSRQSGDNVCHARDG-STLASCGLVGLPPEKPFNISCWSRNMKDLTCR 108
Db 203 VFLS-----DGTINMCOATKPKRIFCTVLFVSKYLEPKNVCSETRDEKFLDGS 253
OY 109 WTPGAGETFL-----HTNYSL 125
Db 254 WEPGV--DTTLWRKORFONTYL 274

RESULT 6
O16542 PRELIMINARY; PRT; 422 AA.
AC 016542: 014626;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=MUSCLE;
MEDLINE: 9539754.
RA CHEREL M., SOREL M., LEBEAU B., DUBOIS S., MOREAU J.F., BATAILLE R.,
MINVIELLE S., JACQUES Y.;
RN [1]
RT Molecular cloning of two isoforms of a receptor for the human
hematopoietic cytokine interleukin-11.
RN Blood 86:2534-2540(1995).
RN [2]
RP SEQUENCE FROM N.A.
RV VAN LEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSIER A.;
RN Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE=PLACENTA;
RA CHEREL M., SOREL M., DUBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
MINVIELLE S.;
RN Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RT EMBL: U32324; AAB36492.1;
RN EMBL: U38102; CAAB6224.1;
RN EMBL: U32323; AAB36491.1;
RN EMBL: U46595; CAAB6570.1;
RN PFAM: PF00041; fn3; 2.
RN PFAM: PF00047; fn3; 1.
SQ SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 10.7%; Score 107.5; DB 4; Length 422;
Best Local Similarity 26.3%; Pred. No. 0.0013;
Matches 40; Conservative 24; Mismatches 67; Indels 21; Gaps 7;

Y 7 GSSLQATCSHGTPGATA-EGLYTFNG--RRLPSLSRLNTSTLALANLNGSRQ 63
Db 41 GRVVKLCC-----PVTAGDPVSWFDEPKILQGPDSGLGHELYLAQDSTDEG--- 92
Y 64 SGDNVCHARDGSIILGSCLYVGLPPEKPFNISCWSRNMKDLTCRTPGAGETFLHTNY 123
Db 92 -----YICQLDGLGCTVTLQGLYPPARPV-VSCQADADYENFSCWPSO--ISGLPTRY 144
Y 124 SLKYLRLVSEKHXMGVPHCEPSLMPYPOG 155
Db 145 LITSYRKTYLVGADSQRRSPSTGP--WPCPODP 174

RESULT 7
O70535 PRELIMINARY; PRT; 1093 AA.
C 070535:
O1-AUG-1998 (TREMblrel. 07, Created)
O1-AUG-1998 (TREMblrel. 07, Last sequence update)
O1-MAY-1999 (TREMblrel. 10, Last annotation update)
LEUKEMIA INHIBITOR FACTOR RECEPTOR ALPHA-CHAIN.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTER-IMMICH; TISSUE=LIVER;
RX MEDLINE: 98007878.
RA AITAMA J., IKEDA-NAIKI S., OHGANE J., MIN K.S., INAKURA T., SASAI K.,
SHIOYA K., OGAWA T.;
RN [1]
RT Molecular cloning of rat leukemia inhibitory factor receptor
RT alpha-chain gene and its expression during pregnancy.
RN Biochim. Biophys. Acta 1353:266-276(1997).
DR EMBL: D86345; BAA25907.1;
DR PFAM: PF00041; fn3; 4.
SQ SEQUENCE 1093 AA; 122394 MW; 23638887 CRC32;

Query Match 10.7%; Score 107.5; DB 11; Length 1093;
Best Local Similarity 24.1%; Pred. No. 0.004;
Matches 28; Conservative 23; Mismatches 44; Indels 21; Gaps 4;

OY 1 DPTLLIGSLQATC---SHGDPGATAEGLYTFNGRRRLPSELRLNTSTLALAN 56
Db 254 DKVLAGSNMTICISTKTVLSGQIGNFRFLHLYG-----ETVAINITLN 299
OY 57 LNSGROSGDNVCHARDGSTLASCGLVGLPPEKPFNISCWSRNMKDLTCRTPG 112
Db 300 IPVS-ENSGSNVIFSTVDD--VGTGVFAGYPPVPOKLSETHDLMEIISWNP 352

RESULT 8
O46561 PRELIMINARY; PRT; 581 AA.
AC 046561;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98001468.
RA BIGNON C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,
DJIANE J.;
RN [1]
RT Long and short forms of the ovine prolactin receptor: cDNA cloning
RT and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents.
RN J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA BIGNON C., DJIANE J.;
RN Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041257; AAB96795.1;
DR PFAM: PF00041; fn3; 2.
RN [1]
RT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
FT SIGNAL 25 581 PROLACTIN RECEPTOR LONG FORM.
SQ SEQUENCE 581 AA; 65235 MW; 6792ATC7 CRC32;

Query Match 9.9%; Score 99.5; DB 6; Length 581;
Best Local Similarity 45.3%; Pred. No. 0.014;
Matches 24; Conservative 4; Mismatches 18; Indels 7; Gaps 2;

OY 76 SLIAGSCLVGLPPEKPFNISCWSRNMKDLTCRTPGAGETFLHTNYSLKXK 128
Db 20 SLINSGS-----PPEKPKLIKCRSPKEKFTTCWEPGADG--LPINITYLTYR 65

RESULT 9

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018880 ID 018880 PRELIMINARY; PRT; 296 AA.
 AC 018880;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR SHORT FORM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97375450.
 RA SCHUIER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal
 tissues";
 RL Endocrinology 138:3187-3194(1997).
 DR EMBL: AF027403; AAB83999.1; -
 DR PFAM: PF00041; fn3; 2.
 SQ SEQUENCE 296 AA; 33854 MW; 8B4CCD8 CRC32;

Query Match 9.7%; Score 98; DB 6; Length 296;
 Best Local Similarity 33.7%; Pred. No. 0.0088;
 Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;
 OY 42 SRLNLTALALANNGSGDNLNCHARGSLASCLYGLPPEKPFNISCWSRN 101
 DB 7 SRVFLFLFLVSLNG--QS-----PPEKPKLVKCRSPG 40
 OY 102 MMDLCRWTPGAGETFLHTNYSIKY 127
 DB 41 KETFTCWMEBGADG--LPTNYLITY 64

RESULT 10
 Q16354 ID 016354 PRELIMINARY; PRT; 206 AA.
 AC 016354;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95286597.
 RA FUH G., WELLS J.A.;
 RT "Prolactin receptor antagonists that inhibit the growth of breast
 cancer cell lines";
 RL J. Biol. Chem. 270:13133-13137(1995).
 DR EMBL: X78505; AAB34470.1; -
 DR PFAM: PF00041; fn3; 2.
 FT NON_TER 1
 SQ SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match 9.4%; Score 95; DB 4; Length 206;
 Best Local Similarity 51.2%; Pred. No. 0.012;
 Matches 21; Conservative 1; Mismatches 17; Indels 2; Gaps 1;
 OY 87 LPPEPFNISCWSRNKDLTCWTPGAGETFLHTNYSIKY 127
 DB 2 LPPEPFNISCWSRNKDLTCWTPGAGETFLHTNYSIKY 40

RESULT 11
 ID 064385 PRELIMINARY; PRT; 432 AA.
 AC 064385;
 SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NRL) (ETL2)
 DE (IL-11RALPHA) (IL11RA1).
 GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE: 95045367.
 RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
 RA GOUCH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
 RT "Cloning of a murine IL-11 receptor alpha-chain: requirement for
 gp130 for high affinity binding and signal transduction";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRYO;
 RA NEUBAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,
 RA GUENET J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6;
 RA GOSSLER A.;
 RL submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUBAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 mouse genome";
 RL Blochem J. 320:359-363(1996).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC CONTAINS ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CAAS2908.1; -
 DR EMBL: U14412; AAS3248.1; -
 DR EMBL: X94162; CA63873.1; -
 DR EMBL: X94163; CA63873.1; JOINED.
 DR MGD: MGI:107426; IL11RA1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; lg; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT CHAIN 1
 FT SIGNAL 23
 FT CHAIN 24
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT CARBOHYD 194 194
 SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

Query Match 9.3%; Score 93.5; DB 11; Length 432;
 Best Local Similarity 27.9%; Pred. No. 0.042;
 Matches 39; Conservative 19; Mismatches 63; Indels 19; Gaps 8;
 OY 21 PGATA-BGLYTFNGRRLPSELRLN--TSLA--TALANNGSROOSGNLYCHANDG 75
 DB 49 PGVAGTPVSWFRDGD-----SRLLOQPSDGLHRLVLAQVDSPE---GTVCQTLIDG 99

QY 76 SILAGSCLYVGPPEKPFENISCSNMKDLTCRWTGAGETFLHTNYSLSKYLRLVRS 135
 DB 100 VSGGWYTLKLGPPARP-EVSCQADVENSCTWSFGQ--VSLGPTRLTYSRKTLPGA 156
 QY 136 XHMGVPCPESLMPYPOGP 155
 DB 157 ESQRESPTSGP--WPCPODP 174

RESULT 12
 P70225 PRELIMINARY: PRT: 432 AA.

AC P70225 009074; (Tremblrel. 02, last sequence update)
 DT 01-FEB-1997 (Tremblrel. 02, last sequence update)
 DT 01-FEB-1997 (Tremblrel. 08, last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11BETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 OS IL11RA2 OR IL-11BETA.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1: TISSUE-TESTIS;
 RX MEDLINE; 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISEL C., HEATH J.K.,
 RA GOSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 RX MEDLINE; 96278810.
 RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 RX MEDLINE; 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT "Identification of a second murine interleukin-11 receptor
 RT alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997)
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.
 CC -1- CONTRAINS ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL; X94157; CAA63872.1; JOINED.
 DR EMBL; X94158; CAA63872.1; JOINED.
 DR EMBL; X94159; CAA63872.1; JOINED.
 DR EMBL; X94160; CAA63872.1; JOINED.
 DR EMBL; X94161; CAA63872.1; JOINED.
 DR EMBL; X98519; CAA67144.1; JOINED.
 DR EMBL; U69491; AAC5111.1; JOINED.
 DR MGD; MG1:109123; IL11RA2.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; fn3; 1.
 DR PFAM; PF00047; fn3; 2.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT CHAIN 1 23
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194

FT CONFLICT 200 200 S -> P (IN CAA63872).
 FT CONFLICT 384 384 V -> L (IN CAA63872).
 SQ SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

Query Match 9.3%; Score 93.5; DB 11; Length 432.
 Best Local Similarity 27.9%; Pred. No. 0.04;
 Matches 39; Conservative 19; Mismatches 63; Indels 19; Gaps 8;

QY 21 PGATA-EGLYWTFNGRRLPSELRLN--TSILA--LALANNGSRQSGDNLVGHARDG 75
 DB 49 PGVSAGTPVSWFRDGD-----SRLLGPDSSGLGRLVLAQVDSDE--GYVQOTLDG 99
 QY 76 SILAGSCLYVGPPEKPFENISCSNMKDLTCRWTGAGETFLHTNYSLSKYLRLVRS 135
 DB 100 VSGGWYTLKLGPPARP-EVSCQADVENSCTWSFGQ--VSLGPTRLTYSRKTLPGA 156
 QY 136 XHMGVPCPESLMPYPOGP 155
 DB 157 ESQRESPTSGP--WPCPODP 174

RESULT 13
 000343 PRELIMINARY: PRT: 440 AA.

AC 000343
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, last annotation update)
 DE INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
 DE (MUTANT INTERLEUKIN-6 RECEPTOR).
 GN IL6RA.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE; 90278354.
 RA SDGITA T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
 RA KISHIMOTO T.;
 RT "Functional murine interleukin 6 receptor with the intracisternal A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis.";
 RL J. Exp. Med. 171:2001-2009(1990).
 CC -1- THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
 CC IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE
 CC REGION CORRESPONDING TO ITS INTRACITOPLASMIC DOMAIN WAS REPLACED
 CC WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE
 CC (IAP) GENE, A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE
 CC ELEMENTS PRESENT IN THE GENOME OF MUS MUSCULUS.
 DR EMBL; X51976; CAA36238.1; JOINED.
 DR PIR; J10144; J10144.
 DR MGD; MG1:105304; IL6RA.
 DR PFAM; PF00041; fn3; 1.
 DR PFAM; PF00047; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT CHAIN 20 440
 FT DOMAIN 1 385
 FT DOMAIN 20 357
 FT DOMAIN 43 96
 FT TRANSMEM 358 385
 FT DOMAIN 386 440
 FT DOMAIN 386 440
 FT DISULFID 47 92
 FT CARBOHYD 32 32
 FT CARBOHYD 55 55
 FT CARBOHYD 150 150
 FT CARBOHYD 440 AA; 47901 MW; EB5E7B93 CRC32;

Query Match 9.2%; Score 93; DB 11; Length 440;

Best Local Similarity 29.3%; Pred. No. 0.048;
Matches 34; Conservative 22; Mismatches 38; Indels 22; Gaps 9;

QY 3 TLIGSSQATCSIHGDPGATAGC---LYWTFNGRLRPLSELSTLALANLING 59
DB 36 TSLGATVTLIC-----PGKEAGNWTIHVYSGSQ-----NEMTTGTIVLRVQL 84
QY 60 SROOSGNLVCHARDGSLAGSC-LYVGLPPEKPFNISCWERN-MKDLTCRWTPGA 113
DB 85 S--DTGDTL-CSLNDH--LVGTVPRLVDPPEED-KLSCFKNPLVNAICEMRPS 134

RESULT 14

Q99650 PRELIMINARY; PRT; 979 AA.
AC Q99650;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ONCOSATIN-M SPECIFIC RECEPTOR BETA SUBUNIT.
GN OSMB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MOSLEY B., DE IMOS C., FRIEND D., BOIANI N., THOMA B., PARK L.,
RA COSMAN D.;
RL J. Biol. Chem. 271:32635-32643(1996).
DR EMBL; U60805; AAC50946.1;
DR PFM; PFM0041; fn3; 4
SQ SEQUENCE 979 AA; 110508 MW; 965DE8BC CRC32;

Query Match

Best Local Similarity 33.3%; Pred. No. 0.14; Length 979;
Matches 21; Conservative 10; Mismatches 26; Indels 5; Gaps 2;

QY 56 NLNCSR--QOSGNLVCHARDGSI---LAGSCLYGLPPEKPFNISCWERNMDLTCRW 110
DB 199 NLNVPFIRNKGITNYCEASQGNVSEGMKGIIVLSVYLEPKDFSCETEDFTLHCTWD 258
QY 111 PG 112
DB 259 PG 260

RESULT 15

062121

AC Q62121; PRELIMINARY; PRT; 856 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PROTEIN TYROSINE KINASE.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94150990.
RA FUJIMOTO J., YAMAMOTO T.;
RT "btl, a mouse gene encoding a novel receptor-type protein-tyrosine
kinase, is preferentially expressed in the brain."
RL Oncogene 9:693-698(1994).
DR EMBL; D17393; BAA04216.1;
DR MGI; MGI:104294; TRO3.
DR PFM; PFM0041; fn3; 2.
DR PFM; PFM0047; fn3; 2.
DR PFM; PFM0069; PKinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

SQ SEQUENCE 856 AA; 93930 MW; 2DFBFC84 CRC32;

Query Match

Best Local Similarity 23.0%; Pred. No. 0.15; Length 856;
Matches 48; Conservative 24; Mismatches 62; Indels 75; Gaps 11;

QY 11 QATCSIHGDPGATAGELYWTFNGRLRPLSELSTLALANLINGSRQSGDVLVC 70
DB 143 QLSCEAVGPPEPT---LYW-WRG-----LTNKGPAPEPFVL-NVTGVTQRT--EFSC 169
QY 71 HARDGSLAGS---CLYGLPPEKPFNISCWERNMDLTCRWTPGAHGETFLH----- 121
DB 190 EARNIKGLATSRPAIVRLQAPPAPEFTVTTISYNASVAVWPGADGLALLHSCVQA 249
QY 121 -----TNSLKYLRLVRSXKHNKGVPHCEPSLMPYP 152
DB 250 HARGEMALAVVVPVPEFTCLNLAIPATVYSLRVR-----CANAL----- 291
QY 153 QGPGP--LHSLXDLGSHOSPRLSKIXCP 179
DB 291 -GPSPTRLGALSDKPS--AAELLRISMP 316

Search completed: September 16, 1999, 20:40:11
Job time: 5562 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:08:16 ; Search time 64.1 Seconds

(without alignments)
11.086 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MVLASSTSIHTMLLMLFHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 188963 segs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	166	1 P50161	Sequence encoded b
2	139	100.0	30	1 W10638	Murine IL-3 signal
3	139	100.0	30	1 W09823	Interleukin-3 sign
4	139	100.0	359	1 W56260	Construct containi
5	139	100.0	30	1 W55017	Murine IL3 signal
6	48	34.5	694	1 W31267	Drosophila frizze
7	46	33.1	116	1 R71911	Antiser specific pro
8	45	32.4	96	1 W46836	Bacillus thuringie
9	45	32.4	652	1 W30637	Human 7-transmembr
10	45	32.4	521	1 W30638	Partial human 7-tr
11	43	30.9	1268	1 W58774	Human breast cance
12	43	30.9	481	1 W55029	G-protein coupled
13	43	30.9	542	1 W55030	G-protein coupled
14	42	30.2	266	1 W71460	Protein encoded by
15	42	30.2	306	1 W90236	E. coli antitoxin
16	42	30.2	299	1 W90237	E. coli antitoxin
17	42	30.2	266	1 W90238	E. coli antitoxin
18	42	30.2	51	1 Y02760	Human secreted pro
19	42	30.2	55	1 Y12970	Protein sequence o
20	41.5	29.9	428	1 W63713	Human htk1 protein
21	41.5	29.9	427	1 W98017	Human calcium acti
22	41	29.5	315	1 R43568	Mouse MSH-R. Melan
23	41	29.5	709	1 R99801	CRIL-7 nerve prote
24	41	29.5	315	1 W37826	Mouse melanocyte s
25	41	29.5	315	1 W87864	Mouse melanocyte s
26	40	28.8	336	1 R28149	Sugar beet beta-1,
27	40	28.8	1276	1 R35199	Mouse multidrug re
28	40	28.8	30	1 R63638	Sheep erythropoiet
29	40	28.8	32	1 R65246	N-terminal of 48 k
30	40	28.8	308	1 R75757	BAV3 ORF2 product.
31	40	28.8	523	1 W78915	Bovine butyrophili
32	40	28.8	248	1 W94567	Mouse major periph
33	40	28.8	45	1 F12840	Amino acid sequenc
34	39.5	28.4	132	1 P70411	ORF 8 gene product
35	39.5	28.4	244	1 W29149	Human high affinity
36	39.5	28.4	244	1 W29149	Human beta subunit
37	39	28.1	1093	1 R05332	Human lymphotoxin
38	39	28.1	1093	1 R56879	Human myotonic dys
39	39	28.1	206	1 R82672	CD45 associating p
40	39	28.1	1989	1 R99640	Peripheral nervous
41	39	28.1	1977	1 R99641	Peripheral nervous
42	39	28.1	467	1 W00382	Bacillus cellulase
43	39	28.1	467	1 W05731	Cellulase. Cellula

ALIGNMENTS

44	39	28.1	81	1 W30082
45	39	28.1	164	1 W38705
Rat perlephrin, GDN				
S. pneumoniae phos				
RESULT	1			
ID	P50161	standard; Protein; 166 AA.		
AC	P50161			
DE	27-NOV-1991 (first entry)			
DE	Sequence encoded by cDNA clone exhibiting multi-lineage cellular			
DE	growth factor activity.			
OS	Mus musculus.			
PN	EP-138133-A.			
PD	24-APR-1985.			
PF	29-SEP-1984; US-539050.			
PR	04-OCT-1983; US-539050.			
PR	19-MAR-1984; US-539050.			
PA	(SCHE) SCHERING CORP.			
PA	(DNAX-) DNAX RES INST MOLEC.			
PI	Yokota T, Lee PD, Remick DM, Aral KI;			
DR	WPI: 85-100349/17.			
DR	N-PSDB; NS0199.			
PT	New poly(peptide)s having growth factor activities - are prepd.			
PT	by recombinant DNA procedures			
PS	Claim 5; Fig 1; 64pp; English.			
CC	The cDNA is derived from messenger RNA isolated from a mouse T-cell			
CC	line after activation with concanavalin A. The cDNA was cloned by			
CC	incorporation into a plasmid vector, which then transformed into			
CC	E.coli. The plasmid vector also contained DNA segments from the SV40			
CC	virus, permitting expression of the cDNA after transfection into a			
CC	mammalian host cell, such as monkey COS-7 cells. The polypeptide			
CC	includes a potential leader sequence of about 19 AAs.			
SO	Sequence 166 AA.			

Query Match 100.0%; Score 139; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MVLASSTSIHTMLLMLFHLGLQASIS 30
1 MVLASSTSIHTMLLMLFHLGLQASIS 30

RESULT 2
ID W10638 standard; Peptide; 30 AA.
AC W10638;
DE 23-JUN-1997 (first entry)
DE Murine IL-3 signal sequence.
DE LERK1 ligand for eph-related kinase; ERK; NLERK2;
DE receptor protein tyrosine kinase; cell proliferation;
DE cell differentiation; cell survival; nerve cell; interleukin-3;
DE IL-3; signal peptide; protein secretion.
OS Mus sp.
PN W09704091-A1.
PD 06-FEB-1997.
PF 19-JUL-1996; AU0460.
PR 20-JUL-1995; AU-004263.
PR 27-NOV-1995; AU-006847.
PR 22-DEC-1995; AU-007299.
PR 05-FEB-1996; AU-007890.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Nicola NA.
DR WPI: 97-133632/12.
PT Nucleic acid mol. encoding ligand for eph-related kinase - useful
PT for treatment of, pref. neuronal, cells to increase survival,
PT proliferation and differentiation
PS Example 3; Page 30; 71pp; English.

CC A peptide sequence (W10638) comprises the signal sequence of
 CC mouse interleukin-3 (IL-3). Mammalian expression vector pEF-BOS
 CC was engineered to contain DNA for the IL-3 signal sequence and for
 CC a FLAG epitope. PCR fragments (see also T60970-72) coding for
 CC mature or soluble NLERK2 (see also W10637), a novel ligand for
 CC eph kinase (LERK), were cloned into the vector to allow prodn. of
 CC recombinant NLERK2 proteins in transfected COS cells.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSSTSIHTMLLMFLHGLQASIS 30

RESULT 3
 W09823
 ID W09823 standard; Peptide; 30 AA.
 AC W09823;
 DT 15-JUL-1997 (first entry)
 DE Interleukin-3 signal peptide.
 KW Interleukin-3; IL-3; signal peptide; NR4; haemopoietin receptor;
 OS Mus sp.
 PN W09715663-A1.
 PD 01-MAY-1997.
 PE 23-OCT-1996; AU00668.
 PR 23-OCT-1995; AU-006135.
 PR 22-DEC-1995; AU-007276.
 PR 09-SEP-1996; AU-002208.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;
 DR WPI; 97-259018/23.
 PT DNA encoding animal haemopoietin receptor which interacts with
 PT Interleukin-13 - useful to treat asthma, allergy or condition
 PS exacerbated by IGE production
 PS Example 2; Page 56; 93pp; English.
 CC Using PCR, a derivative of novel haemopoietin receptor NR4 cDNA was
 CC generated which encoded the Interleukin-3 signal peptide (W09823)
 CC and an N-terminal FLAG epitope tag (W09824) preceding the mature
 CC coding region (Thr27-Pro424) of murine NR4 (see also W09821). The
 CC PCR product was cloned into the mammalian expression vector
 CC pEF-BOS.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSSTSIHTMLLMFLHGLQASIS 30

RESULT 4
 W56260
 ID W56260 standard; Protein; 359 AA.
 AC W56260;
 DT 16-SEP-1998 (first entry)
 DE Construct containing mature interleukin-13 binding protein.
 KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
 KW autoimmune disease; antibody; immunotherapy.
 OS Homo sapiens.
 PN W09810638-A1.
 PD 19-MAR-1998.
 PF 10-SEP-1997; AU00591.
 PR 27-FEB-1997; AU-005374.
 PR 10-SEP-1996; AU-002262.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
 DR WPI; 98-207062/18.
 DR N-PSDB; V22701.

PT New isolated interleukin-13 binding protein - used to develop
 PT products for therapy e.g. for allergic conditions such as asthma or
 PT for diagnosis or detection
 PS Example 14; Page 52-53; 69pp; English.
 CC The IL-13 binding protein and related therapeutic molecules can be used
 CC in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.
 SQ Sequence 359 AA;

Query Match 100.0%; Score 139; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSSTSIHTMLLMFLHGLQASIS 30

RESULT 5
 W55017
 ID W55017 standard; Protein; 30 AA.
 AC W55017;
 DT 28-SEP-1998 (first entry)
 DE Murine IL3 signal sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening;
 OS Mus sp.
 PN W09811225-A2.
 PD 19-MAR-1998.
 PE 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE) DZIELEMSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Meda W, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PS e.g. neuronal cells
 PS Claim 29(1); Page 54; 182pp; English.
 CC The mouse IL3 signal sequence was used to study the expression of mouse
 CC NR6.1. NR6.1 is a form of NR6 a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSSTSIHTMLLMFLHGLQASIS 30

RESULT 6

W31267 standard; Protein; 694 AA.

AC W31267;

DT 27-APR-1998 (first entry)

DE Drosophila frizzled-2 protein (Wnt receptor).

KW Wnt receptor; Drosophila frizzled-2 protein; Dfz2 gene; wingless receptor; Wg receptor; signal transduction; cancer; cell growth; cell proliferation.

OS Drosophila melanogaster.

Key location/Qualifiers

FT Misc_difference 268 /note= "encoded by CAC"

FT Misc_difference 269 /note= "encoded by CAC"

FT Misc_difference 269 /note= "encoded by TGC"

FT Misc_difference 348 /note= "encoded by TA (apparent 1 nucleotide deletion of codon)"

FT Misc_difference 488 /note= "encoded by TTA"

FT Misc_difference 632 /note= "encoded by CTG"

FT Misc_difference 633 /note= "encoded by GCG"

FT Misc_difference 671 /note= "encoded by GCG"

FT Misc_difference 671 /note= "encoded by CG (apparent 1 nucleotide deletion of codon)"

MO9739357-A1.

PD 23-OCT-1997.

PF 11-APR-1997; U06049.

PR 12-APR-1996; US-015307.

PA (UYXO) UNIV JOHNS HOPKINS.

PA (STRD) UNIV LELAND STARFORD JUNIOR.

PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J, Nusse R, Samos CH, Wang Y.

PI WPI; 97-526631/48.

DR N-PSDB; T89885.

PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

PS Claim 2; Page 23-25; 61pp; English.

CC This protein comprises the Drosophila frizzled-2 protein encoded by the Dfz2 gene (see T89885). It is a receptor for wingless (Wg) acting as a signal transducing molecule, and is an example of a Wnt receptor (WntR). Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted for CC compounds involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). CC Modulators identified by the claimed method are useful for CC treatment of diseases related to these conditions.

Sequence 694 AA;

Query Match 34.5%; Score 48; DB 1; Length 694;

Best Local Similarity 31.0%; Pred. No. 16;

Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MYLASSSTSIHMLLLMLLFLHGLQAST 29

DB 383 LTLRESSTGPHSCTLVFLTYFFGMASST 411

RESULT 7

R71911

ID R71911 standard; Protein; 116 AA.

AC R71911;

DT 22-NOV-1995 (first entry)

DE Anther specific protein.

KW Anther specific gene; Brassica napus; antisense RNA; Cruciferae;

KW Pollen formation; male sterile plant.

OS Brassica napus.

PN 307059573-A.

PD 07-MAR-1995.

PF 20-AUG-1993; 206459.

PR 20-AUG-1993; JP-206459.

PA (MITS) MITSUBISHI CORP.

PA (MITU) MITSUBISHI KASEI CORP.

DR WPI; 95-135897/18.

DR N-PSDB; Q87926.

PT A gene expressed specifically in anther(s) - used for the preparation of male sterile Cruciferae plants

PS Claim 1; Page 5; 6pp; Japanese.

CC This sequence is encoded by an anther specific gene derived from CC Brassica napus. This gene may be expressed as antisense RNA in a CC Cruciferae plant causing pollen formation to be modified. This is CC esp. useful in the production of male sterile plants.

Sequence 116 AA;

Query Match 33.1%; Score 46; DB 1; Length 116;

Best Local Similarity 38.5%; Pred. No. 4.3;

Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 5 SRTTSIHTMLLLMLLFLHGLQASTS 30

DB 2 SKITKYSFCLLLVFFLNSQFALS 27

RESULT 8

W46836

ID W46836 standard; Protein; 96 AA.

AC W46836;

DT 11-JUN-1998 (first entry)

DE Bacillus thuringiensis toxin designated 85N2.

KW Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm; Heliothis virescens; Helicoverpa zea.

OS Bacillus thuringiensis.

Key location/Qualifiers

FT Misc_difference 23 /label= unknown

FT Misc_difference 24 /note= "encoded by TAA"

FT Misc_difference 24 /label= unknown

FT Misc_difference 37 /note= "encoded by RAA"

FT Misc_difference 37 /label= unknown

FT Misc_difference 39 /note= "encoded by TAG"

FT Misc_difference 39 /label= unknown

FT Misc_difference 45 /note= "encoded by TAG"

FT Misc_difference 45 /label= unknown

FT Misc_difference 47 /note= "encoded by TAG"

FT Misc_difference 47 /label= unknown

FT Misc_difference 59 /note= "encoded by TGA"

FT Misc_difference 59 /label= unknown

FT Misc_difference 81 /note= "encoded by TAA"

FT Misc_difference 81 /label= unknown

FT Misc_difference 84 /note= "encoded by TAA"

FT Misc_difference 84 /label= unknown

FT Misc_difference 84 /note= "encoded by TAG"

FT Misc_difference 84 /label= unknown

MO9800546-A2.

PD 08-JAN-1998.

PF 01-JUL-1997; U11658.

PR 01-JUL-1996; US-674002.

PA (MYCO) MYCOGEN CORP.

PI Narva KE, Schnepf HE, Stockhoff BA, Walz M, Wicker C; WPI; 98-086971/08.

RESULT 11
 ID W58774 standard; Protein: 1268 AA.
 AC W58774 (first entry)
 DE Human breast cancer gene CH1-9a11-2 protein fragment #1.
 KW therapeutic; screening; diagnostic;
 OS Homo sapiens.
 PN W09738085-A2.
 PD 16-OCT-1997.
 PF 09-APR-1997; U059330.
 PR 10-JUL-1996; US-678280.
 PR 09-APR-1996; US-015167.
 PR 05-JUN-1996; WO-009286.
 PR 06-JUN-1996; US-019202.
 PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
 PI Chen L, Smith H;
 DR WPI: 97-512705/47.
 DR N-PSDB: V10696.
 PT Breast cancer genes - used to develop products to design or screen
 PT diagnostic reagents or therapeutic compounds
 PS Claim 17; Fig 24; 118bp; English.
 CC W58774-W58804 are translated protein fragments from the novel human
 CC breast cancer gene, CH9-2a11-2 isolated from a 3.5 kb DNA fragment.
 CC This fragment can be used for identifying genes and gene products that
 CC are intimately related to malignant transformation or maintenance of the
 CC malignant properties of cancer cells. It can also be used to design or
 CC screen diagnostic reagents or therapeutic compounds. Kits are included
 CC within the scope of the invention.
 SO Sequence 1268 AA;

Query Match 30.9%; Score 43; DB 1; Length 1268;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSTSIHTMLLMFHLGL 25
 DB 17 AIALRTGIIALLRLMLGL 38

RESULT 12
 ID W55029 standard; Protein: 481 AA.
 AC W55029;
 DT 17-SEP-1998 (first entry)
 DE G-protein coupled receptor; short form.
 KW G-protein coupled receptor; gene therapy; abnormality detection;
 OS Homo sapiens.
 PN EP-845529-A2.
 PD 03-JUN-1998.
 PF 27-OCT-1997; 308562.
 PR 29-OCT-1996; JP-286823.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Fukusumi S, Hinuma S, Kawamata Y;
 DR WPI: 98-288746/26.
 DR N-PSDB: V27174.
 PT New human G-protein coupled receptor protein - and corresponding
 PT DNA, ligands, antibodies, etc
 PS Claim 1; Page 42-44; 65pp; English.
 CC This sequence represents a human G-protein coupled receptor of the
 CC invention. The protein or cells expressing the DNA encoding it can be
 CC used to screen for agonists or antagonists of the receptor, which can be
 CC used as drugs for treating various diseases (none disclosed). The DNA can
 CC also be used for practice drug design based on comparisons with
 CC structurally analogous ligands and receptors. DNA encoding the protein
 CC can be used for gene therapy for diseases caused by a deficiency of the
 CC receptor. The DNA can also be used to detect abnormalities in the gene
 CC encoding the receptor. The protein or fragment can be used to determine
 CC levels of receptor ligands in vivo. The antibody can be used in assays to
 CC detect the protein.

SO Sequence 481 AA;

Query Match 30.9%; Score 43; DB 1; Length 481;
 Best Local Similarity 28.6%; Pred. No. 61;
 Matches 8; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY 3 LASSTSIHTMLLMFHLGLQASIS 30
 DB 123 VTSSYSAYAILMLALYFVAVGIVGNTLS 150

RESULT 13
 ID W55030 standard; Protein: 542 AA.
 AC W55030;
 DT 17-SEP-1998 (first entry)
 DE G-protein coupled receptor; long form.
 KW G-protein coupled receptor; gene therapy; abnormality detection;
 OS Homo sapiens.
 PN EP-845529-A2.
 PD 03-JUN-1998.
 PF 27-OCT-1997; 308562.
 PR 29-OCT-1996; JP-286823.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Fukusumi S, Hinuma S, Kawamata Y;
 DR WPI: 98-288746/26.
 DR N-PSDB: V27175.
 PT New human G-protein coupled receptor protein - and corresponding
 PT DNA, ligands, antibodies, etc
 PS Claim 2; Page 45-47; 65pp; English.
 CC This sequence represents a human G-protein coupled receptor of the
 CC invention. The protein or cells expressing the DNA encoding it can be
 CC used to screen for agonists or antagonists of the receptor, which can be
 CC used as drugs for treating various diseases (none disclosed). The DNA can
 CC also be used for practice drug design based on comparisons with
 CC structurally analogous ligands and receptors. DNA encoding the protein
 CC can be used for gene therapy for diseases caused by a deficiency of the
 CC receptor. The DNA can also be used to detect abnormalities in the gene
 CC encoding the receptor. The protein or fragment can be used to determine
 CC levels of receptor ligands in vivo. The antibody can be used in assays to
 CC detect the protein.
 SO Sequence 542 AA;

Query Match 30.9%; Score 43; DB 1; Length 542;
 Best Local Similarity 28.6%; Pred. No. 70;
 Matches 8; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY 3 LASSTSIHTMLLMFHLGLQASIS 30
 DB 184 VTSSYSAYAILMLALYFVAVGIVGNTLS 211

RESULT 14
 ID W71460 standard; Protein: 266 AA.
 AC W71460;
 DT 07-DEC-1998 (first entry)
 DE Protein encoded by ORF 266.
 KW Multiple antibiotic resistance operon; mar; antisense;
 OS Escherichia coli.
 PN US5817793-A.
 PD 06-OCT-1998.
 PF 08-AUG-1994; 225480.
 PR 08-APR-1994; US-225480.
 PR 28-AUG-1992; US-938085.
 PA (TUFT) TUFTS COLLEGE.
 PI Levy SB;
 DR WPI: 98-556472/47.
 DR N-PSDB: V60383.

PT DNA encoding activator of multiple antibiotic resistance operon -
 PT and anti-sense molecule for lowering antibiotic resistance of
 PT bacteria
 PS Disclosure: Columns 35-38; 22pp; English.
 CC The present sequence represents the protein encoded by open
 CC reading frame (ORF) 266 of Escherichia coli multiple antibiotic
 CC resistance (mar) operon. Antisense molecules directed against the
 CC mar operon can be used to lower the resistance of bacteria to
 CC antibiotics.
 SQ Sequence 266 AA;

Query Match 30.2%; Score 42; DB 1; Length 266;
 Best Local Similarity 30.3%; Pred. No. 44;
 Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MYLASTTSHTMLL---LMLFHLGLQASI 29
 DB 161 LILDGSAFMHSLVTDWTLTSLMYLAFVATI 193

RESULT 15

W90236
 ID W90236 standard; protein; 306 AA.
 AC W90236;
 DT 30-MAR-1999 (first entry)
 DE E. coli antibiotic efflux protein fragment #2.
 KW Antibiotic efflux gene; fermentation; L-cysteine; L-cystine; toxic;
 KW N-acetyl-serine; thiazolidine derivative; cellular clearance; secretion.
 OS Escherichia coli.
 PN EP-885962-A1.
 PD 23-DEC-1998.
 PF 22-MAY-1998; 109269.
 PR 19-JUN-1997; DE-026083.
 PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
 PI Leinfelder W, Winterhalter C;
 DR WPI; 99-047559/05.
 PT Microbial strain over-expressing antibiotic efflux gene - for
 PT producing L-cysteine, L-cystine, N-acetyl-serine and/or thiazolidine
 PT derivatives
 PS Claim 5; Page 16-17; 33pp; German.
 CC This sequence is a fragment of an antibiotic efflux protein from
 CC Escherichia coli strain K12 which is used as a method resulting in a
 CC novel microbial strain which is suitable for the fermentative production
 CC of L-cysteine, L-cystine, N-acetyl-serine and/or thiazolidine derivatives
 CC and over-expresses at least one gene coding for a protein that mediates
 CC cellular clearance of antibiotics or other substances that are toxic for
 CC the microorganism. A process is described for producing L-cysteine, in
 CC which intracellularly produced L-cysteine reacts with an intracellular
 CC ketone or aldehyde in a microorganism to form a thiazolidine derivative.
 CC The thiazolidine derivative is secreted from the microorganism by
 CC means of a protein that mediates cellular clearance of antibiotics or
 CC other substances that are toxic for the microorganism, and optionally
 CC after separating the thiazolidine derivative. L-cysteine is recovered by
 CC equilibrium displacement of the reaction equilibrium between L-cysteine
 CC and the thiazolidine derivative in the direction of L-cysteine.
 SQ Sequence 306 AA;

Query Match 30.2%; Score 42; DB 1; Length 306;
 Best Local Similarity 30.3%; Pred. No. 52;
 Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MYLASTTSHTMLL---LMLFHLGLQASI 29
 DB 201 LILDGSAFMHSLVTDWTLTSLMYLAFVATI 233

Search completed: September 17, 1999, 03:08:19
 Job time: 310 sec

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:11 ; Search time 53.94 Seconds

(without alignments)
5.489 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MWLASSTSIHTMLLMFHLGLASIS 30

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database : Issued Patents, AA:*
1: /cgn2-6/ptodata/2/1aa/5A.CONB.pep.*
2: /cgn2-6/ptodata/2/1aa/5B.CONB.pep.*
3: /cgn2-6/ptodata/2/1aa/PTUS9.CONB.pep.*
4: /cgn2-6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	30.9	30	4	5304637-4
2	42	30.2	396	1	US-08-208-007A-13
3	42	30.2	266	1	US-08-225-480-7
4	41	29.5	315	1	US-07-866-979-4
5	41	29.5	315	2	US-08-466-906B-4
6	40	28.8	308	2	US-08-164-292B-18
7	40	28.8	22	2	US-08-446-875-6
8	40	28.8	581	2	US-08-724-334A-3
9	40	28.8	30	3	PCT-US94-04361-31
10	39.5	28.4	244	2	US-07-869-933-32
11	39.5	28.4	244	2	US-08-201-879A-3
12	39	28.1	206	1	US-08-197-793-2
13	39	28.1	206	2	US-08-636-176-2
14	39	28.1	467	2	US-08-727-348-2
15	39	28.1	206	3	PCT-US95-01618-2
16	38.5	27.7	1873	1	US-08-435-675B-4
17	38.5	27.7	1873	1	US-08-336-257A-7
18	38.5	27.7	954	2	US-08-749-169A-3
19	38	27.3	408	1	US-07-916-901-2
20	38	27.3	78	1	US-07-778-413E-12
21	38	27.3	353	1	US-08-118-270-45
22	38	27.3	78	1	US-08-340-102-12
23	38	27.3	402	1	US-08-444-734A-6
24	38	27.3	114	1	US-08-353-324A-3
25	38	27.3	408	1	US-08-351-473B-3
26	38	27.3	78	1	US-08-330-163-8
27	38	27.3	93	1	US-08-480-449-2
28	38	27.3	402	1	US-08-087-772A-15
29	38	27.3	111	1	US-08-417-460-4
30	38	27.3	879	1	US-08-554-612C-1
31	38	27.3	78	2	US-08-482-111-8
32	38	27.3	78	2	US-08-436-420-32
33	38	27.3	114	2	US-08-862-607-3
34	38	27.3	419	2	US-08-270-581-2
35	38	27.3	148	2	US-08-791-924-3
36	38	27.3	114	2	US-08-468-819-4
37	38	27.3	400	2	US-08-103-170-9
38	38	27.3	24	2	US-08-103-170-30
39	38	27.3	353	3	PCT-US93-08528-45

40	38	27.3	93	3	PCT-US95-07294-2	Sequence 2, Appl
41	38	27.3	114	3	PCT-US95-16144-3	Sequence 3, Appl
42	37.5	27.0	1968	1	US-07-745-206A-7	Sequence 7, Appl
43	37.5	27.0	426	1	US-08-455-550-21	Sequence 21, Appl
44	37.5	27.0	1968	2	US-08-455-543A-45	Sequence 45, Appl
45	37.5	27.0	1968	2	US-08-223-305C-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
5304637-4
Patent No. 5304637
APPLICANT: DORSSERS, LAMBERTUS C.J.; WAGEMAKER, GERARD; VOS, YONNE J.; VAN LEEN, ROBERT M.; PERSSON, MARIA L.N.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF HUMAN INTERLEUKIN-3 AND KOTELINS THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/494,182
FILING DATE: 13-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 249,184
FILING DATE: 16-AUG-1988
SEQ ID NO: 4
LENGTH: 139
5304637-4

Query Match 30.9%; Score 43; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLASSTSI 10
DB 1 MWLASSTSI 10

RESULT 2
US-08-208-007A-13
Sequence 13, Application US/08208007A
Patent No. 5501969
GENERAL INFORMATION:
APPLICANT: HASTINGS, ET AL.
TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BROOKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,007A
FILING DATE: March 8, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5501969e
FILING DATE: No. 5501969e
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: LINEAR
MOLECULE TYPE: PROTEIN
US-08-208-007A-13

Query Match 30.2% Score 42; DB 1; Length 396;
Best Local Similarity 69.2% Pred. No. 46;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 TWLILMLFHG 24
Db 3 TLLLLVLELG 15

RESULT 3
US-08-225-480-7
Sequence 7, Application US/08225480
Patent No. 3817793

GENERAL INFORMATION:
APPLICANT: LEVY, STUART B.
TITLE OF INVENTION: MULTIPLE ANTIBIOTIC RESISTANCE OPERON
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,085
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: T0359/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-225-480-7

Query Match 30.2% Score 42; DB 2; Length 266;
Best Local Similarity 30.3% Pred. No. 30;
Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MWLASSSTSIHTMLL-----LMLFHGLQAST 29
Db 161 LIIDGSKTMIHSVLTIDMTTILSLMIAFVATI 193

RESULT 4
US-07-866-979-4
Sequence 4, Application US/07866979
Patent No. 5532347

GENERAL INFORMATION:
APPLICANT: Cone, Roger D
TITLE OF INVENTION: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,979
FILING DATE: 19920410
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-866-979-4

Query Match 29.5% Score 41; DB 1; Length 315;
Best Local Similarity 41.4% Pred. No. 50;
Matches 12; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

OY 3 LASSTSI---HTMLLMLFHGLQA 27
Db 171 IVSSTLFTYKHTAVLCLVTFPLAMLA 199

RESULT 5
US-08-466-906B-4

Sequence 4, Application US/08466906B
Patent No. 5849871

GENERAL INFORMATION:
APPLICANT: Cone, Roger D
TITLE OF INVENTION: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,906B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-906B-4

Query Match 29.5%; Score 41; DB 2; Length 315;
Best Local Similarity 41.4%; Pred. No. 50;
Matches 12; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

OY 3 LASSTST---HTMLLLMLFLHGLQA 27
DB 171 IVSSLTFTTYKHYKAVLCLVTFELMMA 199

RESULT 6
US-08-164-292B-18
Sequence 18; Application US/08164292B
Patent No. 5820868
GENERAL INFORMATION:
APPLICANT: MITTAL, SURESH K.
APPLICANT: GRAHAM, FRANK L.
APPLICANT: PREVEC, LUDVIG
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 345 California Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104-2675
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,292B
FILING DATE: 09-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 29310-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000
TELEFAX: (415) 677-7522
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-164-292B-18

Query Match 28.8%; Score 40; DB 2; Length 308;
Best Local Similarity 45.5%; Pred. No. 68;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 4 ASSTSTHTMLLLMLFLHGL 25
DB 19 ASSPTSMKGFLLIRSLVHCP 40

RESULT 7
US-08-446-875-6
Sequence 6; Application US/08446875
Patent No. 5858751
GENERAL INFORMATION:
APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Keim, Sorge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihadszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 277-1297
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: porcine
FEATURE:
NAME/KEY: Region
LOCATION: 1..22
OTHER INFORMATION: /label=48KDa
OTHER INFORMATION: /note="amino terminal amino acid sequence of the
OTHER INFORMATION: porcine 48 KDa Gal Beta1,3 GalNAc alpha 2,3
OTHER INFORMATION: sialyltransferase"
NAME/KEY: Domain
LOCATION: 5..20
OTHER INFORMATION: /note="putative signal-anchor
OTHER INFORMATION: domain"

STATE: VA
COUNTRY: USA

STATE: VA
COUNTRY: U

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)863-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI beta subunit
US-07-869-933-32

Query Match

28.4%; Score 39.5; DB 2; Length 244;

Best Local Similarity 39.3%; Pred. No. 62; Mismatches 7; Indels 3; Gaps 1;

Matches 11; Conservative 7;

QY 3 LASTSTSHMTLLMLLPHLGLOASIS 30
DB 174 MASFSTEIVVMFLRI--LGISAVS 198

RESULT 11

US-08-201-879A-3

Sequence 3, Application US/08201879A
Patent No. 5807988

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre
APPLICANT: JOUVIN, Marie-Helene
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,879A
FILING DATE: 24-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)863-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI beta subunit
US-07-869-933-32

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/234/NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-201-879A-3

Query Match

28.4%; Score 39.5; DB 2; Length 244;

Best Local Similarity 39.3%; Pred. No. 62;

Matches 11; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

Matches 11; Conservative 7;

QY 3 LASTSTSHMTLLMLLPHLGLOASIS 30
DB 174 MASFSTEIVVMFLRI--LGISAVS 198

RESULT 12

US-08-197-793-2

Sequence 2, Application US/08197793
Patent No. 5510461

GENERAL INFORMATION:

APPLICANT: Meuer, S.
APPLICANT: Schraven, B.
APPLICANT: Schoenhaut, D.
TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,793
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BFI-006CNCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-197-793-2

Query Match

28.1%; Score 39; DB 1; Length 206;

Oy 4 ASSTSIHTMLLMLFHLGL 25
: | | : : | | | | | |
Db 31 SSSVIV--LLELLELLLATGL 50

Search completed: September 16, 1999, 20:41:12
Job time: 5441 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:11 ; Search time 49.27 Seconds
(without alignments)
24.395 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MYLASSITSIHTMLLIMFLHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR-60:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	139	100.0	166	1	ICMS3	Interleukin-3 prec
2	96	69.1	166	1	S07369	Interleukin-3 prec
3	96	69.1	166	1	JC6566	Interleukin-3 beta
4	52	37.4	677	2	S33664	flagella-associate
5	50.5	36.3	437	2	S34959	NADH dehydrogenase
6	48.5	34.9	443	2	F30010	NADH dehydrogenase
7	48	34.5	654	2	S71786	wingless receptor
8	47	33.8	244	2	B69318	nitrate reductase,
9	47	33.8	160	2	B71171	hypothetical prote
10	46	33.1	2073	1	BWASBE	b1me protein Eme
11	46	33.1	451	1	S3612	isocitrate dehydro
12	46	33.1	342	2	F69261	conserved hypochet
13	46	33.1	633	2	AS4366	sodium/phosphate c
14	45	32.4	309	1	S34198	IGE Fc receptor II
15	45	32.4	574	2	S58992	NADH dehydrogenase
16	45	32.4	279	2	E64109	dimethylsulfoxide
17	44	31.7	142	1	S42722	interleukin-3 prec
18	44	31.7	142	1	S42721	interleukin-3 prec
19	44	31.7	130	2	S55171	hypothetical prote
20	43.5	30.9	323	2	A70029	hypothetical prote
21	43	30.9	436	2	S77639	hypothetical prote
22	43	30.9	357	2	H64855	exopolysaccharide
23	43	30.9	493	2	S73890	probable membrane
24	43	30.9	114	2	G71161	hypothetical prote
25	43	30.9	408	2	E70380	Na+/H+-exchanging
26	42.5	30.6	115	2	S26158	NADH dehydrogenase
27	42.5	30.6	115	2	S41842	NADH dehydrogenase
28	42	30.2	500	2	S16872	cytochrome P450 2D
29	42	30.2	396	2	A34401	cathepsin E (EC 3.
30	42	30.2	182	2	S17723	H+-transporting AT
31	42	30.2	70	2	S00408	legumin Ii beta ch
32	42	30.2	266	2	H64907	probable membrane
33	42	30.2	598	2	S75728	hypothetical prote
34	41.5	29.9	357	2	A45619	ubiquitin--cytochr
35	41.5	29.9	631	2	H70154	probable abc trans
36	41.5	29.9	119	2	S40617	NADH dehydrogenase
37	41	29.5	469	1	RGBKCP	nitrogen regulatio
38	41	29.5	468	1	RGBKCP	nitrogen regulatio
39	41	29.5	328	1	QOBEF6	HVLA protein - hu

40	41	29.5	500	2	J00258	cytochrome P450 1s
41	41	29.5	434	2	J00451	cytochrome P450 2C
42	41	29.5	117	2	S58996	NADH dehydrogenase
43	41	29.5	1099	2	A55405	adenylate cyclase
44	41	29.5	118	2	S16762	gonadotropin alpha
45	41	29.5	118	2	A60626	glycoprotein hormo

ALIGNMENTS

RESULT 1

ICMS3

Interleukin-3 precursor - mouse

N/Alternate names: hematopoietic growth factor; IL-3; mast-cell growth factor; multi-C/Species: Mus musculus (house mouse)

C/Date: 18-Apr-1984 #sequence, revision 18-Apr-1984 #text, change 05-Sep-1997

C/Accession: A25481, A01851, A21022, I59024, I53994

R/Campbell, H.D.; Ymer, S.; Fung, M.C.; Young, I.G.

Eur. J. Biochem. 150, 297-304, 1985

A/Title: Cloning and nucleotide sequence of the murine interleukin-3 gene.

A/Reference number: A25481; M01D:85257655

A/Accession: A25481

A/Molecule type: DNA

A/Residues: 1-166 <CAM>

A/Cross-references: GB:X07372; NID:952673; PID:952674

R/Fung, M.C.; Hapel, A.J.; Ymer, S.; Cohen, D.R.; Johnson, R.M.; Campbell, H.D.; Yoon

Nature 307, 233-237, 1984

A/Title: Molecular cloning of cDNA for murine interleukin-3.

A/Reference number: A01851; M01D:84117447

A/Accession: A01851

A/Molecule type: mRNA

A/Residues: 1-166 <FUN>

A/Cross-references: GB:K01850; NID:9198334; PID:9309405

R/Experimental source: myelomonocytic leukemia cell line WEHI-3

R/Yokota, T.; Lee, F.; Renwick, D.; Hall, C.; Araki, N.; Mosmann, T.; Nabel, G.; Canto

Proc. Natl. Acad. Sci. U.S.A. 81, 1070-1074, 1984

A/Title: Isolation and characterization of a mouse cDNA clone that expresses mast-cell

A/Reference number: A21022; M01D:84144843

A/Accession: A21022

A/Molecule type: mRNA

A/Residues: 1-145, 'A', 147-166 <YOK>

A/Cross-references: GB:K01668; NID:9199083; PID:9387421

R/Knepper, T.P.; Ardognet, B.; Schreurs, J.; Delnizer, M.L.

Biochemistry 31, 11651-11659, 1992

A/Title: Determination of the glycosylation patterns, disulfide linkages, and protein

A/Reference number: A38860; M01D:9305774

A/Accession: A38860

A/Contents: annotation

A/Note: disulfide bonds were shown between Cys residues at 43 and either 106 or 105, enesis; the disulfide bond 105-166 is not conserved in most orthologs

R/Miyake, S.; Yokota, T.; Lee, F.; Araki, K.

Proc. Natl. Acad. Sci. U.S.A. 82, 316-320, 1985

A/Title: Structure of the chromosome gene for murine interleukin 3.

A/Reference number: I59024; M01D:85113192

A/Accession: I59024

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-166 <RES>

A/Cross-references: GB:K03233; NID:9198338; PID:9387385

R/Todoroki, K.; Yamamoto, A.; Amanuma, H.; Ikawa, Y.

Gene 39, 103-107, 1985

A/Title: Isolation and characterization of a genomic DDD mouse interleukin-3 gene.

A/Reference number: I53994; M01D:86083183

A/Accession: I53994

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-70, 'R', 72-166 <RE2>

A/Cross-references: GB:M20128; NID:9198384; PID:9387387

C/Comment: This glycoprotein, produced by bone marrow cells, by mitogen or antigen-act

C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; mitogen; monomer; T-cell
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-166/Product: interleukin-3 #status predicted <MAT>
 F:42-113/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:43-106,105-166/Disulfide bonds: #status experimental

Query Match 100.0%; Score 139; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLASSTSTHTMLLMLFHLGLQASIS 30
 DB 1 MVLASSTSTHTMLLMLFHLGLQASIS 30

RESULT 2

507369 Interleukin-3 precursor - rat

N:Alternate names: hematopoietic growth factor; IL-3; mast-cell growth factor; multi-CSF

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1991 #sequence_revision 15-Nov-1996 #text_change 15-Nov-1996

C:Accession: S07369

R:Cohen, D.R.; Hapel, A.J.; Young, I.G.
 Nucleic Acids Res. 14, 3641-3658, 1986

A:Title: Cloning and expression of the rat interleukin-3 gene.

A:Reference number: S07369; MUID:86232609

A:Accession: S07369

A:Molecule type: DNA

A:Residues: 1-166 <COH>

A:Cross-references: EMBL:X03846

A:Note: this sequence, as reported, contains significant sequence differences from some

errata of hematopoietic cells.

C:Genetics: 55/3; 69/3; 101/3; 115/3

C:Superfamily: Interleukin-3

C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; mitogen; monomer; T-cell

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-166/Product: interleukin-3 #status predicted <MAT>

F:40-70/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:105-166/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 82.1%; Score 96; DB 1; Length 166;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MVLASSTSTHTMLLMLFHLGLQAS 28

DB 1 MVLASSTSTHTMLLMLFHLGLQAS 28

RESULT 3

507369 Interleukin-3 beta protein - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 29-Jan-1999

C:Accession: J06566

R:Sandt, M.C.; van Someren, G.D.; van der Velde, I.; van Bekkum, D.W.; Valerio, D.; Not

Gene 211, 151-158, 1998

A:Title: Cloning, biological characterization and high-level expression of rat Interleuk

A:Reference number: J06566

A:Accession: J06566

A:Molecule type: mRNA

A:Residues: 1-168 <ESA>

A:Cross-references: GB:U81492

C:Comment: This protein is a hematopoietic growth factor with a wide range of target cel

C:Superfamily: Interleukin-3

C:Keywords: growth factor

Query Match 69.1%; Score 96; DB 2; Length 166;

Best Local Similarity 82.1%; Pred. No. 5.2e-06;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MVLASSTSTHTMLLMLFHLGLQAS 28
 DB 1 MVLASSTSTHTMLLMLFHLGLQAS 28

RESULT 4

533664 flagella-associated protein flha - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Sep-1998

C:Accession: S33664; C69623; S18993

R:Carpenter, P.B.; Ordal, G.W.

Mol. Microbiol. 7, 735-743, 1993

A:Title: Bacillus subtilis flha: a flagellar protein related to a new family of sig

A:Reference number: S33664; MUID:93225816

A:Accession: S33664

A:Molecule type: DNA

A:Residues: 1-677 <CAR>

A:Cross-references: EMBL:X63698; NID:939916; PID:939917

R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; B

C: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.

A: Erlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Ga

lech, J.; Harwood, C.R.; Hensut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma

Y, M.; Ogawa, K.; Ogilwara, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scen

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S

aeuchl, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tostato, V.; Uchly

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshic

A:Authors: Yoshikawa, H.F.; Zumschein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil

A:Reference number: A69580; MUID:98044033

A:Accession: C69623

A:Molecule type: DNA

A:Residues: 1-677 <KUN>

A:Cross-references: GB:Z99112; GB:AL009126; NID:92633902; PID:el185230; PID:g2634011

A:Experimental source: strain 168

C:Genetics:

A:Gene: flha

C:Superfamily: regulatory protein lcrd

C:Keywords: membrane protein

Query Match 37.4%; Score 52; DB 2; Length 677;
 Best Local Similarity 65.0%; Pred. No. 11;
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 9 SHTMLLMLFHLGLQAS 28
 DB 56 SHTMLLMLFHLGLQAS 75

RESULT 5

534959 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Crithidia oncopelti mitochond

C:Species: mitochondria Crithidia oncopelti

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997

C:Accession: S34959

R:Malov, D.A.; Horvath, A.; Guang II, K.; Kolesnikov, A.A.

submitted to the EMBL Data Library, October 1990

A:Reference number: S34958

A:Accession: S34959

A:Molecule type: DNA

A:Residues: 1-437 <NAS>

A:Cross-references: EMBL:X56015; NID:913879; PID:912881

C:Genetics:

A:Gene: NDA

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 36.3%; Score 50.5; DB 2; Length 437;

Best Local Similarity 34.4%; Pred. No. 12;

Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 1 MYLASSSTSIHTMLLMFHR--LGLQASI 29

Db 131 LVVSSISIMCIIICIIIFHFNLMQSF 162

RESULT 6

F30010

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Leishmania tarentolae mitochondrion

C:Species: Leishmania tarentolae

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Aug-1997

C:Accession: F30010

R:de la Cruz, V.F.; Neckelmann, N.; Simpson, L.

J. Biol. Chem. 259, 15136-15147, 1984

A:Title: Sequences of six genes and several open reading frames in the kinetoplast maxic

A:Reference number: A2848; M01D:85079995

A:Accession: F30010

A:Molecule type: DNA

A:Residues: 1-443

A:Cross-references: GB:M10126

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 34.9%; Score 48.5; DB 2; Length 443;

Best Local Similarity 34.4%; Pred. No. 22;

Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 1 MYLASSSTSIHTMLLMFHR--LGLQASI 29

Db 137 LVVSSISIMCIIICIIIFHFNLMQSF 168

RESULT 7

F30010

NADH dehydrogenase precursor fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Jul-1998

C:Accession: S71786; S78444

R:Bhanot, P.; Bink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Meeke, J.P.; Andrew,

ature 362, 225-230, 1996

A:Title: A new member of the frizzled family from Drosophila functions as a wingless rec

A:Reference number: S71786

A:Accession: S71786

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-694 <BNA>

A:Cross-references: EMBL:065589

A:Note: mRNA was also sequenced

A:Bhanot, P.; Wang, Y.; Nathans, J.

A:Submitted to the EMBL Data Library, July 1996

A:Reference number: S78444

A:Accession: S78444

A:Molecule type: DNA

A:Residues: 1-416, 'T', 418-694 <BNA>

A:Cross-references: EMBL:065589; NID:g1518050; PID:g1518051

A:Genetics:

A:Gene: dfz2

Query Match 34.5%; Score 48; DB 2; Length 694;

Best Local Similarity 31.0%; Pred. No. 37;

Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MYLASSSTSIHTMLLMFHRIGLQASI 29

Db 383 LLNRSSTGPHSCVFLVLYFFGMAS 411

RESULT 8

B69318

nitrate reductase, gamma subunit (narI) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998

C:Accession: B69318

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Wiese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; M01D:98049343

A:Accession: B69318

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-244 <KLE>

A:Cross-references: GB:AE001066; GB:AE000782; NID:g2689389; PID:g2650071; TIGR:AF0546

Query Match 33.8%; Score 47; DB 2; Length 244;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 16 LLMFHRIGLQASIS 30

Db 89 ILNMFHRIGLQASIS 103

RESULT 9

B71171

hypothetical protein PH0566 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

C:Accession: B71171

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; M01D:98344137

A:Accession: B71171

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-160 <KAW>

A:Cross-references: GB:AP000002; NID:g3236129; PID:d1030598; PID:g3256972

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenB

C:Genetics:

A:Gene: PH0566

Query Match 33.8%; Score 47; DB 2; Length 160;

Best Local Similarity 45.5%; Pred. No. 14;

Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MYLASSSTSIHTMLLMFHR 22

Db 134 LALASSEGVFLILALISIFH 155

RESULT 10

BMASBE

hypothetical protein PH0566 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

C:Accession: B71171

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; M01D:98344137

A:Accession: B71171

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-160 <KAW>

A:Cross-references: GB:AP000002; NID:g3236129; PID:d1030598; PID:g3256972

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenB

C:Genetics:

A:Gene: PH0566

b1me protein - *Emicellula nidulans*
 C:Species: *Emicellula nidulans*, *Aspergillus nidulans*
 C>Date: 31-Dec-1991 #sequence, revision 31-Dec-1991 #text, change 24-Oct-1997
 C:Accession: A37879
 R:Engle, D.B.; Osman, S.A.; Osman, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R.
 J. Biol. Chem. 265, 16132-16137, 1990
 A:Title: A negative regulator of mitosis in *Aspergillus* is a putative membrane-spanning
 A:Reference number: A37879; MUID:90375468
 A:Accession: A37879
 A:Molecule type: mRNA
 A:Residues: 1-2073 <ENG>
 A:Cross-references: GB:M59705; GB:J05607; NID:9168026; PID:9168027
 A>Note: In addition to three predicted transmembrane domains, there are several potential
 Asen kinase and one sequence that resembles a nuclear localization signal
 C:Comment: This protein is part of a regulatory pathway that includes the nma protein X
 ter mitosis and prevent them from leaving mitosis.
 C:Genetics:
 A:Gene: b1me
 C:Superfamily: b1me protein
 C:Keywords: cell cycle control; mitosis; transmembrane protein
 F:1623-1643/Domain: transmembrane #status predicted <TM1>
 F:1685-1703/Domain: transmembrane #status predicted <TM2>
 F:1746-1764/Domain: transmembrane #status predicted <TM3>

Query Match 33.1%; Score 46; DB 1; Length 2073;
 Best Local Similarity 47.6%; Pred. No. 1.8e+02;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

3 LASTSTSIHMLLLMLFHL 23
 DB 946 LSNSESHITPLCTILVALHL 966

RESULT 11
 S33612
 Isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) - soybean
 C:Species: Glycine max (soybean)
 C>Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text, change 17-Mar-1999
 C:Accession: S33612
 R:O'dward, M.K.; McDermott, T.R.; Kahn, M.L.
 Plant Mol. Biol. 21, 739-752, 1993
 A:Title: Isolation and characterization of a cDNA encoding NADP(+)-specific isocitrate
 A:Reference number: S33612; MUID:93222474
 A:Accession: S33612
 A:Molecule type: mRNA
 A:Residues: 1-451 <UDV>
 C:Superfamily: Yeast isocitrate dehydrogenase (NADP+)
 C:Keywords: NADP; oxidoreductase

Query Match 33.1%; Score 46; DB 2; Length 451;
 Best Local Similarity 36.7%; Pred. No. 47;
 Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

1 MYLASSTSIHMLLLMLFHLGLQASIS 30
 DB 3 MITSARAAIHITGLCFSLISHLTFYSSQS 32

RESULT 12
 F69261
 conserved hypothetical protein AF0094 - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C>Date: 05-Dec-1997 #sequence, revision 05-Dec-1997 #text, change 05-Jun-1998
 C:Accession: F69261
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 , Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spilggs, T.; Atrialch, P.; Kalne, B.P.; Sykes, S.
 Smith, H.O.; Moose, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A:Reference number: A69250; MUID:98049343
 A:Accession: F69261
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-342 <KLE>
 A:Cross-references: GB:AE001100; GB:AE000782; NID:92689423; PID:92650554; TIGR:AF00

Query Match 33.1%; Score 46; DB 2; Length 342;
 Best Local Similarity 30.0%; Pred. No. 37;
 Matches 9; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

1 MYLASSTSIHMLLLMLFHLGLQASIS 30
 DB 1 MHIGGVVVRIRIILMLFHLGSSNNV 30

RESULT 13
 A54366
 sodium/phosphate cotransport protein, renal - North American opossum
 C:Species: *Didelphis virginiana*, *Didelphis marsupialis virginiana* (North American o
 C>Date: 07-Jul-1995 #sequence, revision 07-Jul-1995 #text, change 17-Mar-1999
 C:Accession: A54366
 R:Sortas, V.; Markovitch, D.; Hayes, G.; Stange, G.; Forgo, J.; Blber, J.; Murer, J.
 J. Biol. Chem. 269, 6615-6621, 1994
 A:Title: Cloning of a Na/P-1 cotransporter from opossum kidney cells.
 A:Reference number: A54366; MUID:94165050
 A:Accession: A54366
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-653 <SOR>
 A:Cross-references: GB:L26308; NID:9425468; PID:9425469

Query Match 33.1%; Score 46; DB 2; Length 653;
 Best Local Similarity 36.7%; Pred. No. 65;
 Matches 11; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

1 MYLASSTSIHMLLLMLFHLGLQASIS 30
 DB 355 ILLAGSLITLCTILVALNLNSVLQGVYA 384

RESULT 14
 S34198
 IGE receptor II, low-affinity - rat
 M:Alternate names: CD23; lymphocyte IGE receptor
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text, change 13-Feb-1998
 C:Accession: S34198
 R:Flores-Romo, L.; Shield, J.; Humbert, Y.; Graber, P.; Audry, J.P.; Gauchat, J.F.;
 submitted to the EMBL Data Library, June 1993
 A:Description: Inhibition of an in vivo antigen-specific IGE response by antibodies
 A:Reference number: S34198
 A:Accession: S34198
 A:Molecule type: mRNA
 A:Residues: 1-309 <FLD>
 A:Cross-references: EMBL:X73579; NID:9313672; PID:9313673
 C:Superfamily: IGE receptor II; C-type lectin homology
 C:Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat
 F:1-25/Domain: intracellular #status predicted <INT>
 F:14-22/Region: stop-transfer sequence
 F:24-46/Domain: transmembrane #status predicted <TM>
 F:47-309/Domain: extracellular #status predicted <EXT>
 F:126-309/Product: soluble IGE-binding factor (29K) #status predicted <IGI>
 F:164-309/Product: soluble IGE-binding factor (25-27K) #status predicted <BFI>
 F:164-288/Domain: C-type lectin homology <LCH>
 F:192-283,260-274/Disulfide bonds: #status predicted

Query Match 32.4%; Score 45; DB 1; Length 309;
 Best Local Similarity 34.5%; Pred. No. 46;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

1 MYLASSTSIHMLLLMLFHLGLQASI 29
 26 LVLYGLITVWVWLLALLMLHMETEKSL 54

ESULT 15

58992

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - earthworm (Lumbricus terrestris)
 Species: mitochondrion Lumbricus terrestris (common earthworm)
 Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 21-Aug-1998
 Accession: S58992

Boore, J.L., Brown, W.M.
 Genetics 141, 305-319, 1995

Title: Complete sequence of the mitochondrial DNA of the annelid worm Lumbricus terrestris
 Reference number: S58985; MUID:96042914

Accession: S58992

Status: preliminary; nucleic acid sequence not shown; translation not shown

Molecule type: DNA

Residues: 1-574 <BOO>

Cross-references: EMBL:U24570

Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Genetics:

Genome: mitochondrion

Genetic code: SCC4

Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Keywords: mitochondrion; NAD; oxidoreductase

Query Match

Best Local Similarity 32.4%; Score 45; DB 2; Length 574;

Matches 11; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

1 MYLASSTSIHMLLLMLFHLGLQASIS 30

364 MIVASLSLYPHNSIMINILFPAVGLTARTS 393

Search completed: September 16, 1999, 20:42:13
 Job time: 5406 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:10:15 ; Search time 35.09 Seconds

(without alignments)
24.166 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MYLASSSTSTHTMLLMFLHGLQASIS 30

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	166	1 IL3_MOUSE	P01586 mus musculu
2	96	69.1	166	1 IL3_RAT	P04823 rattus norv
3	52	37.4	677	1 FLHA_BACSU	P35620 bacillus su
4	51	36.7	115	1 NU3M_BOVAS	P22482 equus asinu
5	51	36.7	115	1 NU3M_HORSE	P48654 equus caball
6	49.5	35.6	115	1 NU3M_CERSI	O03202 ceratotheri
7	49.5	35.6	115	1 NU3M_SHEEP	O96066 rhinoceros
8	49	35.3	115	1 NU3M_SHEEP	O96066 rhinoceros
9	46	33.1	2073	1 BIME_HAENT	P24686 emeritella
10	45	32.4	279	1 DMSC_HAENT	P45002 haemophilus
11	45	32.4	574	1 NU3M_LONTE	O34947 lumbriculus
12	44	31.7	142	1 IL3_CALJA	O28334 callithrix
13	44	31.7	142	1 IL3_SAGE	P51940 drosophila
14	44	31.7	117	1 NU3M_DROSU	O08908 mus musculu
15	44	31.7	722	1 P85_MOUSE	O63788 rattus norv
16	44	31.7	722	1 P85_MOUSE	O63788 rattus norv
17	44	31.7	130	1 YJ02_YEAST	P47010 saccharomyc
18	43	30.9	436	1 EPSE_BURSO	O45411 burholderi
19	43	30.9	493	1 Y130_MYCPN	P75506 mycoplasma
20	43	30.9	357	1 YCFI_ECOLI	P75506 mycoplasma
21	42.5	30.6	115	1 NU3M_FELCA	P48912 felis silve
22	42.5	30.6	115	1 NU3M_HALGR	P38600 halichoerus
23	42.5	30.6	115	1 NU3M_PROVI	O00541 phoca vitul
24	42	30.2	182	1 ATPD_BACFI	P22479 bacillus fi
25	42	30.2	396	1 CATE_HUMAN	P14091 homo sapien
26	42	30.2	500	1 CPD3_RAT	P12938 rattus norv
27	42	30.2	265	1 YDED_ECOLI	P31125 escherichia
28	41.5	29.9	115	1 NU3M_PIG	O79880 sus scrofa
29	41.5	29.9	444	1 NUDM_LOCM1	O36424 locusta mdy
30	41.5	29.9	631	1 Y08A_MYCTU	O11047 mycobacteri
31	41	29.5	1039	1 CP00_RAT	P33773 rattus norv
32	41	29.5	434	1 CYA7_MOUSE	P51829 mus musculu
33	41	29.5	118	1 GLHA_CTEID	P30983 ctenopharyn
34	41	29.5	118	1 GLHA_HYPMO	P30983 ctenopharyn
35	41	29.5	315	1 MSNR_MOUSE	P01727 mus musculu
36	41	29.5	469	1 NTRC_ECOLI	P03329 escherichia
37	41	29.5	469	1 NTRC_KLEPN	P03329 escherichia
38	41	29.5	469	1 NTRC_SALTY	P41789 salmoeilla
39	41	29.5	117	1 NU3M_LONTE	O34950 lumbriculus
40	41	29.5	310	1 US14_HCMVA	P09719 human cytom
41	41	29.5	1029	1 YFC5_YEAST	P43571 saccharomyc
42	41	29.5	332	1 YFEB_ECOLI	P39836 escherichia
43	41	29.5	566	1 YOK4_CAEEL	O09288 caenorhabdi

ALIGNMENTS

RESULT	ID	IL3_MOUSE	STANDARD	PRT	166 AA
AC	P01586	IL3_MOUSE	STANDARD	PRT	166 AA
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998	(REL. 37, LAST ANNOTATION UPDATE)			
DE	INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)				
DE	(MAST-CELL GROWTH FACTOR) (MCSF).				
GN	IL3 OR IL-3.				
OS	MUSCULUS (MURINE).				
OC	EDAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85113192.				
RA	MIRANKA S., YOKOTA T., LEE F., ARAI K.-I.;				
RT	"Structure of the chromosomal gene for murine Interleukin 3.";				
RL	PROC. NATL. ACAD. SCI. U.S.A. 82:316-320(1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85257655.				
RA	CAMPBELL H.D., YMER S., FUNG M.-C., YOUNG I.G.;				
RT	"Cloning and nucleotide sequence of the murine Interleukin-3 gene.";				
RL	EUR. J. BIOCHEM. 150:297-304(1985).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84117447.				
RA	FUNG M.-C., HAPPEL A.J., YMER S., COHEN D.R., JOHNSON R.M.,				
RT	CAMPBELL H.D., YOUNG I.G.;				
RL	"Molecular cloning of cDNA for murine interleukin-3.";				
RN	NATURE 307:233-237(1984).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 86083183.				
RA	TODOKORO K., YAMAMOTO A., AMAMURA H., IKAWA Y.;				
RT	"Isolation and characterization of a genomic DDD mouse Interleukin-3 gene.";				
RL	GENE 39:103-107(1985).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84144843.				
RA	YOKOTA T., LEE F., RENNICK D., HALL C., ARAI N., MOSMANN T., NABEL G.,				
RT	CANON H., ARAI K.-I.;				
RL	"Isolation and characterization of a mouse cDNA clone that expresses mast-cell growth-factor activity in monkey cells.";				
RN	PROC. NATL. ACAD. SCI. U.S.A. 81:1070-1074(1984).				
RP	[6]				
RX	CARBOHYDRATE-BINDING SITES, AND DISULFIDE BONDS.				
RA	KNEPPER T.P., ARBOGAST B., SCHREURS J., DEINZER M.L.;				
RT	Determination of the glycosylation patterns, disulfide linkages, and protein heterogeneity of baculovirus-expressed mouse Interleukin-3 by mass spectrometry.";				
RL	BIOCHEMISTRY 31:11651-11659(1992).				
RP	FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE DIFFERENTIAL THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.				
CC	FUNCTION: THIS CSF INDICES GRANULOCYTES, MACROPHAGES, MAST CELLS, STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.				
CC	STEM CELL MONOMER.				
CC	SUBUNIT: MONOMER.				
CC	TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER CELLS.				
CC	SUBCELLULAR LOCATION: SECRETED.				

CC -1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
 CC -----
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 CC -----
 DR EMBL: K01850; G309405; -
 DR EMBL: K03233; G387385; -
 DR EMBL: X02732; G52674; -
 DR EMBL: M20128; G387387; -
 DR EMBL: M14394; G387387; JOINED.
 DR EMBL: K01668; G387421; -
 DR EMBL: A02046; G344554; -
 DR PIR: A25481; ICMS3
 DR MGI: 96552; IL3.
 DR HSP: P08700; IL3.
 KW CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
 FT SIGNAL 1 26
 FT CHAIN 27 166
 FT DISULFID 43 105
 FT DISULFID 105 166
 FT CARBOHYD 42 42
 FT CARBOHYD 112 112
 SQ SEQUENCE 166 AA; 18540 MW; AA9EB59F CRC32;
 Query Match 100.0%; Score 139; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3; 2e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MYASSTSIHTMLLMLFHLGLOAS 30
 DB 1 MYASSTSIHTMLLMLFHLGLOAS 30
 RESULT 2
 IL3_RAT STANDARD; PRT; 166 AA.
 AC P04823; P70513;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
 DE FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
 DE (MAST-CELL GROWTH FACTOR) (MCGF).
 GN IL3 OR IL-3.
 OS RATIUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATIUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86232609.
 RA COHEN D.R., HABEL A.J., YOUNG I.G.;
 RT "Cloning and expression of the rat interleukin-3 gene";
 RL NUCLEIC ACIDS RES. 14:3641-3658(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ESANDI M.C., VAN SOMEREN G.D., VAN BEKKUM D.W., VALERIO D.,
 RA NOTERBOOM J.L., BOUT A.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -1- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
 CC STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
 CC CELLS.

CC -1- SUBCELLULAR LOCATION: SECRETED.
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 CC -----
 DR EMBL: X03846; G56476; -
 DR EMBL: X03914; E10390; -
 DR EMBL: X03914; E10391; -
 DR EMBL: X03914; E10392; -
 DR EMBL: B81483; G1763673; -
 DR PIR: S07369; S07369.
 DR HSP: P08700; IL3.
 KW CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
 FT SIGNAL 1 27
 FT CHAIN 28 166
 FT DISULFID 43 105
 FT DISULFID 105 166
 FT CARBOHYD 60 60
 FT CARBOHYD 70 70
 SQ SEQUENCE 166 AA; 18630 MW; 6B571582 CRC32;
 Query Match 69.1%; Score 96; DB 1; Length 166;
 Best Local Similarity 82.1%; Pred. No. 2e-06;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 MYASSTSIHTMLLMLFHLGLOAS 28
 DB 1 MYASSTSIHTMLLMLFHLGLOAS 28
 RESULT 3
 FLHA_BACSU STANDARD; PRT; 677 AA.
 AC P35620;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE FLAGELLAR BIOSYNTHESIS PROTEIN FLHA.
 GN FLHA.
 OS BACILLUS SUBTILIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93225816.
 RA CARPENTER P.B., ORDAL G.W.;
 RT "Bacillus subtilis flha: a flagellar protein related to a new family
 RT of signal-transducing receptors";
 RL MOL. MICROBIOL. 7:735-743(1993).
 CC -1- FUNCTION: INVOLVED IN THE EXPORT OF FLAGELLUM PROTEINS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE FLIPEP (FLAGELLA/HR/INVASION PROTEINS
 CC EXPORT PORE) FAMILY.
 CC -----
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 CC -----
 DR EMBL: X63698; G38917; -
 DR EMBL: Z99112; E1185230; -
 DR PIR: S33664; S33664.
 DR SUBTILIST; BG10542; FLHA.

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DR PROSITE: PS00994; FHIPER; 1.
DR PFAM: PF00771; FHIPER; 1.
KW FLNGELLA; TRANSPORT; PROTEIN TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 6 22 POTENTIAL.
FT TRANSMEM 27 43 POTENTIAL.
FT TRANSMEM 52 68 POTENTIAL.
FT TRANSMEM 104 120 POTENTIAL.
FT TRANSMEM 189 205 POTENTIAL.
FT TRANSMEM 230 246 POTENTIAL.
FT TRANSMEM 275 291 POTENTIAL.
SO SEQUENCE 677 AA; 73945 MW; 8CB459D3 CRC32;

Query Match
Best Local Similarity 37.4%; Score 52; DB 1; Length 677;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 9 SIHMLLLMLFHLGLQAS 28
DB 56 SIHPSLLLLFRLGLNVS 75

RESULT 4
NU3M_EQUAS STANDARD; PRT; 115 AA.
P92462;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
MTND3 OR ND3 OR NADH3.
EQUUS ASINUS (DONKEY).
MITOCHONDRION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PERISSODACTYLA; EQUIDAE; EQUUS.
[1]
SEQUENCE FROM N.A.
C TISSUE-KIDNEY;
X MEDLINE; 97032591.
XU X.; GULBERG A.; ARNASON U.;
"The complete mitochondrial DNA (mtDNA) of the donkey and mtDNA
comparisons among four closely related mammalian species-pairs.";
J. MOL. EVOL. 43:438-463(1996).
-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
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EMBL: X97337; E237860;
PFAM: PF00507; oxidored_g4; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
Q SEQUENCE 115 AA; 13030 MW; B3B0653D CRC32;

Query Match
Best Local Similarity 36.7%; Score 51; DB 1; Length 115;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Y 4 ASSTSIHMLLLMLFHL 23
DB 78 ASQTNMLTMLMALVLSL 97

ESULT 5
U3M_HORSE STANDARD; PRT; 115 AA.
P46634;
01-FEB-1996 (REL. 33, CREATED)

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DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
OS MTND3 OR ND3.
OS EQUUS CABALLUS (HORSE).
OC MITOCHONDRION.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; EQUIDAE; EQUUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95047450.
RA XU X.; ARNASON U.;
"The complete mitochondrial DNA sequence of the horse, Equus
cavallus; extensive heteroplasmy of the control region.";
RL GENE 148:357-362(1994).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X79547; G577579;
DR PFAM: PF00507; oxidored_g4; 1.
KM OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13016 MW; C4C338F9 CRC32;

Query Match
Best Local Similarity 36.7%; Score 51; DB 1; Length 115;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 4 ASSTSIHMLLLMLFHL 23
DB 78 ASQTNMLTMLMALVLSL 97

RESULT 6
NU3M_CERSI STANDARD; PRT; 115 AA.
ID 003202;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN MTND3 OR ND3 OR NADH3.
OS CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OC MITOCHONDRION.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; RHINOCEROTIDAE; CERATOTHERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97271644.
RA XU X.; ARNASON U.;
"The complete mitochondrial DNA sequence of the white rhinoceros,
Ceratotherium simum, and comparison with the mtDNA sequence of the
Indian rhinoceros, Rhinoceros unicornis.";
RL MOL. PHYLOGENET. EVOL. 7:189-194(1997).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
CC -----
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CC -----
DR EMBL: Y07726; E275046;
DR PFAM: PF00507; oxidored_g4; 1.

```

KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 12980 MW; 50796E31 CRC32;

Query Match 35.6%; Score 49.5; DB 1; Length 115;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 13; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

OY 4 ASSTSIHMLLLMLFHLGLQASIS 30
DB 78 ASQTINLTKMLTMLLILSL-LAASIA 103

RESULT 7
NM3M_RH10N STANDARD; PRT; 115 AA.
AC 096066;

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN MTND3 OR ND3 OR NADH3.

OS RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).
OG MITOCHONDRION.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; RHINOCEROTIDAE; RHINOCEROS.

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;
RX MEDLINE: 97051708.

RA XU X., JANKE A., ARNASON U.;

RT "The complete mitochondrial DNA sequence of the greater Indian rhinoceros, Rhinoceros unicornis, and the phylogenetic relationship among Carnivora, Perissodactyla, and Artiodactyla (+ Cetacea).";
RL MOL. BIOL. EVOL. 13:1167-1173(1996).

CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

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CC EMBL: X97336; E237876;
DR PFAM: PF00507; oxidored_94; 1.
KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13044 MW; 9FE83B49 CRC32;

Query Match 35.6%; Score 49.5; DB 1; Length 115;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 13; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

OY 4 ASSTSIHMLLLMLFHLGLQASIS 30
DB 78 ASQTINLTKMLTMLLILSL-LAASIA 103

RESULT 8
NM3M_SHEEP STANDARD; PRT; 115 AA.
AC 078753;

DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN MTND3 OR ND3.

OS OVIS ARIES (SHEEP).
OG EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC MITOCHONDRION.

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-MERINOLANDSCHAF; TISSUE-LIVER;

RA HIENDELDER S., LEWALSKI H., WASSMUTH R., JANKE A.;

RT "The complete mitochondrial DNA sequence of the domestic sheep (Ovis aries) and comparison with the other major ovine haplotype.";

RL J. MOL. EVOL. 0:0-0(1998).

CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

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CC EMBL: AF010406; G3445514;
DR OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13102 MW; 2C610097 CRC32;

Query Match 35.3%; Score 49; DB 1; Length 115;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 4 ASSTSIHMLLLMLFHL 23
DB 78 ASQTINLTKMLTMLLILSL 97

RESULT 9
BIME_EMENT STANDARD; PRT; 2073 AA.
AC P24686;

DT 01-MAR-1992 (REL. 21, CREATED)

DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE NEGATIVE REGULATOR OF MITOSIS.

GN BIME.

OS EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
OC EURTILES; TRICHOCOMACEAE; EMERICELLA.

RN [1]
RP SEQUENCE FROM N.A.

RC MEDLINE: 90375468.

RA ENGLE D.B., OSMANI S.A., ROSBOROUGH S., XIANG X.,

RA MORRIS N.R.;

RT "A negative regulator of mitosis in Aspergillus is a putative membrane-spanning protein.";

RL J. BIOL. CHEM. 265:16132-16137(1990).

CC -1- FUNCTION: NEGATIVE REGULATOR OF MITOSIS IN E. NIDULANS. THIS PROTEIN IS PART OF A REGULATORY PATHWAY THAT INCLUDES THE NIMA

PROTEIN KINASE. IT IS REQUIRED TO PREVENT PREMATURE ENTRY INTO

MITOSIS. MUTATIONS TO THIS PROTEIN BOTH CAUSE CELLS TO ENTER

MITOSIS AND PREVENT THEM FROM LEAVING MITOSIS.

CC -1- SIMILARITY: TO MOUSE TSG24 AND YEAST YML17W.

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CC EMBL: M59705; G168027;
DR PIR: A37879; BMASBE.

DR PIR: A37879; BMASBE.

DT TRANSMEMBRANE; MITOSIS.

DT TRANSMEM 342 353

DT TRANSMEM 1623 1643

DT TRANSMEM 1685 1703

DT TRANSMEM 1746 1764

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

POTENTIAL.

POTENTIAL.


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RESULT 12
ID IL3_CALJA STANDARD: PRT: 142 AA.
AC 028334;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
DE FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
DE (MAST-CELL GROWTH FACTOR) (MCGF).
GN IL3.
OS CALITRHX JACCHUS (COMMON MARMOSET).
OC EURARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
OC PRIMATES: PLATYRRHINI: CALLITRICHIDAE: CALLITRHX.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 94153996.
RA BURGER H., MOSTERT M.C., KOK E.M., WAGEMAKER G., DORSSEERS L.C.J.;
RT "Cloning and expression of Interleukin-3 genes of chimpanzee and New
RT World monkeys".
RL BIOCHIM. BIOPHYS. ACTA 1217:195-198(1994).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE: 95018301.
RA BURGER H., WAGEMAKER G., LEUNISSEN J.A.M., DORSSEERS L.C.J.;
RL J. MOL. EVOL. 39:255-267(1994).
CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES (BY
CC SIMILARITY).
CC -1- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
CC STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES (BY
CC SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
CC -----
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CC -----
DR EMBL: X74877; G459436;
KM CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 142 INTERLEUKIN-3.
FT DISULFID 34 102 BY SIMILARITY.
FT CARBOHYD 33 33 POTENTIAL.
SQ SEQUENCE 142 AA; 15980 MW; A83CEFD0 CRC32;

Query Match 31.7%; Score 44; DB 1; Length 142;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
DE FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
DE (MAST-CELL GROWTH FACTOR) (MCGF).
GN IL3.
OS SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).
OC EURARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
OC PRIMATES: PLATYRRHINI: CALLITRICHIDAE: SAGUINUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 94153996.
RA BURGER H., MOSTERT M.C., KOK E.M., WAGEMAKER G., DORSSEERS L.C.J.;
RT "Cloning and expression of Interleukin-3 genes of chimpanzee and New
RT World monkeys".
RL BIOCHIM. BIOPHYS. ACTA 1217:195-198(1994).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE: 95018301.
RA BURGER H., WAGEMAKER G., LEUNISSEN J.A.M., DORSSEERS L.C.J.;
RL J. MOL. EVOL. 39:255-267(1994).
CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
CC -1- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
CC STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
CC -----
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CC -----
DR EMBL: X74878; E211706;
DR EMBL: X74879; E211706; JOINED.
DR HSSP: P08700; IULI.
KM CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 142 INTERLEUKIN-3.
FT DISULFID 34 102 BY SIMILARITY.
FT CARBOHYD 33 33 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 108 108 POTENTIAL.
SQ SEQUENCE 142 AA; 16085 MW; B2C52180 CRC32;

Query Match 31.7%; Score 44; DB 1; Length 142;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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ND3.
DROSOPHILA SUBOBSCURA (FRUIT FLY).
MITOCHONDRION.
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPERA; BRACHYCERA; MUSCOPORPHA; EPHYDROIDEA.
DROSOPHILIDAE; DROSOPHILA.
[1]
SEQUENCE FROM N.A.
STRAIN-SSP. TUE 3.
VOLZ-LINGENHIL A.;
SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
-----
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-----
EMBL; X65129; G506461;
FLYBASE; FBgn0012957; Dsub\mt:ND3.
PFAM; PF00507; oxidored.q4; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SEQUENCE 117 AA; 13427 MW; B8EE2F7A CRC32;

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Query Match 31.7%; Score 44; DB 1; Length 117;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
y 2 VLASSTSIHTMLLLMLFHLG 22
:::||||:||||:|
b 86 IMWTTSTIIFILLIGLYH 106

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ESUTR 15
85B_MOUSE STANDARD; PRT; 722 AA.
008908:
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY BETA SUBUNIT (PI3-KINASE
P85-BETA SUBUNIT) (PTDINS-3-KINASE P85-BETA).
PIK3R2.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
STRAIN-NIH;
MEDLINE; 98241191.
JANSSEN J.W.G., SCHLEITHOF L., BARTRAM C.R., SCHULZ A.S.;
"An oncogenic fusion product of the phosphatidylinositol 3-kinase
p85beta subunit and HMW0R8, a putative deubiquitinating enzyme.";
ONCOGENE 16:1167-1172(1998).
-1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
KINASES, THROUGH ITS SH2 DOMAIN, AND ACTS AS AN ADAPTER, MEDIATING
THE ASSOCIATION OF THE P110 CATALYTIC UNIT TO THE PLASMA MEMBRANE.
-1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
SUBUNITS.
-1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-1- SIMILARITY: CONTAINS 1 RHO GAP DOMAIN.
-1- SIMILARITY: HIGH, WITH OTHER P85-BETA SUBUNITS, AND ALSO TO
P85-ALPHA SUBUNIT.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y13569; E321185;
DR MGD; MGI:1098772; PIK3R2.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
DR PFAM; PF00017; SH2; 2.
DR PFAM; PF00018; SH3; 1.
DR PFAM; PF00620; RHO GAP; 1.
KW SH3 DOMAIN; SH2 DOMAIN.
FT DOMAIN 4 80
FT DOMAIN 125 257 SH3.
FT DOMAIN 324 419 RHO-GAP.
FT DOMAIN 616 710 SH2.
SQ SEQUENCE 722 AA; 81251 MW; C8A703F4 CRC32;

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Query Match 31.7%; Score 44; DB 1; Length 722;
Best Local Similarity 41.7%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
Oy 1 MYLASSTSIHTMLLLMLFHLG 24
::| | | | | | | | | |
Db 207 LVLEPTPLHQALTRFLQHLG 230

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Search completed: September 17, 1999, 03:10:15
Job time: 295 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:11 ; Search time 68.96 seconds
(Without alignments)
26.774 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MVLASSTSIHMTLLMLFHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 201082 segs, 61543640 residues

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_ROOTENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	96	69.1	169	11	P97688	P97688 rattus norv
2	51	36.7	1581	13	073809	073809 fugu rubrip
3	50.5	36.3	437	8	Q34191	Q34191 crithidia o
4	48.5	34.9	437	8	Q03616	Q03616 leishmania
5	47.5	34.5	694	5	Q94916	Q94916 drosophila
6	47.5	34.2	344	2	Q86662	Q86662 streptomyce
7	47.5	34.2	1914	4	Q13129	Q13129 homo sapien
8	47	33.8	244	1	Q29705	Q29705 archaeoglob
9	47	33.8	160	1	Q58301	Q58301 pyrococcus
10	46.5	33.5	115	8	Q92260	Q92260 canis famli
11	46	33.1	342	1	Q30142	Q30142 archaeoglob
12	46	33.1	346	2	P96480	P96480 streptococ
13	46	33.1	414	5	P91486	P91486 caenorhabd1
14	45	32.1	653	6	Q28361	Q28361 didelphis m
15	45	32.4	352	5	Q21917	Q21917 caenorhabd1
16	45	32.4	309	11	Q63097	Q63097 rattus norv
17	45	32.4	107	13	Q90286	Q90286 carassius a
18	44.5	32.0	267	5	Q18135	Q18135 caenorhabd1
19	44	31.7	323	5	Q16396	Q16396 caenorhabd1
20	44	31.7	326	5	Q62449	Q62449 caenorhabd1
21	44	31.7	115	8	Q922Y4	Q922Y4 caenorhabd1
22	43.5	31.3	723	2	Q34616	Q34616 hippopotamu
23	43.5	31.3	751	11	Q60816	Q60816 bacillus su
24	43	30.9	114	1	O58228	O58228 mus musculu
25	43	30.9	391	2	O52060	O52060 pyrococcus
26	43	30.9	408	2	O67072	O67072 salmone11a
27	43	30.9	481	4	O60883	O60883 homo sapien
28	43	30.9	346	8	P92575	P92575 bipes bipor
29	43	30.9	668	10	O48552	O48552 arabidopsis

30	43	30.9	845	10	O04703	O04703 solanum tub
31	42.5	30.6	379	8	O20544	O20544 ctenomys le
32	42.5	30.6	345	8	O78884	O78884 anolis rich
33	42	30.2	293	2	P74826	P74826 sphingomona
34	42	30.2	1218	2	P96057	P96057 salmonella
35	42	30.2	598	2	O55378	O55378 salmonella
36	42	30.2	359	2	O92F85	O92F85 synecocyst
37	42	30.2	102	2	O92521	O92521 bacillus an
38	42	30.2	350	5	P91506	P91506 streptomyce
39	42	30.2	521	5	O17900	O17900 caenorhabd1
40	42	30.2	325	8	O21349	O21349 euhadia her
41	42	30.2	484	10	O24325	O24325 phaseolus v
42	42	30.2	412	10	O80485	O80485 arabidopsis
43	42	30.2	150	10	O80490	O80490 arabidopsis
44	42	30.2	600	11	O920G3	O920G3 mus musculu
45	41.5	29.9	650	2	O52818	O52818 amycolatops

ALIGNMENTS

RESULT 1
ID P97688 PRELIMINARY; PRT: 169 AA.
AC P97688;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98241512.
RA DEL C ESANDI M., VAN SOMEREN G.D., VAN DER VELDE I., VAN BEKKUM D.W.,
RA VALENTE D., NOERBOOM J.L., BOUJ A.;
RT Cloning, biological characterization and high-level expression of
RT rat interleukin-3 using recombinant adenovirus: description of a new
RT splicing variant.*
RL Gene 211:151-158(1998).
DR EMBL; U81492; AAC17704.1;
SQ SEQUENCE 169 AA; 19019 MW; 1EA42F8D CRC32;

Query Match 69.1%; Score 96; DB 11; Length 169;
Best local Similarity 82.1%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MVLASSTSIHMTLLMLFHLGLQAS 28
DB 1 MVLASSTSIHMTLLMLFHLGLQAS 28
RESULT 2
ID 073809 PRELIMINARY; PRT: 1581 AA.
AC 073809;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE LRP1 (FRAGMENT).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RA GELINER K., BRENNER S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005116; AAC34396.1;
DR PFM; PF00008; EGF; 8.
DR PFM; PF00057; IGL_recept_a; 11.

DR PRAM: PF00058; ldl_recept_b; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS01209; LDLRA_1; 9.
 KM Glycoprotein; EGF-like domain.
 FT NON TER 1
 SO SEQUENCE 1581 AA; 176854 MW; 0839098E CRC32;

Query Match 36.7%; Score 51; DB 13; Length 1581;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 4 ASSTSTSHMTMLLMLFHLGLOA 27
 DB 1455 ASSTSTSHMTMLLMLFHLGLOA 1478

RESULT 3
 ID 034191 PRELIMINARY; PRT; 437 AA.
 AC 034191;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT 4.
 GN ND4.
 OS Crithidia oncopelti.
 OC Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S-068;
 RA DMITRIY MASLOV A.;
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S-068;
 RA MASLOV D.A., HORVATH A., GWANG II K., KOLESNIKOV A.A.;
 RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X56015; CAA39491.1;
 KM Mitochondrion.
 SO SEQUENCE 437 AA; 52018 MW; 741F2793 CRC32;

Query Match 36.3%; Score 50.5; DB 8; Length 437;
 Best Local Similarity 34.4%; Pred. No. 11;
 Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

OY 1 MYLASSSTSHMTMLLMLFHLGLOAST 29
 DB 131 LVYSSSSIMCICIIIFHFNVLQSF 162

RESULT 4
 ID 003616 PRELIMINARY; PRT; 437 AA.
 AC 003616;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
 GN ND4.
 OS Leishmania tarentolae (Sauruleishmania tarentolae).
 OC Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 85079995.
 RA LA CRUZ V.F., NECKELMANN N., SIMPSON L.;
 RT "Sequences of six genes and several open reading frames in the
 Kinetoplast maxicircle DNA of Leishmania tarentolae."
 J. Biol. Chem. 259:15136-15147(1984).
 RN [1]

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85297791.
 RA SIMPSON A.G., NECKELMANN N., LA CRUZ V.F., MURICH M.L., SIMPSON L.;
 RT "Mapping and 5' end determination of kinetoplast maxicircle gene
 transcripts from Leishmania tarentolae."
 Nucleic Acids Res. 13:5977-5993(1985).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- COFACTOR: FAD AND IRON-SULFUR CENTRES.
 DR EMBL; M10126; -; NOT ANNOTATED CDS.
 DR PRAM; PF00361; oxidored_q1; 1.
 KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion; FAD; Iron-sulfur.
 SO SEQUENCE 437 AA; 52291 MW; EEF35AF7 CRC32;

Query Match 34.9%; Score 48.5; DB 8; Length 437;
 Best Local Similarity 34.4%; Pred. No. 20;
 Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

OY 1 MYLASSSTSHMTMLLMLFHLGLOAST 29
 DB 131 LVYSSSSIMCICIIIFHFNVLQSF 162

RESULT 5
 ID 094916 PRELIMINARY; PRT; 694 AA.
 AC 094916;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DFZ2.
 GN DFZ2.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
 OC Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96353971.
 RA BHANOT P., BRINK M., SAMOS C.H., HSIEH J.C., WANG Y., MACKE J.P.,
 RA ANDREW D., NATHANS J., NUSSE R.;
 RT "A new member of the frizzled family from Drosophila functions as a
 Wingless receptor."
 Nature 382:225-230(1996).
 RL Nature 382:225-230(1996).
 DR EMBL; U65589; AAC47273.1;
 DR FLYBASE; FB910016797; f22.
 DR PRAM; PF01392; Fz; 1.
 SO SEQUENCE 694 AA; 75437 MW; FDTBOBB9 CRC32;

Query Match 34.5%; Score 48; DB 5; Length 694;
 Best Local Similarity 31.0%; Pred. No. 35;
 Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 1 MYLASSSTSHMTMLLMLFHLGLOAST 29
 DB 383 LMLRSSSTGPHSCTVFLITTFGMASSI 411

RESULT 6
 ID 086662 PRELIMINARY; PRT; 344 AA.
 AC 086662;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
 GN SCA42.06C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA OLIVER K., HARRIS D.,
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MEDLINE: 97000351.
RA REDENBACH M., KIESER H.M., DENAPARTE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RT A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb streptomyces coelicolor A3(2) chromosome.;
RL EMBL: AL031182; CAA20158.1;
SQ SEQUENCE 344 AA; 35350 MW; BD06E656 CRC32;

Query Match 34.2%; Score 47.5; DB 2; Length 344;
Best Local Similarity 46.4%; Pred. No. 23;
Matches 13; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
3 LASTSITHM-LLMLFHLGQASIS 29
40 LPPSHLTHAPLLSLVFSAGLOVAV 67

RESULT 7
ID 013129 PRELIMINARY; PRT; 1914 AA.
C 013129;
T 01-NOV-1996 (TREMblrel. 01, Created)
T 01-NOV-1996 (TREMblrel. 01, last sequence update)
T 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE ZN-15 RELATED ZINC FINGER PROTEIN (RLF).
N RLF.
N Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Mammalia;
C Eutheria; Primates; Catarrhini; Homiidae; Homo.
N [1]
P SEQUENCE FROM N.A.
X MEDLINE: 96133723.
X MAKELA T.P., HELSTEN E., VESA J., HIRVONEN H., PALOTIE A.,
X PELTONEN L., ALITALO K., ALITALO K.;
T "The rearranged L-myc fusion gene (RLF) encodes a Zn-15 related zinc
T finger protein."
L Oncogene 11:2699-2704(1995).
R EMBL: U23277; AAC50386.1;
R PFM: PF00096; ZF-C2H2; 14.
R PROSITE: PS00028; ZINC_FINGER_C2H2; 14.
W Zinc-finger; Metal-binding; DNA-binding.
Q SEQUENCE 1914 AA; 217898 MW; 05BE74D CRC32;

Query Match 34.2%; Score 47.5; DB 4; Length 1914;
Best Local Similarity 45.7%; Pred. No. 98;
Matches 16; Conservative 3; Mismatches 7; Indels 9; Gaps 1;
5 SSTSI-----HTMLLMLFHLGQASIS 30
1043 SSSSTCASKRPTEDTMLLRLKHLKSLKNSIT 1077
RESULT 8
ID 029705 PRELIMINARY; PRT; 244 AA.
C 029705;
T 01-JAN-1998 (TREMblrel. 05, Created)
T 01-JAN-1998 (TREMblrel. 05, last sequence update)

DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE NITRATE REDUCTASE, GAMMA SUBUNIT (NARI).
GN AF0546.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE: 98049343.
RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GINN M., HICKER E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.,
RA OVERBERGER R., GORVINE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTACH P., RAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic,
RT sulphate-reducing archaeon Archaeoglobus fulgidus."
RL Nature 380:364-370(1997).
DR EMBL: AE001066; AAB90687.1;
DR TIGR: AF0546;
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27573 MW; EA12F137 CRC32;

Query Match 33.8%; Score 47; DB 1; Length 244;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
16 LLMLFHLGQASIS 30
89 LLMLFHLGQASIS 103

RESULT 9
ID 058301 PRELIMINARY; PRT; 160 AA.
C 058301;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, last annotation update)
DE 160AA LONG HYPOTHETICAL PROTEIN.
GN PH0566.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
N [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137.
RA KAWABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOTAKA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMITA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIYU A.,
RA KIRUCHI H.;
RT "Complete sequence and gene organization of the genome of a
RT hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000002; BAA29655.1;
SQ SEQUENCE 160 AA; 18153 MW; 7E023984 CRC32;

Query Match 33.8%; Score 47; DB 1; Length 160;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
1 MYLASTSITHM-LLMLFHLGQASIS 22
:||||| :||||| :|||


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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA DU 2., MAGGI L.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U80440; AAB37650.1; -
SQ SEQUENCE 414 AA; 46525 MW; EB685192 CRC32;

Query Match 33.1%; Score 46; DB 5; Length 414;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 15; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

QY 3 LASSITS--HTMILLI---MLFHLGLQASI 29
DB 356 LATTTTFLHSMILLFLYHFFFLALLLTQNI 388

RESULT 14
ID Q28361 PRELIMINARY; PRT; 653 AA.
AC Q28361;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE NA/PI-COTRANSPORTER.
GN NAPI-4.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Metatheria; Didelphimorphia; Didelphidae; Didelphis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EPIITHELIUM, KIDNEY;
RX MEDLINE: 94165050.
RA SORRIBAS V., MARKOVICH D., HAYES G., STANGE G., FORGO J., BIBER J.,
RA MURER H.;
RT "Cloning of a Na/Pi cotransporter from opossum kidney cells.";
RL J. Biol. Chem. 269:6615-6621(1994).
RN [2]
RP SEQUENCE OF 1-89 FROM N.A.
RC TISSUE-KIDNEY;
RA HILFKE H., HARTMANN C.M., STANGE G., MURER H.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: L26308; AAA30978.1; -
DR EMBL: A0003021; CAA05806.1; -
SQ SEQUENCE 653 AA; 70551 MW; A6ED8F28 CRC32;

Query Match 33.1%; Score 46; DB 6; Length 653;
Best Local Similarity 36.7%; Pred. No. 63;
Matches 11; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MVAASSTSIHTMILLMLFHLGLQASIS 30
DB 355 ILLAGSLTLCCTCLLVKLINSVLCQOVA 384

RESULT 15
ID Q21917 PRELIMINARY; PRT; 352 AA.
AC Q21917;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE GPA-7 PROTEIN.
GN
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;

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OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA BARDILL S.;
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCKERRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAUSER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z70686; CAA94612.1; -
DR PFM: PF00503; G-alpha:1.
SQ SEQUENCE 352 AA; 41021 MW; 8BC25EFC CRC32;

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Query Match 32.4%; Score 45; DB 5; Length 352;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 10 HTMILLMLFHLGLQ 26
DB 78 IHSMISIRAFHLOIE 94

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Search completed: September 16, 1999, 20:40:13
Job time: 5564 sec